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Orthomyxoviruses Beyond Influenza A and B: A One Health Perspective on the Emerging Roles of Influenza C and D Viruses

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ABSTRACT

Influenza C and D viruses are emerging but understudied members of the Orthomyxoviridae family with increasing relevance to human, animal, and environmental health. This review examines their virology, ecology, host range, and transmission through a One Health lens. Influenza C remains an endemic human pathogen capable of infecting several mammals, while recent detections in cattle highlight previously unrecognized cross-species exchange. Influenza D has become globally established in cattle and multiple livestock species, with high seroprevalence in bovines and frequent human exposure among cattle workers despite no confirmed illness. Both viruses rely on a single hemagglutinin-esterase-fusion glycoprotein and use 9-O-acetylated sialic acids, features that distinguish them from influenza A and B and indicate unique evolutionary pathways. Their wide host ranges, environmental stability, and undetected circulation demonstrate critical gaps in current surveillance. Strengthening integrated human and animal monitoring and expanding research inclusion of influenza C and D are essential public health priorities.

Keywords: Influenza D virus, Influenza C Virus, One Health, Orthomyxovirus, Zoonoses, Emerging Infectious Disease

1. INTRODUCTION

The family *Orthomyxoviridae* encompasses several genera of enveloped viruses with segmented [1], single-stranded, negative-sense RNA genomes that cause significant respiratory disease in a wide range of hosts [2, 3]. While the influenza A and B viruses are responsible for seasonal epidemics and pandemics [4], the new influenza C and D viruses represent distinct, yet interconnected, genera that have historically received less attention. Their unique virological, ecological, and epidemiological profiles warrant a deeper, more comprehensive evaluation, particularly from a One Health perspective that recognizes the intricate connections between the health of people, animals, and the shared environment [5].

The four genera of influenza viruses are taxonomically distinct and are characterized by key differences in their genomic organization [6]. Influenza A viruses (IAV) and influenza B viruses (IBV) possess eight-segmented, single-stranded, negative-sense RNA genomes [7-9]. In contrast, influenza C viruses (ICV) and influenza D viruses (IDV) are more closely related to each other and are distinguished by having only seven genomic segments [10]. However, a surprising discovery is that despite this difference in genome segments, ICV and IDV virions package eight ribonucleoprotein (RNP) complexes in an identical "1+7" pattern as observed in IAV and IBV [11]. *Orthomyxoviridae* family, transcending the specific number of coding segments. IDV, first detected and isolated in 2011 in the United States from pigs with respiratory illness [12], was officially proposed as a new genus due to its distinct antigenic and genetic divergence from ICV [13]. The rationale for moving beyond an exclusive focus on IAV and IBV is rooted in the One Health framework. Influenza A viruses, with their broad avian reservoir, are the primary focus of pandemic preparedness [14].

However, IDV's established wide host range [15] and widespread circulation in cattle [16] presents a unique and significant zoonotic interface that is being overlooked. Cattle are generally considered refractory to IAV and IBV [17], yet they are the primary host and reservoir for IDV [17]. The high seroprevalence of IDV in cattle [18], its spillover to other livestock in addition to cattle and pigs [19], and the documentation of human seropositivity among those with occupational exposure [20, 21] demonstrate a persistent and tangible zoonotic risk that exists outside the conventional avian-to-human paradigm. This constitutes a critical blind spot in current One Health surveillance systems, which must be addressed to effectively manage future public health threats.

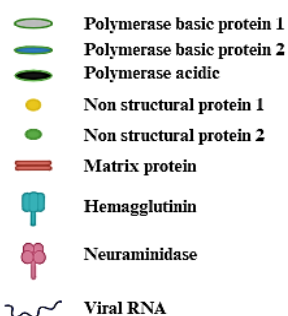
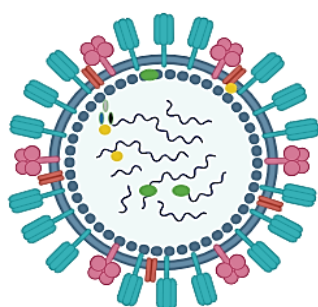
2. VIROLOGY AND GENOMIC FEATURES

The influenza virus belongs to the *Orthomyxoviridae* family, whose members are enveloped viruses that possess segmented, single-stranded, negative-sense RNA genomes [1, 6]. The number of viral RNA (vRNA) segments differs depending on the type of influenza virus; ICV and IDV possess a seven-segmented genome [10], whereas IAV and IBV genomes are composed of eight segments [8]. Each genomic RNA segment exists as a ribonucleoprotein complex (RNP) within the virion [11]. For a progeny virion to be infectious, it must package a complete set of its genomic segments. An interesting finding is that ICV and IDV virions package eight organized RNPs in a "1+7" pattern, consistent with IAV and IBV, despite having only seven genomic segments. This suggests that regardless of genome count, the packaging of eight RNPs is a highly conserved and possibly crucial feature of influenza virion assembly.

