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Review

# Improving Influenza Nomenclature Based on Transmission Dynamics

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**Abstract:** Influenza A viruses (IAVs) evolve rapidly, exhibit zoonotic potential, and frequently adapt to new hosts, often establishing long-term reservoirs. Despite advancements in genetic sequencing and phylogenetic classification, current influenza nomenclature systems remain static, failing to capture evolving epidemiological patterns. This rigidity has led to misinterpretations in public health responses, economic disruptions, and confusion in scientific communication. Existing nomenclature does not adequately reflect real-time transmission dynamics or host adaptations, limiting its usefulness for public health management. The misnomer "swine flu" for the 2009 H1N1 pandemic (A(H1N1)pdm09) has created undue public confusion and potential stigma despite no direct pig-to-human transmission. This review proposes a real-time, transmission-informed nomenclature system that prioritizes host adaptation and sustained transmissibility ( $R_0$ ) to align influenza classification with epidemiological realities and risk management. Through case studies of H1N1pdm09, H5N1, and H7N9, alongside a historical overview of influenza naming, we demonstrate the advantages of integrating transmission dynamics into naming conventions. Additionally, we discuss how a transmission-based framework can enhance public health responses and propose research and surveillance strategies to support its implementation. Adopting a real-time, transmission-informed approach will improve pandemic preparedness, strengthen global surveillance, and enhance influenza classification for scientists, policymakers, and public health agencies.

**Keywords:** influenza A virus; nomenclature; transmission dynamics; zoonotic potential; molecular evolution; public health; virology

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## 1. Introduction

Infectious disease nomenclature serves not only as a technical label for scientists but also as a critical tool in public communication and pandemic response. Historically, influenza A virus (IAV) naming conventions are based on viral characteristics like surface proteins or places of isolation, which fail to convey information about how the virus spreads or host adaptations in real time. This disconnect can hinder public health messaging and response efforts. In this review, we examine existing influenza nomenclature systems and their limitations, and propose an improved framework centered on transmission dynamics. The review begins with an overview of IAV biology and the current naming scheme, followed by a historical perspective on influenza pandemic nomenclature. Core to this review is highlighting why transmission dynamics—such as the ability of a virus to sustain human-to-human transmission or cross-species barriers—should be clearly reflected in virus names. Finally, we outline how a transmission-based nomenclature could be implemented, present supporting case studies, and offer recommendations for integrating this system into global public health and surveillance infrastructure.

### 1.1. Influenza A Virus: An Overview

Influenza A viruses belong to the Orthomyxoviridae family and possess a segmented negative-sense RNA genome. The genome consists of eight segments encoding at least 11 proteins, including the surface glycoproteins hemagglutinin (HA) and neuraminidase (NA), which form the basis of the current subtype classification. There are 18 HA subtypes (H1–H18) and 11 NA subtypes (N1–N11) known, theoretically yielding 198 possible HA/NA combinations, most of which are found in wild

bird reservoirs [1]. Influenza A has a broad host range encompassing birds, various mammals (swine, horses, canines, marine mammals), and humans, reflecting its significant zoonotic and pandemic risk. Two main processes drive viral evolution: antigenic drift (the accumulation of point mutations) and antigenic shift (reassortment of gene segments when a host is coinfecting with multiple strains). These processes enable influenza viruses to evade immunity and occasionally jump between species [2]. Notably, many human influenza pandemics are linked to viruses originating or mixing in animal hosts [3]. Given this dynamic evolution and host range, a static naming convention may fail to capture properties of an influenza strain that are most relevant to its spread and control.

### 1.2. Challenges with the Current Nomenclature System

The prevailing influenza virus nomenclature was established by the World Health Organization (WHO) in 1953 and includes the following components for influenza A: antigenic type (A/B/C), host of origin (if not human), geographic location of isolation, strain number, year of isolation, and HA/NA subtype [4]. For example, **A/California/07/2009 (H1N1)** denotes a strain isolated in California in 2009 with subtype H1N1. This standardized format has utility for basic identification and tracking in research. However, it exhibits several shortcomings in practice:

#### 1.2.1. Focus on Static Attributes

The WHO system emphasizes historical and genetic information (origin and subtype) but does not account for the dynamic epidemiological behavior of the virus captures where and from what species a virus was first isolated, but not how it spreads or adapts thereafter. Key factors such as real-time transmissibility and host adaptation are absent. For instance, genetic sequencing can identify a virus's ancestral origin, but it does not convey whether the virus is currently spreading efficiently in humans or other hosts.

#### 1.2.2. Geographic Labels and Stigma

Names often include a location (e.g., "Asian flu," "Spanish flu"), which may inadvertently stigmatize regions or populations without providing actionable information. A prominent example is the 2009 "swine flu" pandemic initially named "Mexican flu" by some media [5], causing diplomatic tensions and economic impacts on Mexico despite the virus's widespread nature. Geographic names can mislead the public regarding the actual source or risk of a virus and may discourage transparency in reporting outbreaks.

#### 1.2.3. Host-Origin Labels and Cross-Species Complexity

Similarly, host-based labels (e.g., avian influenza, swine influenza) can be confusing when viruses jump species. Common practice is to name a new Influenza viruses after the host species from which they were first isolated, but many strains do not remain exclusive to that host. For example, the A(H1N1)pdm09 virus contained gene segments from avian, swine, and human influenza lineages [6], yet it established itself as a human virus. The PB1 gene of H1N1pdm09 originated in birds, but the virus now circulates predominantly in humans. Likewise, an "avian" H5N1 virus can infect people, and a "swine" virus can re-assort with human strains. Rigid host labels fail to capture these transitions and can cause confusion. For instance, truly swine-adapted influenza strains (like endemic swine H3N2) [7] are distinct from the pandemic H1N1pdm09, yet both have been colloquially termed "swine flu."

#### 1.2.4. Lack of Epidemiological Context

The current nomenclature does not indicate whether a virus is undergoing sustained human-to-human transmission or is only causing sporadic spill over infections. This distinction is crucial for public health. A name like **A/H5N1** gives no indication that, as of now, H5N1 is chiefly a bird virus with rare human cases. Similarly, **A/H7N9** conveys the subtype but not that H7N9 infected over 1,500 humans via poultry exposure with limited, non-sustained human spread [8]. The absence of a

transmission context in names is a missed opportunity to signal the level of pandemic risk associated with a strain.

Due to these challenges, the current naming system can hinder effective risk communication. Health authorities have often needed to introduce ad-hoc nomenclature fixes. For example, during the 2009 H1N1 pandemic, the WHO avoided using geographic or species names and eventually standardized the term **A(H1N1)pdm09** (for “pandemic 2009”) to distinguish the novel human strain from endemic H1N1 viruses and to avoid the misleading term “swine flu” [9]. This change, implemented in 2011, required global coordination but came only after initial confusion. It highlights the need for a proactive naming framework that inherently carries epidemiological meaning, rather than relying on retroactive corrections.

### 1.3. Historical Pandemic Nomenclature

Historical influenza pandemics illustrate how naming conventions have evolved with changing technology. We have reached a point to require a new approach that incorporates epidemiology and transmission dynamics into influenza nomenclature. In the pre-molecular era, history has named pandemics after geographic locations or popular attributions, which bore little relation to the virus’s true origin or characteristics:

- **1889–1890 “Russian Flu”:** The pandemic of 1889, one of the last great pandemics of the 19th century, was nicknamed the “Russian flu” (also “Asiatic flu”) because early reports came from St. Petersburg, Russia. This outbreak caused an estimated 1 million deaths worldwide [10]. There was debate over the etiologic agent – some evidence pointed to an influenza A virus of the H3N8 subtype, while others suspected a coronavirus [11]. Lacking virological information in 1889, the adoption of “Russian flu” presumed a geographic origin. Not surprisingly, the label “Russian flu” did nothing to describe the virus’s behavior; the pandemic spread globally regardless of its Russian association. The use of a place-name also risked stigma, although in this case the term has become primarily historical.
- **1918–1920 “Spanish Flu” (H1N1):** The infamous 1918 pandemic [12] was commonly called the Spanish flu, not because it originated in Spain (in fact, the first known cases were in the United States in early 1918), but because Spain, being neutral in World War I, openly reported on the outbreak while warring nations censored news to maintain morale. The name “Spanish flu” thus reflected political circumstances rather than virology. This pandemic infected roughly one-third of the world’s population and killed an estimated 50 million people, making it the deadliest influenza pandemic on record [13]. The etiologic agent was later identified as an H1N1 influenza A virus. All eight genomic segments of the 1918 virus have since been sequenced from preserved specimens, revealing an avian-derived influenza virus that adapted to humans [14]. However, back a hundred years ago in 1918 people had no conception of subtypes or transmission dynamics – the virus was unnamed except by the misnomer. The term “Spanish flu” provided no useful information on how the virus spread or which populations were at risk, and it unfairly linked the disease to Spain. Modern analyses have shown that the 1918 H1N1 virus became the progenitor of all later influenza A pandemics, but contemporary nomenclature did not capture any of this critical information.
- **1957–1958 “Asian Flu” (H2N2):** The 1957 pandemic came from a novel H2N2 virus that arose from reassortment between an avian influenza virus and the previously circulating human H1N1 strain [15]. It was termed the “Asian flu” because it was first identified in East Asia (with early outbreaks in China and Hong Kong). This pandemic was milder than 1918 but still caused an estimated 1–2 million deaths worldwide. Virologists at the time were able to identify the new H2N2 subtype using serological methods, a significant advance in influenza science and hence the name “Asian H2N2” [15]. While the subtype indicated a new antigen against which few people had immunity, the geographic moniker “Asian” again failed to convey the critical change that made this pandemic possible—the introduction of an avian HA and NA into the human population. Moreover, the name may have contributed to bias or complacency outside of Asia,

despite the virus spreading globally within months. The naming did nothing to highlight the virus's high human transmissibility, which was the key reason it became a pandemic.

