Contrasting the epidemiological and evolutionary dynamics of influenza spatial transmission

Cécile Viboud1, Martha I. Nelson1, Yi Tan1 and Edward C. Holmes1,2

1Fogarty International Center, National Institutes of Health, Bethesda, MD 20892, USA
2Center for Infectious Disease Dynamics, Department of Biology, Pennsylvania State University, University Park, PA 16802, USA

In the past decade, rapid increases in the availability of high-resolution molecular and epidemiological data, combined with developments in statistical and computational methods to simulate and infer migration patterns, have provided key insights into the spatial dynamics of influenza A viruses in humans. In this review, we contrast findings from epidemiological and molecular studies of influenza virus transmission at different spatial scales. We show that findings are broadly consistent in large-scale studies of inter-regional or inter-hemispheric spread in temperate regions, revealing intense epidemics associated with multiple viral introductions, followed by deep troughs driven by seasonal bottlenecks. However, aspects of the global transmission dynamics of influenza viruses are still debated, especially with respect to the existence of tropical source populations experiencing high levels of genetic diversity and the extent of prolonged viral persistence between epidemics. At the scale of a country or community, epidemiological studies have revealed spatially structured diffusion patterns in seasonal and pandemic outbreaks, which were not identified in molecular studies. We discuss the role of sampling issues in generating these conflicting results, and suggest strategies for future research that may help to fully integrate the epidemiological and evolutionary dynamics of influenza virus over space and time.

1. Introduction

With the rapid development and reduced cost of next-generation genome sequencing technologies, gene sequence data for human influenza A virus have become increasingly available at detailed spatial and temporal scales [1,2]. These molecular data have provided important insights into key patterns of influenza viral migration and disease persistence in different geographical regions and at different epidemiological scales. While it has long been known that influenza viruses circulate globally, the existence, location and determinants of a common ‘source’ population from which genetic and antigenic variants might emerge remains a topic of great debate, as does the extent of viral persistence between epidemic seasons within individual localities [3–7].

In parallel to progress in the generation and availability of molecular data, there is a long history of fitting spatial transmission models to influenza epidemiological data, and improvement in computational power has allowed simulation of disease spread at increasingly detailed spatial scales [8–17]. High-resolution disease data now available from non-traditional surveillance sources, such as web searches, electronic medical claim records, cell phone usage and tweets, are becoming essential to validate detailed spatial models [18–20]. In addition, the emergence and rapid global spread of the A/H1N1 pandemic virus in 2009 provide a unique case study to elucidate long-standing epidemiological questions, such as the role of population movements and children on influenza spatial transmission, and to directly compare the findings derived from large-scale epidemiological and molecular data.
The aims of this article are (i) to review efforts to decipher and model the spatial–temporal patterns of influenza virus, using epidemiological and molecular data and (ii) to compare and contrast the findings of these parallel fields. We first explore the spatial dynamics of seasonal influenza based on the increasing wealth of viral gene and genome sequence data, particularly for the A/H3N2 subtype for which most data are available. In comparison, we highlight the insights provided by epidemiological diffusion models. We then discuss the most salient discrepancies between molecular and epidemiological studies, particularly within the context of the 2009 pandemic, and suggest areas for future research to reconcile some of the conflicting findings. Finally, we discuss the implications of spatial studies for public health and control strategies.

2. Spatial dynamics of human influenza based on molecular data

The availability of large-scale gene sequence datasets of human influenza A viruses has provided several key insights into the spatial dynamics of virus transmission at global, national and community scales. The increased number of publicly available human influenza sequences on GenBank (figure 1), from only two whole-genome sequences (and less than 1000 partial haemagglutinin (HA) sequences) in 2000 to more than 6500 genomes (and more than 27 000 partial HA sequences) in 2012, has been instrumental in refining our understanding of the global ecology and migration patterns of influenza, viral persistence between seasonal epidemics and how co-circulating genetic diversity complicates tracing spatial patterns at restricted spatial scales.