A major distinguishing feature of ICV and IDV is their possession of a single, multi-functional spike glycoprotein, the hemagglutinin-esterase-fusion (HEF) protein [22, 23]. This protein combines the separate functions of hemagglutinin (HA) and neuraminidase (NA) proteins found in IAV and IBV [17, 22]. The HEF protein is responsible for receptor recognition [24], viral fusion [25], and the destruction of the host receptor to facilitate virus release [26]. It is composed of three domains: a receptor-binding domain, an acetylsterase domain, and a membrane fusion domain [22, 27]. This HEF protein is not merely a molecular curiosity; it signifies a fundamentally different pathogenic mechanism from that of IAV and IBV. While IAV and IBV must orchestrate the functions of two separate proteins (HA and NA) for entry and release, ICV and IDV achieve both with a single protein (HEF). This unique structure makes the HEF protein a compelling, and to date largely unexploited, target for novel antiviral drug development and for designing a more durable vaccine not prone to rapid antigenic drift, as the HEF protein is antigenically stable. Research on ICV and IDV has concentrated mainly on its only glycoprotein HEF that combines the function of HA and NA of IAV and IBV.

3. MOLECULAR DETERMINANTS OF HOST RANGE AND RECEPTOR USAGE

INFLUENZA A & B (IFA, IFB)



INFLUENZA C & D (IFC, IFD)

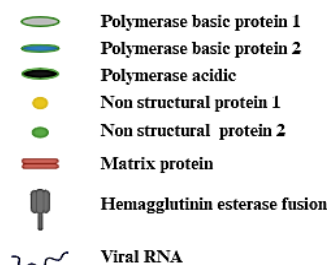
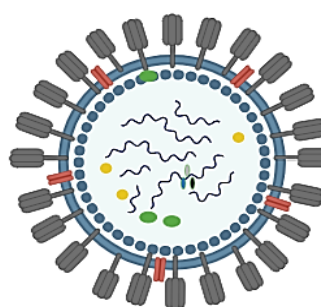


Figure 1. The structural differences of eight segmented influenza viruses (IFA and IFB) and seven segmented influenza viruses (IFC and IFD). (A) Eight-segmented influenza viruses (IAV and IBV) with separately encoded Hemagglutinin (HA) and neuraminidase (NA) proteins for receptor binding and destroying functions, respectively. (B) Seven-segmented influenza viruses with Hemagglutinin–esterase fusion (HEF) protein that combines the dual function of HA and NA. Designed with Biorender.

The receptor specificities of ICV and IDV are key determinants of their host range and species specificity [17]. The cellular receptors for ICV and IDV are 9-O-acetylated sialic acids [29, 30]. This differs from the receptor usage of IAV and IBV which bind to either α 2-6- or α 2-3-linked sialic acids, depending on the host [31, 32]. This distinct receptor-binding mechanism means that the host species barriers for IDV and ICV are completely different from those of IAV AND IBV and require separate research and surveillance efforts.

4. EPIDEMIOLOGY

4. 1. Host range

Influenza C virus (ICV) is primarily a human pathogen [33]. Serosurveys show nearly global distribution and it is a major public health problem [33, 34]. Humans are the main reservoir, and ICV circulates endemically in human populations. However, evidence shows ICV can infect other mammals [35]. Natural or experimental ICV infection has been detected in pigs, dogs, horses, cattle, camelids and rare swine–human transmission [35-41]. Early ICV isolation in pig was in China in 1981 [42] and Japan in 1987 [43], and seroprevalence studies have detected ICV antibodies in mammals in Japan, China, Germany, UK, USA and Kenya [43-47]. Bovine infection with human-lineage ICV has also been reported. An Emerging Infectious Diseases study (2018) found ICV RNA in U.S. cattle with respiratory disease, with isolates ~95% similar to human ICV [115]. Thus, humans are the reservoir, but pigs, dogs, horses, camelids, and even cattle can serve as incidental or intermediate hosts of ICV.

