

MICROBIOLOGY AND VIROLOGY

ECOLOGICAL ASPECTS OF PARAMYXOVIRUS CIRCULATION IN WILD BIRD POPULATIONS ON THE TERRITORY OF CONTINENTAL EURASIA

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ABSTRACT

Background. Avian paramyxoviruses (subfamily Avulavirinae) are widespread avian pathogens that constantly circulate in wild and domestic animal populations. The subfamily Avulavirinae is divided into 3 genera, comprising 22 species. Epizootic surveillance of avulaviruses is conducted worldwide and is of critical importance due to their rapid spread via bird migrations. Avian viruses can cause significant economic damage to the poultry industry both in developing countries and in regions with sustainable economic development. Their infectious potential is of great interest and remains poorly understood.

The majority of intercontinental flyways of migratory birds pass through the territory of continental Eurasia, where large numbers of migratory birds congregate in confined areas during stopovers, nesting and wintering. This creates favorable conditions for virus transmission and the emergence of new genetic variants.

Aim. To analyze the species distribution of paramyxoviruses in wild birds across continental Eurasia.

Materials and Methods. As a result of long-term studies of viruses in wild bird populations across continental Eurasia, avian avulavirus isolates were obtained.

Results. Avian avulavirus isolates of APMV -1, -3, -4, -6, -8, -9, -11, -12, -13, -16, -20, and -21 were obtained. APMV-1 and APMV-4 were detected throughout Eurasia, most frequently in Anseriformes. APMV-3, -6, -9, -11, and -12 were recorded in the European part of Eurasia, APMV-8, -13, and -20 in its central part, and APMV-6, -16, and -21 in the Asian part, in Anseriformes, Passeriformes, Charadriiformes, Ciconiiformes, and Psittaciformes.

Keywords: bird paramyxoviruses, avulaviruses, metaavulaviruses, orthoavulaviruses, paraavulaviruses, continental Eurasia, Newcastle disease virus, wild birds

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ЭКОЛОГИЧЕСКИЕ АСПЕКТЫ ЦИРКУЛЯЦИИ ПАРАМИКСОВИРУСОВ В ПОПУЛЯЦИЯХ ДИКИХ ПТИЦ НА ТЕРРИТОРИИ КОНТИНЕНТАЛЬНОЙ ЕВРАЗИИ

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РЕЗЮМЕ

Цель настоящей работы заключается в анализе видового распространения парамиксовирусов диких птиц на территории континентальной Евразии. Парамиксовирусы птиц (подсемейство Авулавирусы) — широко распространенные патогены птиц, постоянно циркулирующие в популяциях диких и домашних животных. Подсемейство Авулавирусы разделено на 3 рода, включающих 22 вида. Эпизотоологический надзор за авулавирусами ведется по всему миру и очень важен из-за их быстрого распространения благодаря миграциям птиц. Вирусы птиц способны нанести значительный экономический ущерб отрасли птицеводства. Их инфекционный потенциал представляет собой большой интерес и является малоизученным.

Через территорию континентальной Евразии проходит основная часть межконтинентальных перелетных путей мигрирующих птиц, где на ограниченной местности концентрируется огромное количество перелетных птиц во время стоянок, гнездования и зимовок, что создает благоприятные условия для распространения вирусов и возникновения новых генетических вариантов.

В результате многолетних исследований вирусов в популяциях диких птиц на территории континентальной Евразии были выделены образцы авулавирусов птиц АPMV-1, -3, -4, -6, -8, -9, -11, -12, -13, -16, -20, -21. По всей территории Евразии были выявлены АPMV-1 и АPMV-4, наиболее часто — у гусеобразных. Виды АPMV-3, -6, -9, -11, -12 были отмечены в европейской части Евразии, виды АPMV-8, -13, -20 в ее центральной части, виды АPMV-6, -16, -21 в азиатской части у гусеобразных, воробьинообразных, ржанкообразных, аистообразных, попугаевых.