(a) Viral persistence

The study of influenza virus persistence is perhaps the most straightforward utilization of molecular data, and confers one of the most obvious advantages over epidemiological data alone. Studies of intensively sampled localities in temperate regions of the Northern and Southern hemispheres (specifically New York State, USA, Australia and New Zealand) revealed that the A/H3N2 influenza virus rarely persists (if at all) between seasonal epidemics in these locales, suggesting that long-distance, bi-hemisphere migration is essential to sustain global transmission in humans [21,22]. Hence, winter influenza epidemics are not due to the ‘re-igniting’ of viral lineages that survived over the course of the summer. The strong seasonal bottlenecks observed in Bayesian skyline and skyride plots of influenza virus in New York State (USA) and New Zealand (figure 2), which depict changing levels of relative genetic diversity to the next seasonal epidemic in temperate areas, as viruses present at the end of an influenza season are generally genetically different (i.e. fall into different

during summer months in temperate countries, including the USA. As such, the more intensive sampling that took place during the 2009 influenza A/H1N1 pandemic provided a unique opportunity to explore viral persistence patterns in (summer) months that are not traditionally sampled. For example, an unseasonal transmission chain of A/H3N2 influenza virus was identified through 1 June 2009 in New York State and may have persisted later in the summer after sampling was halted [24]. Although of small scale, this study suggests that limited influenza transmission may occur during non-epidemic months and go undetected by traditional surveillance systems. However, limited transmission chains in summer do not significantly contribute genetic diversity to the next seasonal epidemic in temperate areas, as viruses present at the end of an influenza season are generally genetically different (i.e. fall into different
phylogenetic lineages) from those that seed the epidemic in the following winter [21,22]. In addition, all phylogenetic
studies undertaken to date have revealed that multiple
lineages co-circulate within a single geographical locality
during a specific influenza season, indicative of multiple
viral introductions [7,21,22,25].
Although some global phylogenetic analyses have
suggested that a stable influenza virus source population
could exist in tropical regions such as East and Southeast
Asia [3,4], more recent studies focused on Hong Kong and
southern China have not yielded convincing evidence
of viral persistence in these localities, nor of the
consistently higher levels of circulating genetic diversity
expected of a source population [6,7] (figure 2). Finally,
while small chains of influenza A/H1N1 transmission
persisted between the summer and autumn waves of the 2009
pandemic in the UK [26], the time interval between waves
was unusually short, such that they are unlikely to represent
a general phenomenon.

(b) Global ecology
Identifying a geographical source of new antigenic and
genetic variants of influenza virus could potentially improve
early detection and prediction of new vaccine strains. As a
consequence, this question has stimulated great interest.
Early phylogenetic analyses of global influenza datasets led
to the hypothesis of a viral source population for influenza
A/H3N2 located in the tropics, particularly East and
Southeast Asia [3,4]. In particular, influenza viruses from East
and Southeast Asia were found to be the shortest distance
from the main ‘trunk’ of the tree in a global phylogenetic
analysis of the HA1 region, suggesting that they represent a
viable source population [4]. However, subsequent analyses
of longer time-series have revealed that other regions contri-
bute to global diversity, including the USA [5]. Further, recent
studies focused on Southeast Asia suggest that influenza
viruses in this region do not consistently fall at trunk
locations and do not exhibit the patterns of persistence and
genetic diversity expected of a global source population
[6,7] (figure 2). Instead, these phylogenetic data are sug-
gestive of a dynamic ‘metapopulations’ model of global
influenza ecology, such that a multitude of geographical
regions contribute to global viral diversity, and that con-
tributing populations change with time. The sheer number of
subpopulations that exist in the densely populated, highly
connected, and climatically variable regions of East and South-
east Asia may therefore explain the periodic emergence of new
virus variants in this region. It is clear that a complete un-
derstanding of influenza metapopulation dynamics will require
deeper sampling from understudied tropical and subtropical
regions, notably in Africa, India and Latin America, and
from seasonal influenza A/H1N1 and influenza B virus, for
which there is limited information (figure 1). Overall, the
debate over the existence and location of a global source popu-
lation highlights the dangers of drawing strong conclusions
from limited sampling [27].