For Influenza D virus (IDV), it is fundamentally a cattle-associated virus [49]. It was first discovered in U.S. from a domestic pig with influenza-like symptoms in 2011 [50], but it has now been reported widespread in cattle worldwide [48]. Serosurveys in Nebraska, USA between 2003-2004 report very high IDV antibody prevalence in cattle [52]. This serology reports show the same trend with another recent nationwide serology surveillance in cattle USA between 2014-2015 demonstrating that influenza D virus circulated widely in cattle during this period [51]. Beyond cattle, IDV infects a broad range of mammals. Antibodies or virus have been detected in domestic pigs, sheep, goats, camelids, horses, deer, and wild boar [45-56].

Wild mammals such as feral pigs [50], wild boars [56], giraffes [57], and white-tailed deer, kangaroos, wallabies, hog deer [58], have been shown to carry IDV antibodies or virus. Companion animals have recently been implicated. A 2025 surveillance in China found IDV antibodies in 8/360 (2%) pet and stray cats [59]. Beyond United States, distribution is worldwide in countries such as Brazil [60], China [61], Japan [62], France [63, 64], Italy [65, 66], UK [67], Ireland [68] and Canada [69], Namibia [57].

In summary, cattle are the primary host and reservoir of IDV, but the virus infects multiple domestic and wild species (pigs, small ruminants, horses, camels, deer, dogs, cats, etc.). Notably, high IDV seroprevalence in cattle workers indicates frequent exposure, though human infection remains unproven.

4. 2. Geographical distribution

Influenza C (ICV) is globally distributed among humans [70]. Serological studies indicate ICV circulates worldwide. Isolates have been obtained from human and animals in Asia [76], Europe [74, 75], the Americas [72, 73], Australia [71] and Africa. For example, human ICV has been isolated or serologically detected in China, Japan, England, France, Greece, Brazil,

South Africa, the U.S., Canada, Philippines, Cuba, Spain, Italy, India, Finland, Nigeria, and other countries [17]. ICV tends to cause small local outbreaks often in winter [77], but has never caused a large pandemic [78]. Antibody surveys show consistent >50% seropositivity in animals in diverse populations in the U.S., Europe, and Asia. Generally, animal infections by ICV are much rarer; the only confirmed isolations in pigs have come from China in 1981 [36] and Lancaster, UK in 2014 [80], with serological evidence in swine from Japan, USA, but without reported disease [79].

Human-cattle interface is also of interest; ICV was detected in U.S. cattle herds during 2016–18 [81], but apart from this single finding, the full extent of ICV in livestock is largely unknown. It is likely sporadic and inconsistent.

Influenza D (IDV) has a similarly global trend but with emphasis on livestock regions. Since its first discovery in USA, IDV has been reported from various countries including France [64], Mexico [82], Italy [66], Japan [62], China [83], Ireland [68], U.K [84], Canada [69], Denmark [85], Luxembourg [86], South Korea [87], Turkey [88], Australia [89] and Namibia [57], Morocco, Togo, Benin, Kenya [25] and Ethiopia [90]. Prevalence of IDV in cattle is higher, especially in calves. Two studies describe that ~95% of newborn calves had high levels of maternal antibodies against IDV.

Also, a nationwide serological survey in Japan reports an average 30% seropositivity rate in cattle, but the positivity rates varied among regions. The highest detection rates in China was 91% seroprevalence found nationwide in Chinese cattle during the winter of 2022–2023 [91]. In Europe and North America, IDV circulates widely in cattle and swine but with lower seroprevalence; In Africa, IDV circulation has been shown in cattle and small ruminants in Morocco, Togo, Benin, Kenya and Ethiopia [40]. Notably, all surveyed Chinese provinces sampled in 2022–23 had IDV-positive cattle [21]. IDV has even been detected in imported animal products or environments. IDV RNA was found in 14% of air samples from poultry farms in Malaysia [15] suggesting environmental spread. In summary, IDV is now recognized on all inhabited continents, primarily associated with bovine and swine agriculture, whereas ICV remains confined to human and sporadic animal cases globally [20].

