

Migration, Transportation Networks and the Geographical Diffusion of Communicable Diseases

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Abstract

Considering that human mobility plays a major role in the spread of infectious illnesses, mobility does not cause transmission on its own. The geographical spread of infectious diseases at the international, national, regional, and local levels is examined in this study in relation to migration and transportation networks. It uses a qualitative, analytical, and secondary data-based approach, combining official data from the World Health Organization, the United Nations, and the Government of India with peer-reviewed studies on transport modelling, mobility networks, and spatial epidemiology. Three interrelated mechanisms are identified by the analysis: local amplification upon arrival, redistribution via mobility corridors, and disease importation. Network connectivity can shorten the epidemiological distance between settlements, according to evidence from COVID-19, dengue, and malaria. However, the effects of movement vary depending on pathogen biology, route timing, population sensitivity, environmental receptivity, and public health capability. Rapid long-distance importation is particularly important for aviation; national and regional redistribution is supported by rail and road systems; and origin and destination populations are frequently reunited through migration and commuting. India offers a particularly illuminating example due to the extent of internal movement and transportation usage. The paper contends that for densely connected groups, surveillance based just on administrative residence and physical distance is inadequate. While avoiding the stigmatisation of migrants or arbitrary movement restrictions, a network-sensitive approach that integrates epidemiological surveillance with origin-destination flows, transit hubs, and mobility corridors might enhance risk assessment. The study comes to the conclusion that mobility data are best utilised as contextual evidence in surveillance systems that are pathogen-specific, temporally explicit, and ethically regulated.

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Introduction

The geography of communicable disease has always been inseparable from human movement. Trade routes, military campaigns, pilgrimage, labour migration and urbanisation have historically connected populations and transported pathogens between places. What has changed in the contemporary period is not the existence of mobility but its speed, volume, regularity and network complexity. Commercial aviation can link cities on different continents within a single day; railways and highways move very large populations across national territories; and recurrent commuting creates dense daily connections within metropolitan regions. These systems alter the practical meaning of geographical distance. A

settlement that is physically remote may be epidemiologically close to an outbreak centre when it is strongly connected through passenger flows, while a nearby but weakly connected locality may receive infection later. Brockmann and Helbing (2013) formalised this insight through the concept of effective distance, showing that complex epidemic propagation becomes more interpretable when distance is derived from mobility probabilities rather than kilometres alone.

The scale of mobility makes this question increasingly important. United Nations estimates place the international migrant stock at 304 million people in 2024, equivalent to 3.7 per cent of the world population, compared with 154 million in 1990 (United Nations Department of Economic and Social Affairs [UN DESA], 2025). International migration is only one component of mobility. Domestic migration, tourism, commuting, education, pilgrimage, displacement and short-term visits create many more journeys and often involve repeated movement between the same origins and destinations. Recent reviews consequently treat human mobility as a multidimensional process rather than a simple count of travellers. Lessani et al. (2024), synthesising 195 studies across several infectious diseases, found strong evidence that mobility is associated with infectious-disease spread while also identifying major methodological gaps in data integration, geographical coverage and measurement standardisation. Cheng et al. (2025) similarly emphasised the need to connect mobility networks with contact and social networks because movement creates opportunities for exposure but does not itself describe who actually meets whom or under what conditions transmission occurs.

Geographically, three forms of diffusion are particularly relevant. Relocation diffusion occurs when an infected person, pathogen-bearing vector or contaminated object is transported from one location to another. Contagious diffusion involves onward transmission through proximate contacts after arrival. Hierarchical diffusion occurs when disease moves through an urban or transport hierarchy, for example from an international gateway city to regional centres and then to smaller settlements. These mechanisms can operate in sequence: an infection may be imported internationally through aviation, redistributed nationally by rail or road, and amplified locally through households, workplaces or neighbourhood contacts. Transport therefore acts less as a single causal factor than as infrastructure linking epidemiological contexts.

