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Editorial: High-impact respiratory RNA virus diseases

Victor Manuel Petrone-García[1], Inkar Castellanos-Huerta[2]* and Guillermo Tellez-Isaias[2]

[1]Departamento de Ciencias Pecuarias, Facultad de Estudios Superiores Cuautitlán UNAM, Cuautitlán Izcalli, Mexico, [2]Department of Poultry Science, University of Arkansas, Fayetteville, AR, United States

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EDITED AND REVIEWED BY
Michael Kogut,
United States Department of Agriculture,
United States

*CORRESPONDENCE
Inkar Castellanos-Huerta
✉ castellanos.inkar@gmail.com

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Editorial on the Research Topic
High-impact respiratory RNA virus diseases

The text discusses the serious threat of high-impact "respiratory RNA virus" (RRV) infections to global health (1, 2). These viruses can spread rapidly, causing severe respiratory illnesses and significant socioeconomic burdens (3). The emergence and reemergence of these viruses continuously hinder public health preparedness and control measures (1). "RRVs" form a diverse group sharing genetic material of single and double-stranded RNA (4–6). They can lead to various respiratory disorders, from mild symptoms to life-threatening respiratory distress (5).

Notable examples of RRVs include canine distemper virus (CDV) (7) and Newcastle diseases virus (NDV) (8), Influenza virus (IV) (9), porcine reproductive and respiratory syndrome virus (PRRSV) (10), the coronavirus disease 2019 (COVID-19) caused by SARS-CoV-2 (11, 12), and the less well-known African horse sickness virus (AHSV) (13) are some of the most notable high-impact RRVs (14). Past pandemics, like the IV in humans and animals (15, 16) and SARS in the twenty-first century highlighted the challenges of zoonotic transmission and controlling outbreaks (11). The ongoing COVID-19 pandemic demonstrates the relevance of these diseases (17–21) (Jarrah et al.). RRVs can have substantial economic consequences, including disruptions to global trade, tourism, and healthcare systems (22–24). The interconnectedness of global health security underscores the importance of international collaboration, data sharing, and robust surveillance systems to detect and respond to emerging viral threats (25).

RRVs have the potential to spread widely, causing severe respiratory illnesses and far-reaching consequences beyond health, including economic disruptions and impacts on global trade, tourism, and healthcare systems (26). The emergence and reemergence of these viruses continuously challenge public health measures (1). RRVs refer to a diverse group of viruses with RNA genetic material, typically with a protein coat or capsid, surrounding their genome (27), causing various respiratory disorders in human and animal populations. Some RRVs have an envelope derived from the host cell membrane (28). The RNA virus-genomic structure and replication strategies can vary, influencing their ability to infect and replicate within host cells (29). RRVs are characterized by high mutation rates, rapid replication cycles, and the ability to cause various clinical consequences (5, 25, 30). Their genetic structure allows for (+) sense or (–) sense RNA, leading to diverse viral populations (31–33). RRVs reflex a higher mutation rate, enabling them to adapt and evolve rapidly, evading host immune responses and developing resistance to antiviral drugs (25, 34–36). The epidemiology of RRVs varies based on factors such as transmission mode, viral stability, host range, and population susceptibility (19, 37, 38). Some RRVs exhibit seasonal patterns, while others cause sporadic outbreaks or persistent endemic infections (39). The transmission dynamics depend on the specific virus and can occur through respiratory droplets, direct contact, vector-borne transmission, or fecal-oral transmission (19).