(c) Pandemic influenza
The 2009 influenza A/H1N1 pandemic presented a unique
opportunity to integrate molecular and epidemiological ana-
lyses of global and regional spread patterns and epidemic
growth dynamics (summarized in table 1). Using molecular
data from the early phase of the pandemic in Mexico,
Fraser et al. [28] estimated the basic reproduction number
\( R_0 \) of the epidemic to be 1.22 (95% CI: 1.05–1.60), com-
patible with epidemiological estimates ranging between 1.3
and 1.6. The date of onset of the outbreak in the first weeks
of 2009 as inferred from molecular clock-based analyses of
viral sequence data was also in broad agreement with the
first clinical case documented in La Gloria, Mexico, on
15 February 2009 [28,31].
Importantly, the statistical inference of viral migration
pathways and the selection of spatial diffusion models are
now possible with newly developed Bayesian phyloge-
ographic methods, which also account for phylogenetic
uncertainty [36,37]. Such methods were instrumental in track-
ing how the pandemic unfolded across the globe and in
confirming the Mexican origin of the most recent common
viral ancestor in January–February 2009 [32]. In particular,
analysis of viral gene flows suggests an early diffusion
from Mexico into several US states during March and April
2009, with the strongest support for migrations between
Mexico and Texas (where some of the earliest clinical cases
were documented). From the USA, the A/H1N1 virus contin-
ued to spread to Europe and Asia, and the reconstructed
global pandemic spread provides an interesting opportunity
for dynamic visualization using sophisticated tools such as
Google Earth [32]. Overall, these early phylogeographic
studies of viral gene flow are in broad agreement with the
Table 1. Key findings of molecular and epidemiological studies describing the spatial transmission dynamics of the 2009 influenza A/H1N1 pandemic.

<table>
<thead>
<tr>
<th>Pandemic period</th>
<th>Epidemiological studies</th>
<th>Molecular studies</th>
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<tbody>
<tr>
<td>Early pandemic stage</td>
<td>— first cases in an outbreak in the community of La Gloria, Mexico: 15 February 2009 [28]</td>
<td>— most likely time of origin in Mexico: January–February 2009 [28,31]</td>
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<td>(Jan–July 2009):</td>
<td>— little community transmission; multiple introductions</td>
<td>— dissemination from Mexico to the USA during February to April [32]</td>
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<td>— few locations experience spring wave (greater Mexico City area, some US cities, London) [29]</td>
<td>— spread from the USA to Europe and Asia [32]</td>
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<td></td>
<td>— temperate Southern Hemisphere and tropical locations in Asia and Latin America experience summer waves</td>
<td>— spring wave in the USA: strong spatial structure and co-circulating lineages in the USA [33]</td>
</tr>
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<td></td>
<td>— Closing schools early in the pandemic reduces transmission by 30–50%</td>
<td>— summer wave in Scotland: a major lineage originated in UK and other multiple introductions from both international and UK sites [34]</td>
</tr>
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<td>Late stage (Aug–Dec 2009):</td>
<td>— slow spread of the autumn wave in the USA driven by distance; little impact of school closures [30]</td>
<td>— low level of on-site transmission and intensive spatial mixing within an individual community in San Diego [35]</td>
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<td>— great diversity in number, timing, and intensity of pandemic waves between and within countries [30]</td>
<td>— autumn wave in the USA: less spatial structure; single lineage-dominated [33]</td>
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<td></td>
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<td>— single lineage-dominated worldwide in autumn [33]</td>
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<td></td>
<td></td>
<td>— winter wave in Scotland: more diverse genetically with several clades of similar sizes in different locations; extensive mixing [34]</td>
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sequence of pandemic activity experienced by different regions of the world, and with air travel fluxes originating from Mexico [38].