4. 3. Ecological factor

Environmental conditions influence the survival and spread of influenza C and D viruses [92]. Both viruses are enveloped and susceptible to heat, UV, desiccation and disinfectants, but have some distinctive features. Notably, IDV is more environmentally stable than ICV. Laboratory tests show IDV retains infectivity longer under stress conditions than ICV [35]. IDV also replicates at mammalian body temperature (37 °C) whereas ICV optimally replicates at cooler temperature [97]. These differences may help IDV persist in warmer settings (e.g. tropical barns) that would inactivate ICV.

Seasonality may differ between the viruses. Influenza C often peaks in winter in temperate zones (circulating alongside A and B influenza), but serological surveys suggest it can circulate year-round [98, 99]. A peak of the disease was reported in France in winter-spring of 2005 while little ICV was detected in the two following seasons [100]. Also, a similar seasonal pattern was noted in Germany, with a peak of ICV detection in fall–winter–spring of 2012–2013, and minimal detection in the seasons preceding and following [101]. It has also been reported that there was a winter-spring outbreak of 51 cases in the US during 2013–2015, while in the seasons before and after, only 2 and 8 cases were reported, respectively [102]. Furthermore, a single-year study identified a winter-spring seasonality in ICV detection [103].

In most studies, winter–spring seasonality remained consistent, though a year-round detection of ICV was reported in Spain with highest numbers observed in the summer [104]. By contrast, IDV is largely a pathogen of cattle and other livestock, so its “seasonality” follows husbandry cycles; outbreaks often occur in late autumn or winter when cattle are confined. High-density farming environments (feedlots, shared grazing) likely facilitate year-round IDV transmission.

Host population structure is also critical. ICV majorly relies on humans, who mingle widely, whereas IDV depends on livestock trade and movement. Regions characterized by intensive and high-density animal husbandry show higher IDV prevalence [105]. Wild animal reservoirs (feral swine, wild ruminants, wild boar) and companion animals (cats, dogs) may create bridge populations, especially in mixed farming landscapes [106]. Human interventions also affect ecology. Vaccination against IAV/B in humans/swine does not impact ICV/IDV. Lack of targeted surveillance means ICV and IDV often go undetected. Finally, viral genetics play a role: IDV’s broad receptor binding allows infection of diverse cell types, potentially contributing to its wide host range and persistence [35].

4. 4. Transmission mechanism and species spillover

Both ICV and IDV are respiratory pathogens that spread mainly via inhalation of infectious droplets/aerosols and close contact. In ICV, human-to-human transmission is efficient and circulation is continuous in people [93]. ICV can spread within a susceptible population rapidly, with viral shedding for weeks. In swine, experimental studies show ICV transmits from infected pigs to naive pigs by direct contact [94]. Although it is not known whether the virus has been transmitted from pigs to humans or from humans to pigs, but it was strongly suggested that interspecies transmission of influenza C virus between humans and pigs has occurred in nature [95].

Aerosol and fomite spread are also possible. Influenza viruses can persist on surfaces and infect via contaminated fomites, and aerosol transmission of ICV has been documented in animal models (ferrets) and is presumed in humans [95]. Human–swine interfaces pose bidirectional risks. Field serology strongly suggests human–pig ICV transmission, though whether spillover is human-to-pig or pig-to-human remains unclear. Notably, ICV has never been reported from poultry.

Influenza D transmission is similarly via respiratory routes. Direct contact and aerosols efficiently spread IDV in susceptible hosts. In cattle, IDV can transmit rapidly among animals. In a study IDV spread through an entire herd within days [107]. Experimental evidence shows IDV infects ferrets and guinea pigs, indicating airborne transmissibility [108]. Like ICV, contaminated dust and aerosolized particles on farms likely play a role. IDV genomes have been found in bio-aerosol samples in a hospital emergency room in North Carolina hospital air and even public spaces (North Carolina airport) [109, 110].

Though natural IDV cases in humans are not confirmed, seroprevalence in cattle workers (97%) suggests frequent exposure [20]. Interspecies, IDV readily jumps among ruminants. Outbreaks and serosurveys document regular spillover between cattle, pigs, goats, and sheep [45, 110].