- **1968–1970 “Hong Kong Flu” (H3N2):** The 1968 pandemic, caused by an H3N2 virus, named Hong Kong flu, where the virus was first reported in July 1968 [16]. The H3N2 strain emerged through reassortment of the 1957 H2N2 virus with an avian virus (introducing a new H3 HA gene while retaining the N2) [17]. The “Hong Kong flu” caused around 1 million deaths worldwide (some estimates range up to 4 million) and was the least severe of the 20th-century pandemics. By 1968, influenza science had advanced enough that identifying the subtype H3N2 by its surface antigens was possible (often referred to in scientific contexts as “Hong Kong H3N2”). However, public communications still centered on the geographic label. Associating the disease with Hong Kong potentially stigmatized that region and gave a false impression that the threat was localized [18]. In reality, the virus spread internationally within weeks, reaching the United States by that same year. The H3N2 virus became established as a human seasonal strain (replacing H2N2) and continues to circulate today [17]. Knowledge of its efficient human transmission and mild-to-moderate virulence was far more relevant to public health than its geographic origin, yet the name did not reflect those aspects.

These historical examples show a pattern of influenza pandemics being named in ways that emphasize origin or locale (Spanish, Asian, Hong Kong, Russian) rather than the virus's transmissibility or host adaptation [19]. Such names often arose colloquially and stuck due to convenience, but they lack scientific precision and can mislead or stigmatize. In the modern era, virologists do assign subtype designations (e.g., H1N1, H3N2) as was done in 1957 and 1968 (which was a step forward), but subtype alone still conveys limited information about a strain's current epidemiological behavior. For instance, there have been multiple distinct H1N1 influenza pandemics or epidemics (1918, 1977, and 2009) and numerous H3N2 variants; the subtype label doesn't distinguish these in terms of transmission dynamics [20].

**Need for a New Approach:** The inadequacies of historical nomenclature have become evident in recent years. WHO and other bodies now discourage the use of geographic names for new pathogens to avoid stigma (as seen with the naming of COVID-19 variants Alpha, Beta, etc., instead of country names) [21]. Influenza strain naming, however, remains largely rooted in mid-20th-century conventions. Given our improved understanding of influenza ecology, evolution, and the One Health context (the intersection of human, animal, and environmental health), it is timely to refine influenza nomenclature. In particular, incorporating transmission dynamics and host adaptation status into virus names could provide immediate insight into the public health risk a strain poses. In the sections that follow, we explore how the current classification systems for influenza operate, why they fail to capture these dynamic properties, and how a transmission-based naming framework can address these gaps.

## 2. Existing Influenza Virus Classification Systems

Current influenza classification and naming conventions broadly delineated by (a) **phenotypic subtype classification** based on surface proteins, and (b) **host-based classification**. Both used often in scientific and public health communications, typically alongside the standardized strain-naming format described earlier. We review these approaches here to highlight their scope and limitations.

### 2.1. Surface Protein Classification

The accepted convention for classifying influenza A viruses is by their surface glycoproteins: hemagglutinin (H or HA) and neuraminidase (N or NA). As noted, there are multiple HA and NA subtypes, and an isolate is typically referred to by the combination of these, such as H1N1, H3N2, H5N1, etc. This system is useful because the HA and NA are major antigenic determinants; a population's immunity and vaccine design largely focus on these subtypes. For example, the seasonal

flu vaccine might include an H1N1 and an H3N2 strain, referring to the HA/NA of circulating human viruses [22].

Subtype nomenclature readily conveys certain information, especially if only one or a few hosts are involved. For instance, subtype H5N1 is immediately associated with highly pathogenic avian influenza in birds (with occasional human infections), whereas H3N2 is associated with milder, sustained human circulation since 1968. Subtyping also facilitates rapid risk assessment when novel strains emerge; the appearance of an H7 or H5 infection in humans triggers concern due to the known virulence of such subtypes in birds [23].

However, subtype classification alone has significant limitations. There are 18 HA and 11 NA subtypes identified (mostly in birds), theoretically yielding 198 combinations, many of which remain undiscovered in nature. Conversely, viruses of the same subtype can vary greatly in host range and virulence. A case in point is H1N1: this subtype encompasses the 1918 pandemic virus, the 2009 pandemic virus, and various swine and avian strains – a range of viruses sharing the same H1N1 subtype but with very different behaviors. Similarly, H3N2 could refer to a human seasonal flu virus or an avian strain in ducks. Subtyping does not capture these distinctions [1,24].

The subtype-centric naming can also lead to public confusion. The term “H1N1” became infamous during the 2009 pandemic (and is still often labeled “swine flu” today, in 2025). Yet there were H1N1 viruses circulating in humans long before 2009, and others that continue to circulate. In fact, after 2009, both the old seasonal H1N1 (pre-2009 lineage) and the new pandemic H1N1 co-circulated for a time, which required researchers to differentiate them as **H1N1pdm09** vs. **H1N1 (seasonal)** [26]. The average person hearing “H1N1” cannot distinguish between these strains in circulation.

Another element of subtype-based naming is the pathogenicity designation in avian hosts. H5 and H7 avian influenza viruses designated further as **highly pathogenic (HPAI)** or **low pathogenic (LPAI)** based on molecular traits and disease severity in chickens [27]. For example, H5N1, assumed usually as highly pathogenic when discussed. Yet this too is context-specific: H5N1 in a wild bird reservoir [28] might be low pathogenic until it mutates in domestic poultry. Hence, the name “H5N1” by itself does not indicate pathogenicity or transmissibility.

In summary, surface protein classification (H & N) is a necessary component of influenza nomenclature—maintained as a foundational layer in our proposed system—but it addresses primarily the virus’s antigenic identity (important for immunity and virology) rather than its transmission or host-adaptation status. Our analysis suggests that combining subtype information with transmission dynamics in nomenclature could greatly enhance the utility of virus names.

## 2.2. Host-Based Classification

Another traditional way to label influenza viruses is by their host of origin. Terms like “avian influenza,” “swine influenza,” “equine influenza,” and “human influenza” use host descriptors to denote the species in which a virus is currently circulating [29]. This classification stems from the ecology of influenza A: certain subtypes are associated with particular hosts (for example, H3N8 in horses [30,31] and dogs [32]; H1N1 and H3N2 in humans and swine [33]). In research literature and surveillance reports, one often sees tags such as “LPAI H7N9 (avian)” [34] or “variant H3N2 (swine-origin)” [35].

While host labels can be convenient shorthand, they are frequently messy in practice due to cross-species transmission. Influenza viruses do not always respect species boundaries [36]. Swine, for example, are susceptible to avian and human influenza strains and can serve as “mixing vessels” for reassortment. A virus might originate in one species and then adapt to another. The current naming system accounts for the initial host in the strain name (e.g., A/duck/... or A/swine/... if not human), but once a virus becomes established in a new host, the original host-based name may become misleading because a new reservoir host is now sustaining transmission.

A clear illustration is the 2009 H1N1 pandemic virus. It was the product of reassortment among influenza viruses from swine, birds, and humans, and had likely been evolving in pigs for years

before spilling over to humans. However, H1N1pdm09 initially dubbed a “swine flu”, because genetic analysis showed swine lineage origins and early media reports tied it to pig farms—even though from the start, the virus was isolated from humans and spreading widely in humans. It quickly became a predominantly human virus [37]. Calling it a swine flu strain after mid-2009 was inaccurate in terms of ongoing transmission – by then it was a human pandemic strain [38,39]. The host-based label stuck in the public consciousness and caused significant issues: some countries banned pork products and unjustifiably culled pigs, and people were confused about food safety, even though the virus was being transmitted person-to-person [40,41]. The WHO’s adoption of the term **A(H1N1)pdm09** was partly to rectify this issue [9,42,43]. This example underscores how a virus can leap from one host to another, rendering the original host label obsolete or even harmful for communication.