(d) Local transmission

Although molecular data have the potential to reveal detailed spatial patterns defined by individual lineages, the number of influenza viruses that co-circulate in a given locality complicates the study of spatial dissemination at a local scale [39]. Indeed, one of the most consistent and striking observations from studies of localized influenza spread is that even relatively small and isolated US communities harbour multiple geographical lineages, thereby illustrating the fluidity of human movement patterns [25,33]. During the early stage of the 2009 A/H1N1 pandemic in the USA, clear spatial patterns could be detected, as strong founder effects resulted in genetically distinct viral clades sweeping through New York State and Wisconsin in April–May 2009 [33]. However, such spatial structure was broken down by extensive global mixing during the autumn pandemic wave, which was dominated by a single clade that was prevalent in spring in New York City [33]. A slightly different phylogeographic pattern was observed in Scotland, where the spring 2009 pandemic wave was characterized by the expansion of a major clade originating from Birmingham, England, together with multiple introductions from both international and other UK sources [34]. By contrast, the autumn pandemic wave in Scotland was more genetically diverse with several co-dominant clades in individual locations, indicative of widespread gene flow [34]. The examples of the USA and Scotland during the 2009 A/H1N1 pandemic suggest that spatial patterns may vary substantially between temperate locations.

A common observation from numerous community-level studies of genetic diversity during the 2009 pandemic A/H1N1 was the co-circulation of multiple viral clades, which again impeded the detailed analysis of the patterns and dynamics of spatial diffusion [26–28,31–34,36–46]. In Hong Kong, extensive genetic diversity was detected not only at the community level, but also within households and individuals [46]. In the most detailed molecular study of community transmission of influenza virus to date, pandemic A/H1N1 viruses circulating among students at the University of California-San Diego were shown to exhibit little geographical clustering by student residence or city zip code, suggesting that most viral transmission occurred off-campus [35]. Taken together, these findings illustrate the remarkable spatial fluidity of the virus within the community, probably explained by a high degree of human mixing.

Taken together, the complex patterns of viral genetic diversity within individual localities—especially the presence of multiple co-circulating lineages—and lack of sufficient sampling depth have prevented more precise spatial analyses. While major advances in the methods of phylogeographic inference [36,37,47] have facilitated the effective use of gene sequence data to compare competing spatial models in other disease systems (such as animal rabies virus or swine influenza [48–50]), small-scale spatial patterns have not yet been identified for human influenza.

3. Spatial dynamics of human influenza based on epidemiological data

(a) Global spread

Large-scale mathematical and computational transmission models have been used to simulate, in detail, the global spread of pandemic viruses and assess the effectiveness of control measures [11–17,51]. These models typically integrate
information on air travel volumes with local work commute patterns, together with population demographics and seasonality factors. Such large-scale modelling efforts predicted that an early peak of pandemic influenza A/H1N1 virus activity would occur in October/November 2009 in the Northern Hemisphere, several weeks before vaccination campaigns could be carried out, and that antiviral use could delay peak pandemic timing. Further, modelling studies have concluded that substantial reductions in air travel would provide only a short delay in pandemic progression [51,52].

(b) Regional and local spread of influenza

(i) Seasonal influenza

Analysis of influenza epidemiological data at the scale of a country has highlighted the importance of ‘hierarchical’ spread between large population centres of temperate areas. Seminal studies of influenza diffusion in Iceland in the 1960s put forward the concept of gravity models as a useful way to quantify population movements, and hence disease spread [8,9]. Such models assume that population movements are proportional to the population sizes of the donor and recipient locations, divided by the distance between locations. The relative contribution of each factor can be tuned by exponents that are estimated from epidemiological [53,54] or movement data [15,55], making this a particularly flexible model to compare different influenza outbreaks (or different pathogens).