Ключевые слова: парамиксовирусы птиц, авулавирусы, метаавулавирусы, ортоавулавирусы, параавулавирусы, континентальная Евразия, вирус болезни Ньюкасла, дикие птицы

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INTRODUCTION

Viral pathogens are widespread and continuously circulate in human, animal, and bird populations, posing a major threat to health. Viruses of the family *Paramyxoviridae* have a broad host range and are isolated from fish, reptiles, birds, animals, and humans worldwide [1]. Avian viruses (subfamily *Avulavirinae*) – avulaviruses, particularly the Newcastle disease virus (NDV), receive special attention due to their ability to spread rapidly across the globe through bird migrations. Avulaviruses can also cause significant economic damage to the poultry industry, both in developing countries and in regions with sustainable economic development. Many of the known avian paramyxovirus species have been identified through international epidemiological surveillance programs for influenza viruses.

To analyze the species distribution of avulaviruses across continental Eurasia, information was retrieved from the eLibrary.ru, CyberLeninka, ScienceJournals, Scopus, Web of Science, ScienceDirect, SpringerLink, and PubMed databases for the past 10 years.

Avulaviruses cause viral infections in various species of domestic and wild birds [2]. Numerous cases of infection in synanthropic bird species have also been reported [3], which constitute a distinct reservoir where viruses can concentrate, persist, and undergo genetic changes. Synanthropic birds, having been infected with avulaviruses from wild birds, can transmit the infection to domestic poultry. For instance, transmission of Newcastle disease virus from pigeons to chickens has been described [4].

Newcastle disease virus in poultry, which belongs to the genus *Avian orthoavulavirus*, is highly pathogenic and capable of causing massive epizootics among wild and domestic birds. This fact is particularly significant as it poses a major economic threat to poultry industries worldwide. For example, the Advisory Committee of the Eurasian Economic Commission on Dangerous Pathogens has classified NDV as a biosafety level 2 pathogen in the United Kingdom [5].

The infectious potential of other avian paramyxovirus species (hereinafter APMV) remains poorly understood. However, in recent years, these viruses have been increasingly isolated from wild and domestic birds worldwide and represent a potential health threat, as infection of birds with certain virus species (avian paramyxoviruses -2, -3) is associated with respiratory tract lesions, decreased egg production, and neurological symptoms [5]. There is also a possibility of infection in non-avian species. It has been shown that avian paramyxoviruses 1-9, except avian paramyxovirus -5, can replicate in mice and hamsters upon intranasal infection, with avian paramyxoviruses -1, -2, -6, -7, -9 causing broncho-interstitial pneumonia of varying severity and significant weight loss [6].

Classification

Avian paramyxoviruses belong to the subfamily *Avulavirinae*, which is part of the family *Paramyxoviridae*.

Species division is based on hemagglutination inhibition and neuraminidase inhibition assays. According to the latest taxonomic data, the order *Mononegavirales*, subfamily *Avulavirinae* comprises three genera [7]:

Genus *Metaavulavirus* (14 species, including *Avian metaavulavirus* -2, -6; *Avian paramyxovirus* -2, -5-8, -10, -11, -14, -15, -20, -22);

Genus *Orthoavulavirus* (11 species, including *Orthoavulavirus* sp. *Virus*, *Antarctic penguin virus* A, B, C, *APMV* -1, -9, -12, -13, -16, -21, *AOAV* -12);

Genus *Paraavulavirus* (including species *Paraavulavirus* -3, -4).

Viruses APMV -1, -9, APMV -2, -5-8, and species APV -3, -4 were isolated and characterized before 1980, while APMV -10, -11, APMV -12, -13 were identified between 2005 and 2013. APMV -14, isolated from a duck in Japan in 2011 [8], AMV-15, isolated from a sandpiper (Bonaparte's sandpiper, family *Scolopacidae*) in Brazil in 2012 [9], and APMV -16, isolated from a wild duck in South Korea in 2014 [10], were included in the subfamily *Avulavirinae* in 2018 [11]. Antarctic penguin viruses A, B, C were isolated from Antarctic penguins (Chinstrap penguin, Adelie penguin) in 2017 [12]. Also, in 2013 and 2014, AMV-20 (GenBank: MH844489.1) was isolated from gulls in Kazakhstan [13]. APMV-21 was isolated from wild birds in South Korea in 2017 [14]. APMV-22 was isolated from samples collected from red turtle doves in Taiwan [15].