Another example is H5N1 avian influenza. H5N1 was first recognized in 1997 in Hong Kong’s poultry (with some human infections) [44,45], and it re-emerged in 2003 to spread epizootically in birds across Eurasia and Africa. It is often called “bird flu” because it primarily affects birds and poultry. However, H5N1 has infected hundreds of humans (often with severe outcomes), as well as various mammalian species (cats, tigers, seals, etc.). In recent years, the H5N1 clade 2.3.4.4b virus has caused infections in a wide range of mammals, including outbreaks in farmed mink and wild mammals [46]. If H5N1 were to mutate to sustain transmission in mammals or humans, the label “avian influenza” would no longer be appropriate. We would need to quickly signal that the virus is no longer just a bird threat. Current practice would be to note this in prose (e.g., “H5N1 adapted to mammals”), but the nomenclature itself does not change unless a completely new subtype or strain name is assigned.

Host-based naming also struggles when influenza viruses circulate in multiple species simultaneously. Influenza A typically has reservoirs in wild birds [47], but many strains have jumped to domestic poultry, swine, horses, dogs, etc. [48,49]. For instance, an H3N2 lineage that originated in birds jumped to pigs and humans (the 1968 pandemic strain in humans, which later even jumped to dogs) [50]. Similarly, certain H1N1 and H3N2 viruses circulate endemically in swine herds and occasionally infect humans (these are termed variant viruses, like H1N1v or H3N2v). In those cases, what do we call the virus? If it’s in pigs we might say “swine H3N2,” and if it infects a human we say “variant H3N2,” but genetically it can be nearly the same virus. The label changes with the host context, which can be confusing if not carefully explained.

In summary, host-of-origin terminology is a double-edged sword: it highlights the ecological source of a virus (important for veterinary and One Health contexts), but it can become misleading if the virus expands beyond that host. A more dynamic naming system would update the host descriptor when a virus establishes sustained transmission in a new host. Our proposed transmission-based nomenclature (see Section 4) aims to do exactly that – for example, an “H5N1-Avian” could become “H5N1-Mammal” if evidence of sustained mammalian spread emerges. In this way, the name itself would keep track of the virus’s host adaptation status.

Before detailing the proposal, we first summarize the key limitations of the current nomenclature approach that motivate the need for change.

### 3. Limitations of the Current Nomenclature System

Under the status quo, influenza nomenclature provides static labels that often fail to convey epidemiologically significant information. The main shortcomings are: (a) static attributes are emphasized over dynamic behavior, (b) host labels can be misleading, and (c) public health communication is hampered.

#### 3.1. Static Attributes

The current system labels viruses based on their genetic subtype and initial isolation context, which remain fixed even as the virus spreads and evolves. This static approach neglects the changing transmission dynamics and phenotypic behavior of the virus. For instance:

### 3.1.1. Geographic and Historical Emphasis

Including a place name in the virus's label (e.g., "Asian flu" for H2N2, "Spanish flu" for H1N1) may provide a sense of origin, but it lacks information on the current situation and can even be misleading. Such labels may stigmatize regions without offering any insight into the virus's present threat level. A person hearing "Asian flu" learns nothing about how contagious or virulent the virus is, or whom it is primarily affecting.

### 3.1.2. Genetic Ancestry vs. Current Behavior

Modern strain names often incorporate clade or lineage markers (for example, "**A(H5N1) clade 2.3.4.4b**" or "**A/California/07/2009 (H1N1)**"), which reflect genetic relationships. While valuable for scientists tracing evolution, these designations do not indicate whether the virus is spreading efficiently in humans or other hosts at that time [51]. A name locked to genetic identity can quickly become outdated in meaning. For example, H7N9 in 2013 was labeled as an avian-origin virus, yet five years later thousands of human infections had occurred, mostly via widespread poultry-to-human transmission [52,53]. The genetic label remained the same even as public health concerns grew.

### 3.1.3. No Temporal Component

Other than the strain's isolation year (which is used in full strain names), there is typically no indication of time in influenza naming. Thus, the nomenclature doesn't readily distinguish a **2009-era "swine flu" H1N1 virus** from a **2019 descendant** of the same lineage. In contrast, epidemiologists often have to introduce terms like "seasonal H1N1 (2015)" vs. "pandemic H1N1 (2009)" to clarify which virus they mean. A more dynamic system might include temporal markers to denote when a major host-transition event occurred (e.g., adding the year a virus adapted to humans).

Influenza viruses are moving targets – they mutate, reassort, and adapt (for example, H5N1 adapting to infect dairy cattle and mink in recent outbreaks) [54]. A static name captures them like a snapshot, potentially missing the "movie" of their spread. This can lull observers into a false sense of familiarity ("oh, it's just H5N1; we've seen that for years") when in reality the risk profile may change if a virus breaches new species barriers or gains transmissibility. The nomenclature needs to be more fluid to reflect such shifts.

## 3.2. *Misleading Host Labels*

As discussed, naming by host origin can be problematic when a virus jumps hosts. The nomenclature often fails to distinguish between a virus's historical origin and its current main host, leading to confusion:

### 3.2.1. Persistence of Origin Labels

The 2009 H1N1 example shows how the "swine flu" label persisted even after the virus became a human pandemic strain. Similarly, the influenza research community still refers to the **1918 virus** as an "avian-like H1N1," yet in 1918 it was obviously a human epidemic. The label emphasizes where it came from (historical host = birds), not where it is (current host = people). In day-to-day public health usage, we did not give the 1918 virus an updated name like "human-adapted H1N1" at the time—it was only later characterized as such in retrospective research. This lag in language can affect how seriously the public and policymakers take emerging infections. If H5N1 were to start spreading easily among people, continuing to call it "avian influenza H5N1" might downplay the new reality that it has evolved into a human epidemic.

### 3.2.2. Conflation of Distinct Strains

Host labels can cause different viruses to be conflated. For example, **H1N1 in swine** (classic swine flu) versus **H1N1pdm09 in humans** are distinct lineages, but the shared "swine" association

caused public misunderstanding. Another case is the generic term “bird flu,” which has been applied to both H5N1 and H7N9 (among others). If someone says “bird flu outbreak,” it could refer to very different viruses with different human risk levels. Yet the host-oriented name obscures the distinction. During 2013–2017, China experienced hundreds of human infections with H7N9 avian influenza – a situation quite distinct from H5N1 “bird flu” in other countries. A layperson will not grasp this nuance from names alone.

### 3.2.3. Zoonotic vs. Sustained Transmission

It is critical to distinguish a virus’s true pandemic risk by whether it is merely causing zoonotic infections or has achieved sustained human-to-human transmission. Current nomenclature does not encode this difference. For instance, both H5N1 and H1N1pdm09 have at times been called broadly “avian influenza” or “swine influenza,” but H1N1pdm09 achieved efficient human transmission ( $R_0 > 1$  in humans) whereas H5N1 has not (only rare small clusters). Without additional explanation, the public might think “bird flu” in 2006 (H5N1) and “bird flu” in 2013 (H7N9) were similar scenarios, yet in reality neither involved sustained human-to-human spread – H5N1 remained a bird-to-human spillover threat, and H7N9 was largely a zoonotic epidemic tied to poultry markets [53]. A naming scheme that explicitly tags a virus as, say, “H7N9-Avian” indicates its primary host context (birds). Hypothetically, if H7N9 began spreading between humans, it might be renamed “H7N9-Human.” Such clarity is missing in our current static labels.

### 3.3. Public Health Communication Challenges

Because of the above issues, the current nomenclature can impede effective communication and timely response:

#### 3.3.1. Stigma and Concealment

Countries might hesitate to report novel viruses if they fear being permanently associated with a pandemic (the “Spanish flu” effect). A neutral, behavior-based naming system could reduce this disincentive by not embedding a location in the public name. Instead of “Country X flu,” a name could focus on the host or transmission mode (e.g., “avian-to-human flu 20XX”), which is less stigmatizing and more descriptive of the situation. Transparency in reporting outbreaks is essential, and naming conventions should facilitate rather than hinder it.

#### 3.3.2. Public Misunderstanding

The public often has limited scientific knowledge of influenza. If names are misleading, people may under- or over-estimate the threat. For example, the term “**low pathogenic avian influenza**” (LPAI) refers to pathogenicity in birds, but a strain that is LPAI (mild in poultry) can still infect and severely harm humans (as H7N9 did). Someone might falsely assume “low pathogenic” means it’s not dangerous to anyone. Likewise, during the 2009 pandemic, some people avoided pork products due to the term “swine flu,” despite there being no risk of infection from properly cooked pork – a costly misunderstanding for agriculture. A well-designed nomenclature could improve risk communication by immediately conveying the nature of spread (e.g., “human-transmissible flu strain”) rather than a possibly irrelevant origin.