While direct bird-to-mammal transmission has not been observed, wild mammals (e.g. wild boar) could carry IDV between farms [120, 121]. Both ICV and IDV transmit by respiratory routes; ICV predominates in human populations, whereas IDV transmits efficiently in mixed livestock settings and can infect multiple mammalian hosts.

Table 1. Summary of the seroepidemiological studies of ICV conducted in humans and other animal species.

Host	Rate % (Total)	Region
Cattle	94.6	Ireland
Bull	68	Argentina
Human	4.9	Italy
Swine	5.9	Luxembourg
Cattle	80.2	Luxembourg
Cattle	47.2	France
Small ruminants	1.5	France
Cattle	48.5	Japan
Feral swine	19.1	USA
Small ruminants	8.8	USA
Poultry	0	USA
Cattle	77.5	USA
Newborn calves	98	USA
Human (cattle exposed)	97	USA
Human (non-cattle exposed)	18	USA
Cattle	31.5	Senegal
Cattle	1.9	Benin
Cattle	10.4	Togo
Cattle	0	Cote d voire
Cattle	35	Morocco
Cattle	0	Kenya
Cattle	80	Italy
Equine	1	Italy
Swine	20	Italy

Wild boar	51	Italy
Cattle	91.4	China
Pig	3	China
Goat	1	China

Table 2. Comparative clinical and epidemiological characteristics summary of influenza c and influenza d viruses.

Feature	Influenza C Virus (ICV)	Influenza D Virus (IDV)
Primary Host	Human	Cattle
Other Susceptible Species	Pigs, dogs, cattle (sporadic)	Pigs, goats, sheep, camelids, horses, wild ruminants, cats
Human Infection	Common, mild (Significant in children)	High seroprevalence among cattle workers but no confirmed clinical disease
Clinical Signs in Primary Host	Mild to moderate URT disease; bronchiolitis; croup; pneumonia	Mild to moderate respiratory disease; contributes to BRD; worsens bacterial coinfection
Disease Severity	Severe in infants and immuno-compressed individuals	Mild alone but severe in BRD complex
Transmission Mode	Human to human via droplets, close contact	Cattle-to-cattle; multi-species; aerosols; farm/environmental persistence
Environmental Stability	Moderate	High (stable in aerosols)
Public Health Impact	Underdiagnosed contributor to pediatric respiratory disease	Zoonotic exposure concern; unclear clinical impact in humans
Diagnostic Inclusion	Rarely included in routine human practice	Rarely included in cattle respiratory screening
Vaccine Availability	None	None (Experimental vaccine showed promising protection)

URT – Upper Respiratory Tract

BRD – Bovine Respiratory Disease

5. HUMAN EXPOSURE AND ZOOONOTIC RISK

People with livestock contact have the highest exposure risk. Numerous studies show that dairy and cattle workers frequently encounter IDV. For example, 97% of Florida cattle-workers

had IDV antibodies compared to less than in 20% of non-exposed adults [111]. Another U.S. field study of 31 dairy workers (across five herds) found IDV RNA in the nasal wash of 67% of participants on at least one of five consecutive days [112]. Notably, these workers reported no increase in symptoms during IDV exposure [112]. By contrast, swine veterinarians in Italy showed only 5% IDV seropositivity [113], reflecting the lower prevalence of IDV in pigs. In summary, cattle-related occupations show high IDV exposure (very high seroprevalence and viral detection in workers [111, 112], whereas human illness from IDV has not been observed. For ICV, exposure is ubiquitous in the general population (young children often highly seroconvert) [114] and data on livestock-worker exposure are lacking. Nonetheless, the discovery of ICV in pigs and cattle raises the possibility of occasional animal-to-human exposure. One U.S. cattle ICV isolate contained gene segments from both bovine and human ICV lineages indicating genetic mixing. This finding suggests that farm workers might occasionally encounter novel reassortant ICV strains, though no human cases from such events have been documented.

Both viruses are also evolving host ranges. ICV was first isolated in humans in and later found in pigs and dogs until recently it was not known to infect large livestock. In 2016-18, ICV was detected in ~4% of U.S. cattle with respiratory disease and the ICV genomes were 98% identical to each other [115]. Also, the bovine ICV isolates showed high nucleotide identity (95%) with human ICV isolate C/Mississippi/80, suggesting the ability of human strains to infect cattle or vice versa [115]. This high genetic similarity implies possible cross-species transmission of ICV, although no confirmed cases of animal-origin ICV causing human illness have been reported [70, 115].