Ecological Aspects of Avulavirus Circulation in Wild Bird Populations of Continental Eurasia

Continental Eurasia is a vast territory through which most intercontinental migratory flyways of birds pass: the East Asian-Australasian, Central Asian, West Asian-East African, Mediterranean-Black Sea, and Atlantic flyways [16], where large numbers of migratory birds concentrate in confined areas during stopovers, nesting, and wintering. Currently, there are about 250 species of wild birds that are natural carriers of NDV and other avulaviruses. Thus, favorable conditions are created for the further spread of various avulavirus types among birds and infection of healthy individuals. In this regard, monitoring of viral diseases in birds and characterization of obtained virus isolates are of great importance. Surveillance of avulaviruses in natural environments, as well as in high-risk areas for virus transmission between domestic and wild birds, will provide information on the ecology, epizootiology, and genetic relationships of viruses. These data can offer insight into currently circulating virus types and contribute to risk assessment of epizootics in domestic and wild bird populations.

Ecological Aspects of Avian Avulavirus-1 Circulation in Wild Bird Populations

Avian Avulavirus-1 is currently the most studied, as it includes all strains of NDV, which is economically

significant for poultry production due to the high contagiousness of the disease it causes in commercial and domestic poultry. Infection with viruses of this species can vary in severity – from asymptomatic or mild carriage to severe disease, accompanied by fever, respiratory tract lesions, pneumonia, multiple hemorrhagic lesions of internal organs, CNS involvement, encephalitis, leading to death [5]. Based on pathogenicity, these strains are classified as velogenic, mesogenic, and lentogenic types. The varying levels of pathogenicity are determined by the amino acid sequence composition of the protease cleavage site of the F_0 [17]. NDV strains cause viral diseases in wild and domestic birds. A separate group includes avulavirus-1 strains infecting wild and domestic pigeons, which are also contagious to other bird species, posing a primary threat to domestic and commercial poultry populations [17].

NDV is endemic to developing countries in Africa, Asia (India, Pakistan, Iran), and Central America with predominantly agricultural economies, where poultry production plays a significant role. Despite vaccination programs, periodic outbreaks are also recorded in developed countries such as the USA, Australia, and the EU. NDV was first characterized in 1926 in Indonesia and the United Kingdom, then in 1928 in India, and in the 1920s-1950s caused the first panzootic wave of Newcastle disease. The virus subsequently spread to eastern regions of Eurasia, causing a second wave of epizootics in Middle Eastern and European countries in the 1960s. Phylogenetic analysis has shown relatedness between isolates collected in Denmark, Sweden, Switzerland, and Austria and Middle Eastern isolates from the 1960s, whereas isolates from Germany, Belgium, the Netherlands, Italy, and Spain had a more recent origin and were novel to the European region, being genetically similar to isolates from the Far East [18]. In the 1980s, no major NDV outbreaks were observed in European countries, but since the early 1990s, the number of registered NDV cases has been steadily increasing. In 1996, NDV caused outbreaks in Scandinavian countries, and a genetically related NDV strain was isolated from birds in Germany in 1993–1996, then in Finland and Denmark in 2001 [19], as well as in Sweden and Denmark in 2002–2004. In the period 2000–2009 and in 2016, pigeon NDV infections were regularly reported in Europe. In Switzerland in 1996, antibodies to APMV-1 were found in 10 % of wild birds during serological surveys. Individual NDV epizootic outbreaks were recorded in Italy from 1990 onward, and then almost annually from 2000 to 2009 in wild mallard populations. In 2005, PPMV-1 strains were isolated from various bird species: mallards (order Anseriformes) and robins (order Passeriformes); similar isolates were also identified in northern Italy from pigeons. NDV cases were reported in Austria in 2004 and in France in 2006 in Columbidae birds [19]. Virological screening of samples from wild waterfowl in Finland in 2006–2010 detected 39 NDV strains. Positive NDV samples were most frequently found