#### 3.3.3. Policy and Response Delay

Public health measures often rely on clearly recognizing a virus’s status. If the name does not make it obvious that a virus has switched from animals to people, officials might delay interventions. Consider how quickly we would react to reports of “**sustained human H5N1 influenza**” versus just “**H5N1 avian influenza cases.**” The former phrasing (which a transmission-based nomenclature would inherently provide) triggers a sense of urgency. The latter might sound like the familiar

sporadic bird-to-human events we've seen for years. Thus, a dynamic naming system could prompt swifter responses when a virus meets criteria for higher pandemic risk.

In summary, current influenza naming conventions, while deeply entrenched and useful for virological documentation, suffer from inflexibility and lack of epidemiological context. These limitations can obscure critical changes in a virus's behavior and impede clear communication. The following section introduces a proposed framework to address these issues by incorporating transmission dynamics into the nomenclature.

#### 4. Proposed Framework: Transmission-Based Nomenclature

To enhance influenza nomenclature, we propose a framework that retains essential virological information (such as subtype and origin) but **adds transmission dynamics and host adaptation status** as key elements of the name. The goal is a system in which the name of the virus evolves in tandem with the virus's demonstrated behavior, especially with regard to which host(s) are sustaining transmission.

##### 4.1. Core Principles

The transmission-based nomenclature framework rests on four core principles:

1. **Dominant Host Adaptation:** The naming should reflect the current primary host in which the virus is spreading sustainably. In practical terms, this means identifying the host species or category where  $R_0 > 1$  (i.e., the virus can maintain chains of transmission). For example, if an H5N1 virus is initially circulating in birds ( $R_0 > 1$  in bird populations) and only sporadically infecting humans ( $R_0 \sim 0$  in humans), it would be labeled with an **"-Avian"** marker. If it later adapts to enable efficient human-to-human transmission ( $R_0 > 1$  in humans), the host marker in the name would switch to **"-Human."** This principle ensures the name always points to the epidemiologically most relevant host. It is important to define host categories broadly (e.g., human, avian, swine, equine, or potentially a general "mammalian" category for non-human mammals) for simplicity.
2. **Dynamic Updates:** Updating of host descriptors happens only upon significant changes in transmission dynamics, not for minor or transient events. In other words, nomenclature changes are triggered by clear evidence of sustained transmission in a new host or a fundamental change in the virus's behavior, rather than every small cluster or mutation. This avoids instability in naming. Once a virus is shown to establish a self-sustaining transmission cycle in a new host population, it merits a naming update. However, the original name and classification can be retained in scientific records for continuity. An updated name signals to public health that "this is effectively a new phase" for the virus. If multiple hosts maintain the virus in parallel (e.g., some influenza strains co-circulate in pigs and humans), the naming could include both or could default to the host representing the greatest public health concern (perhaps using a hierarchy like Human > other mammals > birds, since a human-adapted virus usually implies the highest pandemic risk).
3. **Integration with Genetic Data:** The scheme will still retain subtype and other genetic identifiers as needed, but these will not be the sole focus of the public-facing name. Genetic nomenclature (like clade numbers or lineage names) can be appended or kept in parenthetical notation for scientists. For example, a full name might be **"H7N9-Avian (Yangtze River Delta lineage)"** to satisfy both needs. Crucially, however, the primary name used in public communication would be the transmission-based one, emphasizing that H7N9 is currently an avian virus, while detailed genetic info is secondary. This integration ensures that valuable molecular data is not lost—researchers can still trace origins and relatedness—but by not prioritizing genetic lineage in the primary name, we reduce confusion for policymakers and the public, focusing their attention on what matters for control (how and where the virus is spreading now).

4. **Transparency and Clarity:** The naming system should incorporate temporal markers or neutral geographic markers when relevant to track epidemiology, but do so in a way that avoids blaming specific regions. For instance, using the year of emergence or host switch can provide a time reference (as done with “pdm09” for the 2009 pandemic). If needed, broad regional terms might be used without stigma – e.g., “**H5N1-Mammal-Europe2022**” could denote a mammalian-adapted H5N1 first noted in Europe in 2022, without singling out a particular country. However, any geographic element would be included only for context and not as a core part of the virus’s identity. The priority is clarity about what the virus is doing. Thus, the naming framework strives to be unambiguous and easily interpretable: anyone reading the name should be able to glean the subtype, the primary host of spread, and possibly a timeframe indicator, all of which are directly relevant to risk assessment.

These principles collectively aim to produce names that are scientifically sound yet adaptable. The system acts almost like an annotation of the virus’s status: as the virus evolves, so does its nomenclature classification. This is analogous to how storm naming escalates (tropical depression → tropical storm → hurricane categories) to signal changing status—except here the progression is in virological and epidemiological terms.

#### 4.2. Illustrative Implementation of Transmission-Based Naming

To make the proposed framework more concrete, we provide examples of how it could be applied to known influenza A viruses. These examples demonstrate the naming conventions and the conditions under which names would update:

##### 4.2.1. Example 1: H1N1pdm09 (2009 Pandemic Strain)

*Initial name:* When the virus emerged in 2009, it should have been named “**H1N1-Human-2009**” (or simply *H1N1-Human (2009)*), reflecting that it was a novel H1N1 sustaining human-to-human transmission starting in 2009. This emphasizes the virus’s pandemic spread in humans. Indeed, the virus quickly became the dominant human seasonal flu strain after 2009. *Rationale:* The virus demonstrated  $R_0 > 1$  in humans almost immediately in multiple countries. Under our system, the host descriptor “-Human” indicates this is a human-transmissible strain. The inclusion of “2009” as a temporal marker distinguishes it from other H1N1 variants. (In practice, WHO named it A(H1N1)pdm09, which is very similar in concept—subtype plus a pandemic year tag. Our system formalizes this kind of designation.) *Updated name:* Considering its status today, it is still an H1N1 circulating predominantly in humans (as an endemic seasonal virus), so it would remain **H1N1-Human** in the nomenclature. If it were to hypothetically jump back into animals and form sustained lineages there distinct from the human strain, we might label those separately (e.g., **H1N1-Swine-201X** for a lineage derived from the 2009 virus now established in pigs). In fact, such spillback into swine has happened to some degree, though those viruses are often referred to as variant swine influenza [56].

##### 4.2.2. Example 2: H5N1 Highly Pathogenic Avian Influenza

*Initial name:* “**H5N1-Avian.**” For decades since its emergence, H5N1 has primarily circulated in birds, so the name conveys that the virus’s dominant host is avian. This covers the situation up to the present, where H5N1 is causing a global panzootic in wild birds and poultry. *Trigger for update:* If a particular H5N1 clade acquires the ability for sustained mammalian transmission (for instance, an H5N1 strain spreading efficiently among mink [57], or an outbreak in mammals with clear mammal-to-mammal contagion), the name could be updated to “**H5N1-Mammal**” (optionally with a year or clade notation, e.g., *H5N1-Mammal-2024*). This would immediately signal that H5N1 is no longer just a bird problem. If, furthermore, it started spreading among humans (and meets criteria for human adaptation), it would change to “**H5N1-Human.**” Not every single mammalian case would prompt a change – only evidence of sustained transmission in that new host. For example, the large H5N1

outbreak in a Spanish mink farm in 2022 suggested some mink-to-mink transmission [57], but whether it was sustained or just a one-farm event is still under study. One might wait for confirmation of onward spread beyond a single cluster. On the other hand, the ongoing spread of H5N1 in wild mammals (e.g., among seals in multiple colonies) [58,59] and even domestic dairy cattle [60,61] might prompt a “-Mammal” designation if shown to be widespread and self-sustaining. *Outcome*: At the time of writing, H5N1 remains principally avian, so it stays **H5N1-Avian**. If a change happens, the year of that shift could be appended (e.g., *H5N1-Mammal-2023* if that were the year it first sustained mammalian transmission). Genetic clade information (like 2.3.4.4b) might still be mentioned in scientific contexts but would not appear in the primary name.

#### 4.2.3. Example 3: H7N9 Avian Influenza

*Initial name: “H7N9-Avian.”* When H7N9 virus was first detected in humans in 2013 in China, it was traced to poultry sources [62]. Through 2017, H7N9 caused five epidemic waves in humans, totaling 1,568 laboratory-confirmed cases with ~39% mortality. However, nearly all those cases were due to repeated spillovers from infected chickens at live bird markets, not sustained human transmission. Under our framework, throughout that period H7N9 would retain the “-Avian” label because its propagation depended on birds (indeed, interventions like closing poultry markets sharply reduced human cases). *Trigger for update*: If at any point H7N9 had evolved to spread easily from human to human (signs of community transmission, clusters beyond households, etc.), the name would have switched to “**H7N9-Human**.” In reality, that did not occur; instead, H7N9 was largely controlled by a poultry vaccination program in 2017 and human cases dwindled. So H7N9 remains an avian virus in nomenclature. (If it ever re-emerges or if limited human-to-human spread is observed in the future, one might consider an intermediate label like “H7N9-Zoonotic” or “H7N9-Avian?” to denote uncertainty, but it’s probably better to reserve renaming for confirmed sustained transmission events to avoid confusion.)