Analyses of seasonal influenza epidemics in the USA have shown that regional disease spread is best approximated by gravity models driven by work commutes, suggesting that adults are responsible for influenza dissemination at large scales [15]. Long-range population commutes driven by air travel, especially between the East and West coasts, synchronize epidemics across the lower continental US states. In addition, population size was a particularly important driver of disease spread, with larger population centres experiencing earlier epidemic onset than less populous US locales [15]. Analysis of high-resolution seasonal influenza data from France has confirmed the very high synchrony of epidemics in this well-mixed population, with no particular transportation mode dominating disease spread [56,57]. In Japan, analysis of hospitalized influenza cases in the Fukuoda prefecture revealed early transmission clusters in the largest population centres, followed by later diffusion in rural areas [58], consistent with the ‘hierarchical’ spread of the disease in the USA [15].

In contrast to the relatively well-characterized seasonality and diffusion patterns of influenza in temperate areas of the Americas, Europe and Asia, the transmission dynamics of influenza in the tropics has proved to be an enigma [59]. In Brazil, seasonal influenza activity starts early in the remote equatorial regions of the north and travels over the course of a three-month period to the more temperate areas of the south during their winter season [60]. These diffusion patterns are in contrast to the hierarchical spread of influenza observed in temperate locales, as the largest and best-connected cities in Southern Brazil experience late onset of viral activity [60]. Even though there is an apparent travelling wave of influenza originating in the equatorial regions of Brazil, consistent with the concept that the tropics serve as a source population of virus variants, these diffusion patterns have yet to be confirmed by geographically representative gene sequence data. Indeed, external disease drivers such as environmental or demographic factors (e.g. temperature or birth rates) can be spatially structured, producing apparent spatial structure in the seasonal timing of epidemics. For instance, despite the presence of spatial structure in epidemiological data for respiratory syncytial virus and rotavirus, there is no (or limited) pathogen diffusion between individual locations [61,62]. In this case, phylogenetic approaches are more powerful than epidemiological models in their ability to disentangle the role of intrinsic and extrinsic drivers on disease dynamics.

(ii) Pandemic influenza

The 1918 pandemic presents a particularly interesting case study owing to its unusual severity, making it relatively straightforward to characterize spatial patterns in epidemiological data. Detailed studies of disease diffusion in rural and urban areas of England and Wales have highlighted the rapid spread of the lethal autumn wave of 1918, with larger and more urban population areas experiencing earlier disease onset, reminiscent of the spread of seasonal epidemics in the USA [10,63]. Pandemic diffusion was much slower and less synchronous in the USA than in the UK, probably owing to less intense population mixing in the USA [54] and geographical differences in non-medical interventions between US cities [64,65]. With only 16 partial haemagglutinin HA1 virus sequences available from this historical pandemic to date [66], it is unfortunately impossible to compare diffusion patterns identified in epidemiological data with those derived from analysis of molecular data.

Although earlier pandemics predate the era of modern virology by several decades, a recent analysis of epidemiological records dating back to the 1889 pandemic have highlighted the rapid regional spread of the disease in Europe and the Americas via the railway network [67]. Unfortunately, no viral specimens have been preserved from this era. While virological and epidemiological surveillance networks were in place during the more recent pandemics of 1957 and 1968, lack of spatially disaggregated data for these relatively mild events has hampered analyses of disease spread. Country-level epidemiological studies have provided evidence for regional differences in the timing and intensity of the 1968 pandemic, potentially linked to differences in circulating viruses and prior immunity [68]. In the early 1960s, mathematical metapopulation models were developed to simulate the spread of influenza in 126 cities of the Soviet Union based on the air traffic transportation network [11]. These models were expanded on a global scale to reproduce broad diffusion patterns of the 1968 pandemic in 52 cities [69]. Recent efforts to incorporate international travel data in disease spread models have built heavily on these seminal efforts, relying on the theoretical concept that speed of spread should increase proportionally to population movements. However, few studies have attempted to match long-term trends in diffusion patterns of influenza epidemics with changes in human mobility, as seen over the past decades [70–73].