in Eurasian teal and mallards. The highest NDV prevalence among wild birds was recorded in 2010 at 11.8 %. Phylogenetic analysis of these samples revealed their close relatedness to strains from wild and domestic birds in China [20]. In 2010, a study of NDV prevalence among wild mallard populations captured in Sweden during the autumn migration found that 1 % of birds were infected with NDV. Phylogenetic analysis showed close relatedness to strains from central and northern Europe, as well as to a small group of strains isolated from birds in southeastern China [20]. NDV strains detected in 2006–2008 in wild waterfowl populations in Luxembourg were genetically close to viruses found in birds in Finland. These data suggest the potential spread of NDV by migratory birds [21]. In Serbia, NDV was detected in wild birds (mallard, Eurasian sparrowhawk, collared dove, feral pigeon) in 2007, phylogenetically close to strains from China. However, it was noted that the strain isolated in Serbia was genetically similar to samples most commonly isolated in Europe at that time from domestic poultry, suggesting that domestic birds could have been the source of infection for wild birds [19]. From 2010 to 2016, 35 fatal cases among wild birds caused by NDV were detected in Catalonia (northern Spain), with the number of infections increasing over this period. Most cases were recorded from September to February, which the authors attribute to favorable conditions for virus persistence in the environment (in water) during this period, as NDV is transmitted via the fecal-oral route [22]. During viral infection surveillance in Romania from 2010 to 2016, antibodies to NDV were detected in 5.4 % of the wild bird population, *the first* such detection in this territory [23]. These data indicate active circulation of NDV strains among wild waterfowl and Columbidae, as well as further spread of NDV across continental Europe [24]. In Russia, in 2001, NDV isolates were obtained from wild birds in the Astrakhan region (Volga River basin): little tern, great cormorant, coot, whiskered tern, and common redshank. In 2001, an NDV strain was isolated during virological monitoring of wild bird populations in Primorye. In 2004, an NDV strain was isolated from teal, which exhibited greater pathogenic properties compared to the 2001 isolate [25]. NDV isolates were also obtained from wild ducks in Adygea in 2008 and from a pigeon in Altai in 2010 [26]. In 2011, NDV was isolated from a wild mallard in Yakutia, phylogenetically close to strains from China, Japan, and South Korea [27]. From 1998 to 2005, periodic NDV outbreaks were observed in domestic poultry in Kazakhstan and Kyrgyzstan [28]. During virological surveillance in 2011 and 2014, APMV-1 viruses were detected in wild birds from 17 families across nine regions of Kazakhstan [28]. Nine NDV isolates were obtained from virological analysis of wild birds in South Korea during 2007–2010, and their similarity to isolates from live bird markets in Korea and China was noted, confirming the role of wild migratory birds in NDV spread [29]. Regular NDV outbreaks have been reported in China

since 1996. Genetic analysis of NDV isolates has shown that NDV can actively mutate, generating unique variants with novel properties and pathogenic potential capable of causing a panzootic in the Asian region in the future [30]. In India in 2012, cases of NDV infection in wild peafowl were reported, with strains genetically related to those from Western Europe, Israel, Indonesia, Taiwan, and India [31]. A large number of NDV outbreaks were recorded in Pakistan during 2010–2012, including among captive wild birds [17]. The presented data show that NDV is persistently present and continuously circulates in the European and Asian parts of Eurasia, periodically causing epizootics among wild and domestic birds. A case of mixed infection of a wild mallard with NDV and Avian Avulavirus-4 was noted in Israel in 1997. The fact of mixed infection of a single individual with different paramyxovirus species is of great importance for epizootiology, as it may alter the clinical presentation of diseases, enhancing or attenuating their severity [32].