These examples show that the naming would include the subtype (HxNy), a host marker (Human, Avian, Swine, etc.), and optionally a time or episode marker (year of emergence or host jump). The subtype informs about the virus’s virology, the host marker tells the current epidemiological context, and the time marker can differentiate separate emergences of what might nominally be the same subtype. For instance, **H1N1-Human-1918** vs **H1N1-Human-2009** would denote the two different H1N1 pandemics, which have distinct lineages, but the public-facing name makes clear they are separate events.

Under this system, the formal strain names (with exact strain IDs) remain for lab records, but public communications and high-level discussions would refer to the transmission-based names. The framework can also extend to influenza B (which only infects humans and seals — one could label lineages as Human or Seal if it ever became necessary) and potentially to other emerging viruses for consistency.

By adopting transmission-based nomenclature, we maintain clarity as viruses evolve. It is a proactive approach: rather than language lagging behind the virus (as happened when we added “pdm09” after the fact in 2009), the naming framework is built to update in step with key epidemiological shifts. This could significantly improve how scientists, officials, and the public perceive and respond to emerging influenza threats.

## 5. Case Studies Supporting the Proposed Framework

To further illustrate and validate the proposed transmission-based nomenclature, we examine three case studies in detail: the 2009 H1N1 pandemic (**H1N1pdm09**), the persistent avian influenza **H5N1**, and the zoonotic **H7N9** virus in China. Each case demonstrates particular challenges of the current naming system and shows how a transmission-focused name could provide clearer insight. We also draw on data and events associated with these viruses to underscore the importance of nomenclature that reflects transmission dynamics.

### 5.1. H1N1pdm09 (2009 “Swine Flu” Pandemic)

**Background:** The 2009 pandemic H1N1 virus emerged in April 2009 and swept across the globe within months. Genetic analysis revealed an extraordinary origin: it was a quadruple-reassortant virus combining gene segments from North American swine, Eurasian swine, avian, and human influenza lineages. Specifically, its HA, NP, and NS genes traced to a classical swine H1N1 lineage; its PB2 and PA genes to North American avian influenza; its PB1 gene to a human H3N2 virus (which itself had originally come from birds); and its NA and M genes to a Eurasian swine H1N1 lineage. This mosaic virus had been incubating in pig populations (likely in Mexico) for years before spilling over to humans around 2009.

When the virus first infected humans, it was quickly dubbed “swine flu” in the media because of its swine origins. However, within weeks it was clear that the virus was transmitting efficiently human-to-human in many countries – it had become a human-adapted strain. The continued use of “swine flu” caused public confusion and significant economic damage to the pork industry (as discussed earlier). Epidemiologically, H1N1pdm09 caused a pandemic with an estimated ~284,000 deaths in the first year (based on later CDC models, since many deaths were never lab-confirmed) and it disproportionately affected children and non-elderly adults. By August 2010, WHO declared the pandemic over, and the virus had become endemic as part of seasonal influenza. In hindsight, adopting nomenclature like “**H1N1-Human (2009)**” to reflect its sustained human circulation would have helped decouple it from the swine influenza misnomer. Indeed, this virus is still circulating today (2025) as one of the seasonal influenza A strains.

**Nomenclature Issues:** Initially, formal communications used names like “Influenza A (H1N1) 2009” and later “**A(H1N1)pdm09.**” These were fairly technical and not immediately adopted by the lay media, which stuck with “swine flu.” The host-based label misled some into thinking the virus was coming directly from pigs at the point of infection (that may have been true for some early human cases, but soon human-to-human transmission dominated). Also, once it became a seasonal strain after 2010, calling it “pandemic H1N1” was no longer appropriate, yet simply calling it “H1N1” could cause confusion with other H1N1 viruses. Essentially, we lacked a clear, simple name that indicated “a novel human-transmissible virus of swine origin.”

**How a Transmission-Based Name Helps:** Under our framework, as soon as it was determined that sustained human transmission was occurring (which was evident by May–June 2009), the virus would be labeled **H1N1-Human-2009** (which could be abbreviated in media as “2009 human H1N1”). This name directly conveys that it is an H1N1 influenza virus adapted to humans as of 2009. It avoids the term “swine” entirely, removing the implication about pigs, and instead highlights the important fact: it’s now a human epidemic. The year tag “2009” distinguishes it from any previous human H1N1 lineage. As the virus persisted in humans beyond 2009, the name **H1N1-Human** would continue to apply, perhaps with the year dropped once it was clearly an established endemic strain. If one needed to discuss historical context or differentiate it, the year could be included (e.g., “the post-2009 H1N1-Human virus”).

This naming would have been useful when, for example, scientists later discussed antigenic drift of the “pandemic H1N1” virus in the following years – they could have simply referred to the **human H1N1 lineage**. In fact, today we have two influenza A subtypes in seasonal circulation: H1N1 and H3N2, both adapted to humans. Calling them **H1N1-Human** and **H3N2-Human** in a formalized way might make it clearer that these are human-adapted strains, as opposed to the many H1N1 or H3N2 variants existing in animals.

To summarize this case: H1N1pdm09 demonstrates that once a virus makes the jump to sustained human transmission, the nomenclature should promptly reflect that shift. A transmission-based name would have improved public understanding and reduced misnomers. It also highlights that such a name can remain relevant long after the initial event (as that virus became a new seasonal lineage).

## 5.2. H5N1 (“Avian Influenza” with Pandemic Potential)

**Background:** Influenza A(H5N1) first gained worldwide attention in 1997, when an H5N1 highly pathogenic avian influenza (HPAI) virus in Hong Kong infected 18 people, killing 6. After aggressive poultry culling ended that outbreak, H5N1 resurfaced in 2003 and spread epizootically across Asia, Europe, and Africa, becoming entrenched in poultry in many countries. From 2003 through 2021, the WHO documented 863 human H5N1 cases with 455 deaths, an exceptionally high average case fatality rate (~53%). Nearly all these cases were due to direct contact with infected birds – human-to-human transmission was extremely rare and self-limited. H5N1 thus became the poster child of a deadly zoonotic virus that had **not yet achieved person-to-person spread**. Scientists and public health officials have long been concerned that H5N1 could mutate or reassort to gain transmissibility among humans, potentially causing a severe pandemic.

In late 2021, a new chapter began: H5N1 clade 2.3.4.4b, which had been circulating in birds, sparked a panzootic in wild birds and poultry across multiple continents. This led to unprecedented numbers of outbreaks in wild birds and domestic flocks. With so many viruses in circulation, spillovers into mammals started occurring more often. Since 2022, H5N1 has infected an array of mammalian wildlife (foxes, mink, skunks, dolphins, bears, seals, etc.), likely through predation or scavenging of infected birds. Notably, an outbreak in a Spanish mink farm in late 2022 suggested that the virus may have spread between mink (mink-to-mink) after an initial introduction. In early 2023, Peru reported over 600 sea lion deaths associated with H5N1, again raising alarms that mammal-to-mammal transmission might be happening in colonies of animals with close contact. Additionally, H5N1 was detected in early 2024 on several dairy cattle farms in the United States, with evidence pointing to cow-to-cow transmission (a completely unexpected host for avian flu). These events have not yet led to efficient human-to-human transmission, but they indicate the virus is **expanding its host range** in the animal kingdom.

Human cases of H5N1 remain very sporadic; a handful of cases (often single isolated infections or small family clusters) occurred in 2022–2023 in Asia and one in 2023 in South America (Ecuador), mostly involving high-risk exposure to birds. No sustained human spread has been observed to date. The risk to the general public is still considered low, but the situation is closely monitored by organizations like the U.S. CDC and the WHO.

**Nomenclature Issues:** H5N1 has almost universally been termed a “**bird flu**” or “**avian flu**.” This is accurate in that birds are the reservoir and main transmission host. However, with the virus now jumping into mammals at an unprecedented scale, the blanket “avian flu” term may obscure the growing risk. If we wait until human transmission is detected to change how we refer to H5N1, we might be too late in galvanizing certain preparedness steps. Also, multiple variants of H5N1 exist across different genetic clades, but they are all simply called H5N1, so discussions often have to specify clade or region to avoid confusion (e.g., “H5N1 clade 2.3.4.4b in mammals” versus “H5N1 clade 2.2 in Egypt,” etc.).