IDV is primarily a cattle virus [113]. Since then, its RNA and antibodies have been found in cattle and other mammals worldwide (pigs, small ruminants, camelids, rodents) under experimental or field conditions. Cattle appear to be the main reservoir driving IDV circulation. Although serological and molecular evidence indicate human exposure, no symptomatic human infections have been confirmed so far. IDV genome fragments have been detected in a swine-farm worker's nasal wash (Malaysia) and in aerosols at a U.S. airport and hospital [44, 111, 116], and high IDV antibody levels have been found in cattle-exposed people [111, 112]. However, to date no replication-competent IDV has been isolated from humans and CDC has noted that IDV is not known to cause illness in people. In summary, ICV is endemic in humans (causing mild respiratory infection) and can infect livestock, whereas IDV is endemic in cattle with frequent human exposure but no confirmed human disease.

6. ONE HEALTH SURVEILLANCE AND INTEGRATION

Global surveillance for influenza C and D is still nascent. Human influenza surveillance networks focus majorly on A and B and rarely target C or D. A recent review noted that “most countries do not have active and comprehensive surveillance” of zoonotic influenza at the human-animal interface which underestimates the true burden of zoonotic influenza diseases [117]. Nonetheless, some countries and research groups have begun integrated surveillance efforts. In Japan, a five-year clinical study (Jan 2018–Mar 2023) screened 2,144 respiratory patients for ICV and IDV by duplex RT-PCR [118]. They detected three ICV cases (lineages C/Kanagawa and C/SãoPaulo) but no IDV, and recommended adding IDV to routine monitoring to assess its public-health impact. On the animal side, targeted testing has revealed

both viruses. For example, another Japanese serosurvey (2020–23) found 27% cattle seroprevalence for ICV and 48% for IDV [119]. These studies demonstrate local surveillance efforts. A One Health approach linking veterinary and clinical data is needed to contextualize such findings. The One Health paradigm should incorporate human, animal, and environmental health to confront emerging zoonotic viruses [111], but systematic data integration remains limited in the context of Influenza C and D [117].

7. CONCLUSIONS

Influenza C and D viruses are no longer peripheral curiosities in Orthomyxoviridae research; they are active distinct players with proven One Health significance. Influenza C persists as an endemic human pathogen capable of infecting multiple mammalian hosts, and bovine detections genetically close to human strains demonstrate genuine cross-species exchange that merits heightened attention and Influenza D has emerged as a globally distributed, cattle-associated respiratory virus with high seroprevalence in bovine populations and repeated detections in other domestic and even wild mammals. Several virological features explain why ICV and IDV deserve dedicated surveillance and attention. Both viruses use 9-O-acetylated sialic acids and rely on a single multifunctional hemagglutinin-esterase-fusion (HEF) glycoprotein for attachment, fusion, and receptor destruction; the HEF is antigenically more stable than the HA/NA pair of IAV/IBV and therefore represents an attractive, underexplored target for antiviral and vaccine design.

Human exposure at the animal–human interface is concerning. Seroepidemiological work and field sampling repeatedly show markedly higher IDV antibody prevalence among cattle-exposed workers and detectable viral RNA in occupational communities. These data indicate frequent human exposure even in the absence of confirmed, symptomatic human infections to date, and they underscore the importance of targeted occupational surveillance and serology studies. From a One Health perspective, the current surveillance and preparedness posture is insufficient. Routine influenza surveillance emphasizes IAV and IBV, leaving ICV and IDV under-detected in both human and veterinary streams. Integrating multiplex molecular testing for ICV/IDV into existing human and animal diagnostic pipelines, expanding serosurvey among livestock and exposed workers, and sampling environmental aerosols in high-risk settings would close critical gaps in early detection.

We recommend the following near-term priorities; (1) implementation of coordinated human–animal surveillance platforms in regions of intensive cattle production, (2) systematic occupational cohort studies with longitudinal sampling to determine whether transient human infections occur and whether they are clinically silent or under-recognized, (3) characterization of HEF antigenic drift and cross-lineage immunity to evaluate vaccine feasibility, (4) investigation of IDV environmental persistence and farm-scale transmission dynamics to identify practical mitigation measures and (5) rapid publication of sequences to enable global molecular epidemiology and reassortment screening.

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