According to reports on avian paramyxovirus detection in the European Union in 2016, 12 countries reported no paramyxovirus isolates on their territory (Croatia, Estonia, Finland, Hungary, Northern Ireland, Latvia, Lithuania, Luxembourg, Norway, Poland, Greece), while 19 countries reported detection of avian paramyxoviruses. Among these, 11 EU countries recorded avulavirus cases in wild birds: Austria – Avian Avulavirus-1 in feral pigeons; Belgium – Avian Avulavirus-1 in pigeons, Avian Avulavirus-3 in captive Psittaciformes, Avian Avulavirus-6 in mallards. In Cyprus, positive samples of Avian Avulavirus-1 were found in urban pigeons; in the Czech Republic – Avian Avulavirus-1 in collared doves; in Denmark – Avian Avulavirus-1, -4 in wild mallards and Avian Avulavirus-9 in farmed mallards. In France – Avian Avulavirus-1 in doves and pigeons; in Italy – in doves and sparrowhawks; in the Netherlands – in wild and urban ducks; in Portugal – in common and collared doves; in Slovakia – in pigeons and common doves; in Spain – in doves, Eurasian tawny owls, and pigeons. The final report on avian paramyxovirus detection noted that in 2016, three NDV epizootics were recorded in EU countries compared to two in 2015, indicating a persistent and increasing threat of new epizootics. The report also noted a large number of infections in pigeons and Columbidae, which may contribute to virus spread in commercial and domestic poultry populations. It also emphasized the particular importance of monitoring not only Avian Avulavirus-1 but also other avian avulavirus species [33]. Surveillance of other Avian Avulavirus species has shown their constant presence in wild bird populations of continental Eurasia. Thus, serological surveys of 18 wild bird species in Andalusia (southern Spain) in 1990–1992 detected antibodies to all Avian Avulavirus-1–9 species except Avian Avulavirus-5. Among waterfowl, Avian Avulavirus-8 (43 %) and Avian Avulavirus-6 (21 %) predominated, mainly in Anseriformes, while among non-aquatic

bird species, Avian Avulavirus-2 (60 %) in sparrows constituted the largest proportion. It was also noted that the highest antibody levels to avulaviruses were recorded from May to September, during the period of maximum juvenile density in bird flocks [3].

Ecological Aspects of Avian Avulavirus-3 Circulation in Wild Bird Populations

Isolation of an Avian Avulavirus-3 strain was reported only once – from Psittaciformes in Belgium in 2016. Avian Avulavirus-3 infection caused encephalitis in birds of this family. Avian Avulavirus-3 can also infect chickens and turkeys, causing respiratory tract lesions of varying severity, pancreatitis, and CNS involvement in passerine birds [5, 33].

Ecological Aspects of Avian Avulavirus-4 Circulation in Wild Bird Populations

Avian Avulavirus-4 has become widespread across continental Eurasia. It is typically isolated from wild waterfowl. It was first isolated from a duck in Hong Kong in 1975, and subsequently from mallards, grey ducks, teals, and geese during surveillance programs in the USA and China. In Eurasia, Avian Avulavirus-4 was isolated in Italy from mallards and ducks, and in Belgium from mallards in 2006 and 2007, respectively [34]. In 2016, it was isolated from wild mallards in Denmark [33]. In Ukraine, Avian Avulavirus-4 isolation cases were reported in 2010 from mallards, teals, and starlings; in 2011–2013 from mallards, and in 2014 from teals [35]. In Russia, Avian Avulavirus-4 was isolated from teals in 2017 and 2018, and from a mallard in 2019 [25]. In Kazakhstan – from wild Anseriformes on Lake Alakol and from a curlew on the Caspian Sea coast in 2003 and 2009 [36]. In Mongolia – from mallards in 2012 [37]. In China, Avian Avulavirus-4 isolates were obtained during 2012–2016 from wild waterfowl (mallard, swan, greater white-fronted goose, and grey duck) [38]. In South Korea, Avian Avulavirus-4 samples were isolated in 2006, 2007, 2009–2014, 2016, and 2017 from wild waterfowl (mallard, grey duck) [39]. The pathogenic potential of Avian Avulavirus-4 is poorly understood. Experimental infection of chickens caused moderate pneumonia and catarrhal tracheitis.

Ecological Aspects of Avian Avulavirus-6 Circulation in Wild Bird Populations

Avian Avulavirus-6 is also most frequently isolated from wild waterfowl. This serotype was first isolated in 1977 in Hong Kong from a duck. In 2007, an isolate from a teal in Italy was characterized as Avian Avulavirus-6 [5]. It was also isolated in 2007 and 2016 in Belgium [33]. In 2003, it was isolated in Russia in Primorye from grey herons [3], and in 2009 from a teal [40]. In Kazakhstan – from a red-crested pochard in 2013

[41]. In China, Avian Avulavirus-6 samples were isolated from wild mallards in 2001, 2011, and 2015 [41]. In South Korea – from wild ducks in 2010, 2011, 2013, and 2014 [42]. The infectious properties of Avian Avulavirus-6 are poorly understood. It is known that Avian Avulavirus-6 is avirulent for chickens, but causes moderate respiratory disease and reduced egg production in turkeys.