**How a Transmission-Based Name Helps:** In a transmission-based framework, as of 2023 we would label the circulating strain as **H5N1-Avian** (since birds are the sustaining host). We would continue to monitor mammalian clusters closely. The moment evidence meets a defined threshold for sustained mammal-to-mammal transmission (for example, a certain number of non-contained outbreaks among mammals, or a calculated  $R_0 > 1$  in a mammalian species), we would update the name to **H5N1-Mammal-(Year)** for that lineage. For instance, the outbreaks in mink and sea lions in 2022–2023, if confirmed as ongoing mammal-to-mammal transmission, could justify an “**H5N1-Mammal-2022**” designation for that specific context. If the virus then adapts further to humans (a scenario we fear but have not yet seen), any sustained human transmission would trigger a renaming to **H5N1-Human**.

Such naming would make communications more precise. Officials could say, “We now have H5N1-Mammal strains identified, which signals the virus has adapted to at least some mammalian species – we are escalating preparedness.” This could correspond, for example, to initiating human vaccine seed strain development for that lineage. If, unfortunately, H5N1 ever shows person-to-

person spread in a community, calling it **H5N1-Human** immediately frames it as a pandemic threat requiring aggressive containment. It would distinguish that scenario from the decades of referring to H5N1 as a zoonotic avian flu. Additionally, by encoding the year of adaptation, we help researchers track evolutionary events. (It is conceivable that multiple distinct H5N1 mammalian adaptations could occur in different places/times – each might get its own label like *H5N1-Mammal-2024A* vs *2024B* if needed.)

In the meantime, while H5N1 remains an avian virus with only sporadic spillover, the name **H5N1-Avian** reinforces that the primary risk is via contact with infected birds. It also hints at the control strategy – namely, that controlling the virus in birds is key to reducing human risk. If that name were to change, it would serve as a red flag that our priorities must shift to containing it among mammals or humans. In this way, nomenclature would be aligned with action.

### 5.3. H7N9 (*Avian Influenza with Limited Spillover*)

**Background:** H7N9 influenza virus emerged in China in 2013 as a low-pathogenic (in birds) virus in poultry that caused severe illness in humans. Over the next few years, it caused annual winter epidemics linked to live bird markets. By 2017, H7N9 had evolved into a highly pathogenic form in birds, leading to even larger outbreaks in poultry and more human cases in the fifth wave (2016–2017). Cumulatively, as noted, H7N9 infected over 1,500 people and killed about 600 [53,55]. Its case fatality (~39% among hospitalized patients) was extremely high, though there may have been undetected mild cases. Importantly, H7N9 did **not** transmit easily between humans; most human cases were isolated or, at most, in small family clusters. The Chinese government's introduction of a poultry vaccination program in late 2017 dramatically reduced H7N9 incidence. After 2019, no new human cases have been reported, and H7N9 is presumed controlled, at least for now.

H7N9 remains notable for pandemic planning because it showed that an avian virus could adapt well enough to infect humans in large numbers while still not achieving full human transmissibility. It's a reminder that the barrier between efficient zoonotic infection and sustained human spread is a critical tipping point in pathogen evolution.

**Nomenclature Issues:** Throughout the event, H7N9 was known simply as “H7N9” or “avian influenza H7N9.” Early on, officials often referred to it as a “novel avian influenza A(H7N9) virus,” highlighting that it was of avian origin and new to humans. After a few years, however, it wasn't “novel” anymore. All human cases were clearly linked to poultry exposure, so one might argue the name was adequate during the outbreak. However, as years passed, the public could lose sight of the fact that this remained a bird virus and not a human-to-human virus. It also co-existed with H5N1 in some regions, leading to media confusion at times (two different “bird flu” threats simultaneously). If H7N9 had ever started spreading in people, we would have had to adjust how we talk about it yet again.

**How a Transmission-Based Name Helps:** Initially—and indeed throughout its known course—**H7N9-Avian** would be the designation. This asserts that birds (specifically chickens in live markets) were the reservoir sustaining the virus. Public health messaging can then emphasize controlling the virus in poultry to stop human cases. If evidence had emerged of sustained human transmission (for example, a sizable cluster not linked to a market, or signs of community spread), an update to **H7N9-Human** would signal a dire change. In reality, that never happened, so a change in nomenclature was unnecessary. In a sense, the fact that the name remained H7N9-Avian communicates that despite numerous human cases, the virus never established a foothold in humans; it **always** required the avian source. This helps maintain focus on the true source of risk.

One might consider whether H7N9 needed any temporal or geographic marker in its name. Since it was essentially one protracted outbreak in one country (all cases in China from 2013–2018 [63] by a particular lineage), an extra label was not really necessary. Had it spread significantly to other countries, perhaps something like **H7N9-Avian-China** could be contemplated, but we prefer to avoid geographic terms if possible. The year of emergence (2013) could be included as H7N9-Avian-2013 to distinguish it from other purely avian H7N9 strains elsewhere (there are other H7N9

viruses circulating in birds globally that never infected humans). However, to keep names short, it's reasonable to omit the year unless needed for clarity.

In summary, H7N9's case reinforces that the absence of a host update in naming (remaining "-Avian") is itself informative under our system. It means public health interventions should focus on the animal source, and that sustained human-to-human spread never became a feature of that virus. This conservative approach ensures that the nomenclature, while dynamic, does not fluctuate unnecessarily or cause confusion with too-frequent changes. Not every zoonotic virus will get a new label—only those that truly shift their transmission mode.

These cases illustrate the limitations of static nomenclature and underscore the necessity of dynamic classification frameworks that evolve with real-time transmission data. A transmission-based nomenclature is feasible and advantageous. In each instance, it either clarifies the situation retrospectively or would have improved communication during the event. H1N1pdm09 shows how quickly a name might need to change (within weeks) when a species jump happens.

## 6. Implications of Transmission-Based Nomenclature

Adopting a transmission dynamics-based naming system for influenza viruses has implications for science, public health, and policy. It could influence how we prioritize research, how vaccines are developed, and how the public perceives different influenza threats. In this section, we explore key areas where a transmission-based nomenclature could add value or change current practices, specifically in enhancing vaccine development and improving public health communication. We will also touch on implications for global surveillance and intersectoral collaboration, which are expanded upon in Section 7 (implementation strategies).

### 6.1. Enhancing Vaccine Development

Influenza vaccine strain selection is a process that must anticipate which strains will be predominant in the upcoming season or could cause a pandemic [64–66]. A naming system that highlights which host a virus is adapted to can provide guidance for these decisions. For example, if a virus is labeled "-Human," that flags it as a current threat to humans and a candidate for inclusion in vaccines or for pandemic stockpile efforts. Conversely, a virus labeled "-Avian" or "-Swine" might not warrant a human vaccine unless it shows signs of moving toward humans.

Take H5N1: if one day we have an **H5N1-Human** strain, it would be immediately obvious that developing or updating an H5 vaccine for humans becomes urgent. In the current system, H5N1 is already recognized as a potential pandemic strain, but the nomenclature does not differentiate between the H5N1 causing poultry outbreaks versus a hypothetical H5N1 that has adapted to people. Transmission-based naming would make that distinction explicit and immediate.

Another benefit is streamlining communication within the vaccine development community. Researchers working on a strain labeled "**H7N9-Avian**" know they are dealing with a zoonotic virus, which might warrant certain actions (e.g., creating and stockpiling vaccines in case it shifts, but not deploying them widely unless and until it does). If that virus were to become "**H7N9-Human**," it might then be considered for inclusion in seasonal flu vaccines in affected regions or trigger mass immunization campaigns. In other words, the name itself encapsulates the risk level. This clarity could also help with regulatory and funding decisions. For instance, releasing funds for vaccine development might be easier to justify when the virus carries a "-Human" designation, indicating a clear and present human health risk.

During the 2009 H1N1 pandemic, one challenge was that the virus emerged and spread so rapidly that by the time a vaccine was produced, the pandemic had already peaked in many places [67,68]. Part of the delay in recognizing the scope of the threat was initial confusion and mixed messaging; if an official label "H1N1-Human-2009" had been applied as soon as sustained transmission was verified, it might have more quickly signaled vaccine manufacturers to switch gears from seasonal to pandemic vaccine production. (In practice, they did pivot by June 2009, but clearer nomenclature could only have helped by removing ambiguity.)

Moreover, for seasonal vaccine updates, consider a scenario with multiple co-circulating strains of the same subtype, e.g. we may have simultaneous circulation of an **H3N2-Human** (the current endemic strain) and an **H3N2-Swine** that occasionally infects humans (as a variant). If the swine-derived virus starts increasing in prevalence in humans (but still isn't sustaining human transmission), our naming might temporarily label such isolates in humans as **H3N2-variant** or similar. If it crosses the  $R_0 > 1$  threshold to become human-adapted, it would be renamed **H3N2-Human-20XX**. Such clarity would immediately tell vaccine strain selection committees that a new human-adapted lineage has joined the mix and might need representation in the vaccine if it begins to compete with the older lineage.