The 2009 A/H1N1 pandemic provides an opportunity to undertake a detailed validation of existing diffusion models, aided by high-resolution epidemiological data. Accordingly, the spring wave of the pandemic in the USA was characterized by sporadic outbreaks in northeastern and midwestern
cities, with pronounced activity in New York City and Boston. By contrast, dissemination of the autumn wave was unexpectedly slow, originating in Georgia–Alabama in late August and travelling westwards and northwards over a three-month period [30]. While school closure may have had some effect on reducing transmission in late summer [30,74], the particularly slow diffusion and late pandemic onsets in well-connected northeastern US cities are difficult to reconcile with existing pandemic diffusion models relying on ‘hierarchical spread’ [12,13]. Further, these epidemiological patterns are in contrast to findings from molecular data, which reveal the existence of several introductions into large northeastern cities in early autumn, which failed to ignite an epidemic [33].

It has been speculated that important details of the transmission process, human mobility or prior immunity, may not be accurately captured by existing pandemic models, including the exact role of school-age children, who are less mobile than adults [15]. More broadly, we lack a complete understanding of the variation in the intensity, timing and number of pandemic waves experienced by different cities of the same state (such as New York), which could be a complex function of connectivity, seasonality, school terms and prior immunity [75].

4. Discussion

With the availability of increasingly large volumes of molecular and epidemiological data, it has become possible to study influenza migration and transmission patterns at various spatial and temporal scales. Overall, the findings derived from large-scale molecular and epidemiological studies of inter-regional or inter-hemispheric spread in temperate regions are in broad agreement, revealing intense epidemics followed by deep troughs strongly driven by seasonal bottlenecks, multiple viral introductions, and lack of sustained viral persistence between epidemics [3,21,23,76,77]. However, there are important differences in studies conducted at smaller spatial scales, most likely reflecting the inadequate sampling of smaller molecular studies given the number of co-circulating lineages. As a case in point, country-specific epidemiologic studies reveal spatially structured diffusion patterns (e.g. the autumn wave of the 2009 pandemic in the USA [30], seasonal epidemics in Brazil [60], or hierarchical spread driven by population size and distance (seasonal influenza in the USA [15,54]), which have not yet been clearly observed in molecular data. Such discrepancies prevent the complete integration of epidemiological and evolutionary models for spatial data, as proposed in early visions for the field of phylodynamics [78].

Despite the limitations of current molecular studies, one key advantage they have over epidemiological data is that they allow the exact characteristics of influenza virus to be determined (e.g. specific type, subtype and lineage). Indeed, there are inherent dangers in basing all epidemiological estimates on incidence of influenza-like illnesses (ILI), which by definition must also contain cases owing to other respiratory pathogens. It is estimated that in a typical season, only one-third of ILI cases are caused by an influenza virus infection, with the highest influenza aetiological fraction observed near the time of the epidemic peak, during more severe outbreaks, and in young and middle-aged adults [29]. During the 2009 A/H1N1 pandemic, which occurred at an unusual time of the year when circulation of other respiratory pathogens was limited, the proportion of ILI caused by an influenza virus reached 40–60% [79,80]. The bias introduced by non-influenza pathogens can be reduced by relying on timing of peak ILI incidence, or on ILI rates in excess of a seasonal baseline, which are highly correlated with viral activity data, especially in influenza A/H3N2 seasons [15,81,82]. However, in contrast to molecular studies, epidemiological data cannot provide more detailed information on the spread of individual viral lineages that may differ in major phenotypic properties such as antigenicity [2,25] and capacity for drug resistance [83,84].

As noted earlier, the most obvious and severe limitation of molecular data is that, although it provides a uniquely powerful retrospective vision on the pathways of viral transmission, it is subject to strong sampling bias, particularly when viruses are collected for the purpose of vaccine strain selection. Although efforts by the National Institute of Allergy and Infectious Diseases-led Influenza Genome Sequencing Project have increased the availability of population-based collections of viral sequences, and specifically those based on complete viral genomes [1,2], the influenza virus specimens collected have tended to come from localities that are able to sample. Hence, there is still limited molecular information from locales that might harbour the most interesting patterns of genetic diversity, particularly in tropical regions. Phylogeographic analyses can draw migrational links only between populations for which samples are available, and hence may provide a false picture of the frequency of connections between undersampled geographic localities. Similarly, there is relatively little effort to collect samples outside the typical influenza season in temperate areas, nor from the full spectrum of clinical cases, although these may be central to understanding spatial viral dynamics. This problem is most acute at smaller spatial scales in which most samples are not given a sufficiently distinct spatial identifier (such as a GPS location) to enable detailed phylogeographic analysis. For the future, it will be essential to undertake both large-scale and structured sampling of influenza virus from diverse geographical locations and from diverse patient groups.