Ecological Aspects of Avian Avulavirus-8 Circulation in Wild Bird Populations

Avian Avulavirus-8 was first isolated from a Canada goose in 1976 among waterfowl of the Atlantic flyway, and then from a wild pintail duck in 1978 in Japan. In Eurasia, Avian Avulavirus-8 isolates were obtained in Mongolia from wild waterfowl in 2012 [37] and in Kazakhstan from wild waterfowl (waders, whooper swans, greater white-fronted geese) in 2013 [36]. Avian Avulavirus-8 isolates are most frequently found in waterfowl, but a case of antibodies to Avian Avulavirus-8 in chickens has been noted, as well as its ability to replicate in mammals (hamsters, mice, rhesus macaques).

Ecological Aspects of Avian Avulavirus-9 Circulation in Wild Bird Populations

Avian Avulavirus-9 isolation cases were reported in Italy in 2004, 2007, and 2008 in wild waterfowl of the Anatidae family (pintail, mallard, wigeon) [5]. In Denmark in 2016, an Avian Avulavirus-9 infection case was noted in farmed mallards. Avian Avulavirus-9 can infect other animal species (mice, hamsters, macaques) with clinical signs of disease.

Ecological Aspects of Avian Avulavirus-11 Circulation in Wild Bird Populations

In 2010, an Avian Avulavirus-11 isolate was obtained from a snipe in France. The habitat of these birds includes muddy shores and wetlands. Phylogenetically, its closest relative is Avian Avulavirus-2. The Avian Avulavirus-11 sample was obtained from a bird without clinical signs. Its pathogenic potential and virulence properties have not yet been studied [5].

Ecological Aspects of Avian Avulavirus-12 Circulation in Wild Bird Populations

In Italy in 2005, as part of an influenza virus surveillance program, an Avian Avulavirus isolate was obtained from cloacal swabs of wigeons (order Anseriformes) and was characterized as a new species, Avian Avulavirus-12. Serological testing with Avian Avulavirus-1-9 antisera showed genetic relatedness of the Avian Avulavirus-12 isolate to Avian Avulavirus-1, and to a lesser extent to Avian Avulavirus-9. Virulence tests on day-old chicks demonstrated low

virulence of Avian Avulavirus-12 for chickens (ICPI 0.45) [5].

Ecological Aspects of Avian Avulavirus-13 Circulation in Wild Bird Populations

Avian Avulavirus-13 was isolated during annual viral surveillance of wild bird populations in Kazakhstan in 2013 from a greater white-fronted goose. Phylogenetically, Avian Avulavirus-13 is closest to Avian Avulavirus-12, as well as to Avian Avulavirus-1 and Avian Avulavirus-9 [43].

Ecological Aspects of Avian Avulavirus-16 Circulation in Wild Bird Populations

In 2014, as part of an avian influenza surveillance program in southeastern South Korea, a novel paramyxovirus sample was isolated from the feces of wild birds inhabiting wetlands. Morphologically, viral particles exhibited pleomorphic shapes typical of paramyxoviruses, with characteristic surface glycoprotein arrangements. Serological tests identified this paramyxovirus sample as a novel species, Avian Avulavirus-16. Phylogenetically, it is most closely related to Avian Avulavirus-1, followed by Avian Avulavirus-9, -12, and to a lesser extent -13. Serological testing of samples from various wild bird species showed that Avian Avulavirus-16 was found only in Anseriformes (Eurasian teal, Eurasian wigeon, mallard, and spot-billed duck) [10].

Ecological Aspects of Avian Avulavirus-20 Circulation in Wild Bird Populations

In Kazakhstan in 2013 and 2014, a novel avian paramyxovirus was isolated from nasopharyngeal and cloacal swabs of wild black-headed gulls (order Charadriiformes) and characterized as Avian Avulavirus-20. Morphological examination showed that virions had the structure typical of paramyxoviruses. Virological studies demonstrated the absence of pathogenic properties of Avian Avulavirus-20 in infected chickens. It is important to note that Avian Avulavirus-20 was isolated only from Laridae, whereas most avulavirus species are characteristic of Anatidae. It can be hypothesized that Charadriiformes may have greater susceptibility to Avian Avulavirus-20 [13].