In summary, transmission-based nomenclature provides a heuristic for vaccine targeting. It identifies which virus lineages are in which hosts, thereby guiding the strategic focus of vaccine research, development, and stockpiling. It complements genetic characterization with an extra layer of phenotypic relevance, essentially differentiating "**is this virus currently a human problem or an animal problem?**" – a key question for vaccine strategy.

## 6.2. Improving Public Health Communication

Perhaps one of the strongest arguments for transmission-based naming is the benefit to communication and public education. When an outbreak occurs, the public's understanding (or ignorance) of what is happening can influence everything from personal protective behaviors to acceptance of control measures. A naming system that inherently reduces confusion and conveys risk can improve the effectiveness of communication.

**Reducing Stigma and Panic:** By avoiding geographic names, the proposed nomenclature prevents the unfair blaming of regions or ethnic groups for a virus. It focuses attention on the true source of risk – the infected host species and the virus's mode of spread. This can make public messaging more factual and targeted. For instance, telling people "*H5N1-Avian is spreading in our poultry – avoid contact with sick birds*" is more precise than "*bird flu is here*," which might cause people to fear wild birds indiscriminately or, conversely, not realize that their backyard chickens are the real risk. Similarly, when COVID-19 variants were named by Greek letters instead of countries [69], it helped shift discourse away from finger-pointing and towards discussing the characteristics of the variants. We could see a parallel in flu: no more revival of "Spanish flu" or "Asian flu" terminology – instead, names like **H1N1-Human-1918** (when discussing the 1918 pandemic virus in hindsight), which are neutral and descriptive.

**Clarifying Transmission Risk:** A dynamic name would convey when a virus has become more dangerous to humans. If the public hears that an "*avian influenza*" has changed to a "*human influenza*" in its naming, that inherently warns them that person-to-person spread is now happening, and thus they might need to take precautions (like wearing masks or avoiding crowds, as advised by health authorities). Conversely, as long as it's "*avian influenza H7N9*," an informed member of the public understands that preventing infection involves avoiding poultry exposure, and that they won't catch it from a neighbor who hasn't been around birds. This could prevent both overreaction and underreaction. During the H7N9 outbreaks, there was worldwide fear that it might spark a pandemic, but there was also the understanding that it wasn't spreading in communities. Clear naming could reinforce that nuance: for example, health agencies repeatedly referring to it as "**H7N9 avian virus**" helped remind people that transmission was limited to bird exposures. If in a hypothetical scenario it had become "**H7N9 human virus**," that shift in terminology would have been a clear public alert.

**Media and Public Discourse:** The media often struggles with scientific nuance in the midst of an outbreak. For example, headlines might say "scientists fear bird flu may start a pandemic," which is not very specific. If instead the official language classifies viruses in terms of their transmission capability (not yet human-adapted vs. human-adapted), then reporters have a straightforward way to phrase their stories. They could say "*Currently H5N1 is labeled an avian virus, meaning it does not spread among people. Officials are watching closely in case it shifts to a human-adapted virus.*" This is easier for the public to follow and injects a clear scientific assessment into the coverage. It may also reduce

sensationalism, because the terms are somewhat technical but still understandable. The difference between a zoonotic threat and a human epidemic would be baked into the name, and thus naturally conveyed in reporting. During crises, consistent terminology is crucial – for example, the shift to calling the 2009 H1N1 strain “pandemic (H1N1) 2009” once it was established created consistency in official documents. A transmission-based scheme would similarly provide a consistent vocabulary, with terms like “human-adapted flu strain” appearing directly in the name.

**Education and Awareness:** Over time, if this nomenclature is adopted, the public may become more literate in the concepts of zoonosis and host jumps. People would get used to hearing terms like “mammalian-adapted flu” or “avian-origin flu” and understand the difference. This would be analogous to how terms like “variant” or “spillover” became commonly understood during COVID-19. As a result, it could become easier to explain why certain measures (culling chickens, vaccinating pigs, closing animal markets) are needed for an “avian” virus versus why travel restrictions or social distancing might be needed if it becomes a “human” virus. The name itself sets the context for the type of response required.

Overall, tying nomenclature to transmission dynamics yields *dynamic communication*: the name changes when the situation changes, ensuring that the name of the virus aligns with the message health authorities need to convey. This stands in contrast to static names that require additional explanations as the situation evolves (e.g., “Yes, it’s called swine flu, but now you can catch it from people, not pigs...”). By reducing those explanatory gaps, we can deliver information more efficiently and, hopefully, improve public compliance with recommendations. As noted by commentators, clear terminology is a critical part of public health transparency and trust.

Having considered the advantages in specific domains like vaccines and communication, we next turn to the practical aspects of making this nomenclature system a reality. In the final sections, we will discuss what changes in surveillance, policy, and collaboration would be required to implement transmission-based naming on a global scale, and provide recommendations for next steps.

## 7. Integration into Global Public Health and Surveillance Systems

Implementing a transmission-based influenza nomenclature in practice will require coordinated efforts across scientific, public health, and policy domains. Here, we outline strategies and recommendations for integrating this naming framework into global surveillance systems and pandemic preparedness activities. Key considerations include establishing clear criteria for renaming, ensuring transparency of data, achieving international consensus, and fostering cross-disciplinary collaboration (a One Health approach) to inform naming decisions. By proactively developing the infrastructure and agreements needed, the global community can be better prepared to adopt transmission-based names that improve pandemic response.

### 7.1. Strengthening Surveillance and Research to Inform Nomenclature

A transmission-focused naming system is only as good as the data that drive it. To determine *when* a virus has achieved sustained transmission in a new host (and thus merits a naming update), we need robust surveillance and research efforts:

#### 7.1.1. Enhanced One Health Surveillance

Influenza surveillance should explicitly integrate human, animal, and environmental health monitoring. Programs like the WHO’s Global Influenza Surveillance and Response System (GISRS) and veterinary networks under FAO/OIE (now WOAHA) must share data in real time. Surveillance in poultry, swine, wild birds, and even farmed wildlife or companion animals can provide early warning of viruses adapting to new hosts. For example, if a jump from birds to mammals is detected (as with H5N1 in mink or seals), veterinary authorities should alert public health officials immediately. Joint investigations can then assess if mammal-to-mammal transmission occurred. Surveillance protocols should define what evidence (e.g., multiple detections in the same species,

genomic changes associated with adaptation, etc.) would trigger considering a host category change for the virus's name. Strengthening lab capacity to sequence and characterize viruses from different hosts, and adopting a coordinated One Health surveillance strategy, are crucial.

#### 7.1.2. Transmission Studies and Thresholds

Crucial research includes identifying markers of sustained transmission. This involves field epidemiology (monitoring clusters and calculating  $R_0$  when possible) and laboratory studies (e.g., ferret transmission experiments to see if a virus can spread via respiratory droplets in a mammalian model). By correlating genetic changes with transmissibility data, scientists might predict when a virus is nearing a phenotypic shift. These findings should feed into risk assessments. A multidisciplinary expert group (virologists, epidemiologists, veterinarians, etc.) must regularly review emerging influenza strains and advise whether to trigger a nomenclature update. For instance, if unusual clusters of H7N9 without bird contact had appeared, this group would evaluate if criteria for adding the “-Human” designation were met. The establishment of formal criteria or a decision algorithm is necessary – for example: *“If  $R_0$  is estimated  $> 1$  in a new host, or there is confirmed sustained transmission beyond 1–2 generations in a non-reservoir host, then update the host label.”* These criteria should be internationally recognized so that naming decisions are transparent and based on scientific evidence.

#### 7.1.3. Data Sharing and Transparency

Open data sharing is fundamental. Countries should promptly share virus sequence data and epidemiological findings on platforms like GISAID, and report any unusual transmission events through WHO and WOAHA channels. The naming framework itself could incentivize transparency: since it avoids country names, countries might be more willing to report outbreaks (knowing they won't be “blamed” in the virus's name). An emphasis on transparency is paramount for international cooperation. When surveillance data is openly available, the global scientific community can help detect patterns that indicate a host adaptation. For example, multiple labs analyzing H5N1 sequences from disparate mammal cases might independently notice the same adaptation markers, collectively building the case for a naming update.

#### 7.1.4. Historical Analysis and Baseline

Researchers should retrospectively apply the framework to past events (as we have partly done in this paper) to develop a baseline and refine the criteria. By simulating how we would have renamed past viruses, we can test the logic and fine-tune thresholds. This also helps train current epidemiologists in the new way of thinking. For instance, analyze the 1918, 1957, 1968, 1977, and 2009 pandemics: at what point in those outbreaks would available data have justified switching to a “-Human” label? We might find that in 1918 it would have been perhaps too late (given poor surveillance), whereas in 2009 it could have been flagged by early May 2009 based on outbreak investigations. These lessons can calibrate our present-day criteria.