This review highlights how molecular analyses of influenza dynamics in localized communities have generally failed to provide clear evidence of spatial structure. To be informative, future studies will require greatly expanded and more structured sampling, perhaps by more than an order of magnitude over what is currently available. Inference of spatial structure in phylogeographic methods relies on the occurrence of nucleotide substitutions across the influenza virus genome. The rapid pace of human movement compared with the relatively slow pace of mutational fixation, coupled to the sparseness of sampling, is the most likely reason why there is a disconnect between those spatial patterns inferred from epidemiological and molecular data. However, the exact extent of sampling required to capture spatial patterns at smaller scales remains unclear, even for more remote localities.

For the future, it will also be important to go beyond molecular analyses limited to the HA1 domain of the influenza virus haemagglutinin. Although these are very informative about antigenic evolution, and provide an essential comparative dataset, they often lack the phylogenetic resolution required to precisely infer spatial dynamics, particularly at
localized spatial scales. In addition, segments other than the HA can present different phylogeographic patterns owing to frequent reassortment events, which may be essential to the development of both antigenic diversity [2,3] and drug resistance [83,84]. Hence, the analysis of complete genome sequences should be a priority to improve both the resolution and usefulness of future phylogeographic studies [2]. Deep intra-host sequencing may also prove to be a useful tool in elucidating detailed spatial transmission patterns, such as within-households, revealing transmission linkages that would otherwise not be detected by population consensus sequencing [85,86].

Another interesting area for future research is the issue of viral introductions and how it relates to seasonal drivers of transmission, which remain debated for influenza and other respiratory infections [87–89]. It will be useful to reconcile findings from molecular studies demonstrating multiple viral introductions over long periods of time in individual locations [25,33], with the unimodal and strikingly seasonal shape of influenza epidemics illustrated by epidemiological data. It remains unclear whether seed is constant throughout the year or highly seasonally dependent, and whether seed varies with travel volumes globally. Further, the exact relationship between viral dispersal and human mobility remains debated, with some epidemiological studies suggesting that population mixing is high in Northern Hemisphere temperate locations [56,57,73], and that changes in domestic and international connectivity may matter only in extreme situations such as isolated islands [71]. Molecular studies explicitly contrasting travel movements with patterns of viral seeding and migrations in well-sampled global locations would help quantify this relationship with better resolution than in previous studies [32].

Finally, we believe that it will be necessary to heavily sample locations that are strongly connected by human movements but which experience different climatic and influenza seasonality patterns, as these may provide insights into the drivers of influenza seasonality. Some areas of Latin America offer great opportunities in this respect, including the coastal, mountain and jungle areas of Peru [90] and Brazilian states [60], where pronounced geographical structure in timing and seasonal characteristics of epidemics has been identified. Whether these distinct spatial patterns observed in epidemic data can be reconciled with molecular patterns remains unclear.

A better integration of molecular and epidemiological models for the spatial transmission of influenza would benefit public health and help guide intervention strategies. In particular, clarification of the global migration patterns of influenza viruses and the existence of source populations, across different viral subtypes, would be helpful to focus surveillance efforts and improve vaccine design. Further, the projected impact of travel restrictions and border screenings would benefit from a better understanding of the global migration of influenza virus. Similarly, a better understanding of spatial dynamics at a local scale could help identify foci of influenza transmission and fine-tune the effectiveness of localized interventions, such as school closure or household prophylaxis. In conclusion, we believe that synergies between epidemiological and evolutionary studies of influenza spatial transmission will ultimately be helpful to improve predictive models and guide pandemic preparedness plans.

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