Ecological Aspects of Avian Avulavirus-21 Circulation in Wild Bird Populations

In 2015, a novel avian paramyxovirus, Avian Avulavirus-21, was isolated from the feces of wild migratory birds in South Korea (Cheonsu Bay, western region of South Korea). Among the wild birds found in this area are numerous waterfowl such as the greater white-fronted goose, bean goose, black crane, ruddy shelduck, white-tailed sandpiper, common sandpiper,

wood sandpiper, yellow-billed egret, Eurasian spoon-bill, as well as the Japanese buzzard, Eurasian hobby, grey-headed bunting, and Japanese shrike [14].

Vaccination Challenges

Currently, low-pathogenicity strains such as LaSota are used for NDV vaccination of domestic and commercial poultry. However, their ability to provide sufficiently effective immune responses against new wild strains phylogenetically distant from vaccine strains remains questionable [19, 44]. Another current issue in poultry vaccination is the interspecies transmission of vaccine virus strains from domestic poultry to wild birds. Various outbreaks caused by vaccine strains in wild birds have been identified in Mexico, Japan, and Finland [44, 45]. In light of this situation, the strategy and criteria for vaccine strain selection need to be reconsidered. Continuous monitoring of wild and synanthropic bird species for viral infections is also essential.

Practical Applications of Avulaviruses

An oncolytic effect has been discovered in some paramyxoviruses (NDV), allowing their use in the development of antitumor therapies [46].

The replication characteristics and conserved genomic properties make them suitable and safe for the development of vector vaccines. Currently, there is an urgent need for effective vaccines against highly virulent NDV strains. Naturally occurring low-virulence NDV strains are currently used as live attenuated vaccines against NDV. However, as a result of routine vaccination, domestic poultry in some cases becomes less sensitive to currently used vaccines. Avulavirus species that do not cause clinical signs of disease could serve as material for the development of recombinant NDV vaccines [47].

CONCLUSION

From the data presented, it is evident that the primary carriers of avulaviruses among wild birds are waterfowl. The most widespread and best studied is Avian Avulavirus-1, known as Newcastle disease virus. Its reservoir and vectors in the wild are most frequently birds of the orders Anseriformes and Columbiformes. Cases of Avian Avulavirus-1 detection have also been recorded in birds of the orders Passeriformes, Galliformes, Gaviiformes, Strigiformes, and Accipitriformes, indicating a wide diversity of potential hosts and vectors for this virus. The particular attention to this avulavirus variant is explained by the fact that it causes massive epizootics among domestic poultry, primarily chickens.

Avian Avulavirus-3 has been isolated only once (Belgium) from captive Psittaciformes in the European part of continental Eurasia.

Avian Avulavirus-4 has most frequently been recorded in the Asian part of Eurasia (China, South Korea). Avian Avulavirus-4 has been isolated from waterfowl of the order Anseriformes, but also from Passeriformes and Charadriiformes.

Avian Avulavirus-6 has been recorded across the entire territory of Eurasia in birds of the orders Anseriformes and Ciconiiformes.

Avian Avulavirus-8 has been isolated in central Eurasia (Kazakhstan and Mongolia) from birds of the orders Anseriformes and Passeriformes.

Avian Avulavirus-9 has been recorded only in the European part of Eurasia, in Anseriformes.

Avian Avulavirus-11 has been isolated only once – in France from a snipe (order Charadriiformes).

Avian Avulavirus-12 was isolated from Anatidae in the European part of Eurasia (Italy). Avian Avulavirus-13 (from Anseriformes) and Avian Avulavirus-20 (from Charadriiformes) were isolated in central Eurasia (Kazakhstan). Avian Avulavirus-16 was isolated from Anatidae in South Korea (Asian part of continental Eurasia). Avian Avulavirus-21 was isolated from wild migratory birds in South Korea.

The analysis of available literature data indicates that avulaviruses are widely distributed in wild bird populations across the entire territory of Eurasia. The epidemic and epizootic potential of these viruses, with the exception of Avian Avulavirus-1 (Newcastle disease virus), remains poorly understood, and these viruses may pose a potential threat to humans and, particularly, to poultry production, underscoring the need for their surveillance in the wild.

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