Diagnosing RRV diseases involves various laboratory techniques, including molecular methods like polymerase chain reaction (PCR) (40–43) (Machado et al.), and serological tests to detect viral genetic material or antibodies (ELISA test) (44–48). Overall, understanding the characteristics, transmission, and diagnostic methods of RRVs is crucial for effectively combating these infections and improving global health preparedness. Some examples of RRVs are briefly described below:

a) SARS-CoV-2 has a single-stranded (+) sense RNA virus genome, which means it can serve as a messenger RNA (mRNA) for protein synthesis once it enters a host cell (9, 49). The genome structure includes regions encoding structural and non-structural proteins (50, 51). Its genome can undergo mutations, leading to the emergence of different variants that may impact transmissibility, virulence, and vaccine efficacy (52–54). Continuous monitoring of viral genomic sequences helps researchers understand the evolution and spread of the virus (18, 23, 55) (Padilla-Blanco et al.). Diagnosing in animals is crucial for understanding its impact on animal health and welfare, studying transmission dynamics, adopting a One Health approach that considers human, animal, and environmental health, and enhancing public health and epidemiological surveillance (56). Animals can become infected with SARS-CoV-2 through zoonotic transmission, and studying such cases provides valuable data for tracking the virus's spread and assessing its potential impact on human populations. Collaborative efforts between human health professionals and veterinary experts are essential for comprehensive disease surveillance, prevention, and control (18, 57).
b) PRRSV is a significant viral pathogen affecting pigs worldwide (58). It is an enveloped, single-stranded RNA virus, family *Arteriviridae*, genus *Betaarterivirus* (59), with a genome containing several ORFs encoding viral proteins, including structural and non-structural proteins (60–62). There are two major genotypes: PRRSV type 1 (PRRSV-1) and PRRSV type 2 (PRRSV-2) (63). PRRSV is characterized by causing reproductive failure, respiratory illness, and immunosuppression in pigs (64). Its genetic diversity challenges disease control and vaccine efficacy (65, 66). Recently a new type of active vaccine demonstrated superior results against the PRRSV (Trevisan et al.).
c) IV is an enveloped RRV of the *Orthomyxoviridae* family classified into four genera: *Alphainfluenzavirus* (influenza A virus, IAV), *Betainfluenzavirus* (influenza B virus, IBV), *Gammainfluenzavirus* (influenza C virus, ICV), and *Deltainfluenzavirus* (influenza D virus, IDV) (67–69). The viral genome comprises segments of single-stranded RNA, encoding structural and non-structural proteins (68, 70). The replication and transcription processes involve interactions between viral components and host cell machinery (71). Influenza viruses can cause seasonal flu outbreaks (Fujiwara et al.), occasionally leading to pandemics (15, 16).
d) NDV is an enveloped, single-stranded RNA virus belonging to the *Avulavirus* genus in the *Paramyxoviridae* family (72). It affects domestic poultry and wild bird species (72). NDV has a non-segmented RNA genome, and its replication and transcription processes involve interactions between the viral polymerase complex and viral RNA (73, 74). Vaccination is crucial for controlling NDV outbreaks (8).
e) CDV is a highly contagious viral disease affecting dogs and other *Canidae* family members (75, 76). It belongs to the *Morbillivirus* genus within the *Paramyxoviridae* family (77). The CDV genome is segmented RNA and encodes various structural and non-structural proteins (78). Vaccination is the most effective preventive measure against CDV (79, 80).
f) AHS, a member of the *Orbivirus* genus within the *Reoviridae* family (13, 81), has a segmented genome with 10 RNA segments, each encoding specific proteins (82, 83). The virus is primarily transmitted through insect vectors, and vaccination and vector control are essential for disease prevention (82). AHS can cause various clinical signs, varying from peracute to chronic (Adesola et al.). Research focuses on understanding the viral genome and developing effective control strategies (83).

The challenges of prevention, diagnosis, and treatment are examined, highlighting the necessity for continuous research, surveillance, and preparedness. To mitigate the effects of RRVs, it is essential to prioritize surveillance, prevention, diagnostics, and research efforts while fostering collaboration among scientists, healthcare professionals, and policymakers to enhance global preparedness for future outbreaks.

Author contributions

VP-G: Conceptualization, Formal analysis, Investigation, Writing—original draft, Writing—review and editing, Data curation, Methodology, Supervision. IC-H: Investigation, Writing—original draft, Writing—review and editing, Software, Visualization. GT-I: Funding acquisition, Supervision, Writing—review and editing, Project administration, Resources, Validation.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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