In summary, to implement naming changes swiftly and appropriately, we need a strong evidence base. Investments in surveillance and research – especially aimed at detecting cross-species transmission events – are investments in better naming and thus better warning systems. As one FAO strategy document notes, a One Health approach with integrated data is key to contextualizing and responding to influenza threats in a globalized world. This includes strengthening real-time surveillance integration so that we can promptly update naming conventions. With such systems in place, the decision to label a virus “-Human” or “-Mammal” would come as a natural conclusion of the data, not a subjective or controversial call.

## 7.2. Fostering Transparency, Coordination, and Collaboration

Implementing transmission-based nomenclature globally will require consensus and cooperation among international bodies, national governments, and scientific experts. Several steps can facilitate this:

### 7.2.1. International Endorsement and Guidelines

The World Health Organization (WHO), in collaboration with the World Organisation for Animal Health (WOAH, formerly OIE) and the Food and Agriculture Organization (FAO), should convene an expert working group to formalize the nomenclature scheme. These organizations have the legitimacy to set naming standards – much as WHO has done for COVID-19 variants and for past influenza nomenclature decisions [4,9]. The working group can develop a guidance document that defines the naming format, criteria for updates, and procedures for announcing a name change. Having WHO/FAO/WOAH jointly issue this guidance will embed One Health principles and ensure both human and animal health sectors are integrated. The document should also encourage countries to adopt the terminology in their reporting and publications. This top-down endorsement is crucial to achieving uniform usage; otherwise, disparate naming conventions could proliferate in different regions.

### 7.2.2. Coordination Mechanism

We propose establishing a **Nomenclature Coordination Committee**, possibly under the existing WHO framework (e.g., as part of GISRS or as an adjunct to the WHO influenza strain selection committee). This committee would review data and decide on nomenclature changes in real time. It would include members from WHO, WOAH, FAO, leading researchers, and representatives from heavily affected countries. If surveillance data suggests a virus has met criteria for a host-label change, the committee can rapidly confer (virtually, if needed) and make a determination. Once a decision is made, WHO and WOAH can simultaneously issue alerts to inform all member states that, for example, *“Influenza A H5N1 clade X is now being designated as H5N1-Mammal to reflect documented mammalian transmission,”* providing a summary of evidence [70]. This ensures that communication of the change is through official channels, reaching national influenza centers, veterinary authorities, and ministries of health together. Such coordination was exemplified in 2011 when WHO consulted with partners to standardize the term A(H1N1)pdm09; a similar collaborative approach can be used for dynamic naming updates.

### 7.2.3. National Adoption and Integration

Countries should integrate the new nomenclature into their pandemic preparedness plans and communication strategies. National influenza centers and outbreak response teams could include in their standard operating procedures a step to check WHO updates on nomenclature. If a virus of concern gets reclassified, national authorities should update public messaging, guidelines, and possibly policy measures accordingly. For example, an animal outbreak that leads to a “-Mammal” classification might prompt a country to activate certain preparedness steps (like increasing PPE use for responders dealing with animal outbreaks, reviewing human vaccine seed strains, etc.), analogous to moving to a higher phase in WHO’s pandemic alert system. The naming system, in effect, can complement or enhance existing pandemic phase alerts by providing a more granular, virus-specific warning. National adoption also means training health communicators to use the terms correctly, so that press releases and risk communication align with the new nomenclature.

### 7.2.4. Cross-Disciplinary Collaboration

The very nature of transmission-based naming encourages collaboration between virologists, epidemiologists, veterinarians, and ecologists. Deciding what a virus is “demonstrating” in terms of transmission requires input from all these domains. We recommend more joint analyses and publications across sectors. For instance, after a major spillover event, a One Health investigation

team can publish a report that not only describes the outbreak but also explicitly assesses whether criteria for sustained transmission were met [71]. This team approach has been shown to be feasible in some instances (e.g., joint human-animal investigations of H7N9 outbreaks in live markets). Institutionalizing such collaborations will yield more coherent data to inform naming decisions. The One Health High-Level Expert Panel (OHHLEP) emphasizes the importance of communication, coordination, collaboration, and capacity (the “4 Cs”) in managing zoonotic threats. Applying those same 4 Cs here: ensure constant **communication** between human and animal health sectors about viral spread; **coordinate** on interpreting what the data mean; **collaborate** on the response, including on what to call the virus; and build **capacity** to do all this in every country.

### 7.2.5. Transparency in Decision-Making

Whenever a naming update happens, it should be carried out with full transparency. The scientific rationale (e.g. data on cases, R0 estimates, genomic sequences) should be made available alongside the announcement. This allows the broader scientific community to understand and, if needed, debate or validate the decision. Transparent criteria and evidence help maintain trust in the process. Just as WHO publishes vaccine strain selection reports, naming decisions and their justifications could be shared in outlets like the Weekly Epidemiological Record or WHO’s Disease Outbreak News. By being open about the process, we also invite independent researchers to potentially spot aspects that official channels might miss – essentially, extra sets of eyes on the data can only help.

Implementing these coordination and transparency measures will ensure that transmission-based nomenclature is not just an academic idea, but a practical tool ingrained in the global influenza governance structure. The ultimate aim is that when the next potential pandemic virus emerges, the world will have a naming system that immediately reflects its status and risk, enabling faster consensus on actions. As one Lancet commentary noted, building global preparedness for avian influenza requires strong international coordination and communication – and naming conventions should be part of that preparedness [70].

Finally, while we have focused on influenza, it’s worth noting that the principles here could extend to other emerging viruses. The COVID-19 experience taught us the value of clear, easy-to-understand variant naming. In the future, perhaps even novel pathogens might have naming schemes that incorporate transmission mode or reservoir. (Imagine if “2019-nCoV” had been called something like “**Airborne-CoV-2019**” once it was known to be primarily airborne human-to-human – it might have signaled the response needed more clearly.) Influenza, with its long history of problematic naming and rich surveillance data, can lead the way in this nomenclature innovation.

## 8. Conclusions

The continual threat of influenza pandemics demands that we leverage all available tools to improve preparedness and response – including the tool of nomenclature. This review has highlighted that traditional influenza naming conventions, focused on static characteristics like subtype, host of isolation, and geography, fall short of conveying crucial information about how a virus is spreading and in what host. We have presented a framework for transmission dynamics-based nomenclature that addresses these gaps by making the virus’s current behavior – its predominant host and transmissibility – central to its name.

By examining historical and contemporary cases (1918 H1N1, 1957 H2N2, 1968 H3N2, 2009 H1N1pdm, H5N1, H7N9), we illustrated how a dynamic naming system could have provided clearer guidance and reduced confusion. In particular, labeling viruses as “-Human”, “-Avian”, “-Swine”, etc., at appropriate junctures would have signaled the shifting risk profiles of those viruses. The proposed system is not meant to replace detailed scientific classification, but rather to augment it for public health purposes – marrying the genomic era’s insights with real-world epidemiology *in the very naming of the virus*.

Key benefits of this approach include improved public communication (names that inform rather than mislead), enhanced international transparency (no country or region is unfairly tied to a virus's identity), and potentially faster mobilization for vaccine development and control measures (since the name itself can act as a call to action when it changes). The case studies of H1N1pdm09, H5N1, and H7N9 show that the framework is applicable to both rapid-onset pandemics and smoldering, persistent zoonotic threats.

We have also outlined how to implement this naming system within the existing global public health infrastructure. Success will depend on strong One Health surveillance, clear criteria for transmission thresholds (e.g.,  $R_0 > 1$  in a new host), and close cooperation between organizations like WHO, WOA, and FAO, as well as national authorities. Importantly, the scientific community must build consensus on this paradigm shift so that virologists and epidemiologists speak with one voice when recommending a naming update. Early buy-in and pre-established protocols (ideally agreed upon before the next crisis) will make it easier to execute name changes in the heat of an outbreak.

There will undoubtedly be challenges. Deciding exactly when a virus has "sustained" transmission can be contentious if data are limited. We must be cautious to avoid premature or overly frequent changes that could sow confusion. The system should be flexible but with a bias toward stability until a true shift is evident. It will also be important to continuously evaluate the impact of any new nomenclature on public understanding – does it truly reduce misperceptions? Ongoing risk communication research will be valuable after introducing such a scheme.

In conclusion, a transmission-based nomenclature for influenza is a logical evolution in the way we talk about and classify these viruses, reflecting a parallel evolution in our scientific understanding of them. What we call a virus is not merely a technical detail; it can influence preparedness, public fear or complacency, economic decisions, and international relations. Getting the name right means getting a head start on the response. As we stand in an era of rapid information and misinformation, having clear, informative, and adaptable names for pandemic threats is increasingly critical. We recommend that global health authorities pilot this nomenclature for upcoming influenza virus variants of concern and incorporate it into pandemic planning exercises. The next time an influenza virus emerges from nature with the potential to ignite a pandemic, a name that encapsulates its transmission dynamics could help the world recognize the danger for what it is – and respond with unity and clarity.

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