The relationship is also pathogen-specific. Respiratory infections can move rapidly through highly connected populations when infected travellers are infectious during or soon after travel. Vector-borne diseases such as malaria and dengue involve an additional ecological requirement because the arrival of an infected person does not guarantee local transmission; competent vectors, suitable climatic conditions and adequate contact between humans and vectors are required. Vaccine-preventable and enteric infections introduce still different combinations of susceptibility, immunity, sanitation and contact structure. This variation is why broad statements that 'travel spreads disease' are analytically weak. The more useful question is when mobility changes the probability of importation, where the imported infection is likely to arrive, and under what destination conditions it can generate sustained transmission.

India is especially relevant to such analysis because its population is connected through extensive internal migration and multimodal transport systems. The Periodic Labour Force Survey report on migration estimated an all-India migration rate of 28.9 per cent for July 2020-June 2021 under its usual-place-of-residence definition, with substantial differences by sex and urban-rural location (Ministry of Statistics and Programme Implementation [MoSPI], 2022). This figure belongs to that survey period and should not be treated as a 2026 estimate. Transport volumes are also extremely large. The Ministry of Railways reported 741 crore passenger journeys during financial year 2025-26, up from 716 crore in 2024-25 (Press Information Bureau [PIB], 2026). These figures indicate

connectivity and movement intensity, not disease transmission; nevertheless, they illustrate why transport networks are relevant to spatial surveillance in India.

Recent research has advanced understanding of mobility and disease but remains disproportionately shaped by COVID-19. Studies using mobile-phone traces, Google mobility indicators, air-passenger data and migration records produced a large evidence base during the pandemic, whereas comparable integration is less developed for vector-borne and other communicable diseases (Lessani et al., 2024). In addition, analyses often treat administrative units as self-contained containers even though transport corridors cross district and state boundaries. A further limitation is the tendency to combine different forms of movement - permanent migration, circular migration, commuting and tourism - under a single mobility label. The present study addresses these gaps by synthesising transportation and migration evidence within a geographical framework that separates importation, redistribution and local amplification, and that compares transport modes and disease mechanisms rather than assuming a uniform mobility effect.

Accordingly, the study pursues four objectives: to identify the principal geographical mechanisms through which migration and transport networks shape communicable-disease diffusion; to compare the roles of aviation, rail, road and recurrent mobility across spatial scales; to evaluate international and Indian evidence for respiratory and vector-borne diseases; and to assess how network information can strengthen proportionate public-health surveillance. Four corresponding research questions guide the paper: through what mechanisms do mobility networks alter disease geography; how do effects differ by transport mode, spatial scale and pathogen; what does recent evidence reveal about importation and local amplification; and how can mobility information improve surveillance without treating travellers or migrants themselves as epidemiological hazards? The paper's contribution is therefore conceptual and comparative: it integrates transport geography, migration studies and spatial epidemiology within a single network-sensitive framework.

2. Literature Review

A central development in the literature has been the shift from Euclidean distance to network-based representations of epidemic space. Brockmann and Helbing (2013) demonstrated that the apparently irregular arrival of an epidemic across a transportation network can be represented more coherently through effective distance derived from passenger-flow probabilities. This framework does not eliminate conventional geography; rather, it shows that physical distance is filtered through connectivity. Klamser et al. (2024) extended this logic to country-specific import risk within the world air transportation network, illustrating how network structure can be used to estimate the relative likelihood that active cases leaving an outbreak origin will reach different destination countries. Such approaches are particularly useful early in an outbreak when identifying likely importation pathways may be more actionable than explaining transmission after widespread community circulation.

Metapopulation and mobility-network models provide a complementary perspective. They represent cities, districts or other population units as locally interacting populations connected by flows. Soriano-Panos et al. (2022) reviewed models that explicitly distinguish movement, interaction and return, emphasising that recurrent mobility differs from permanent relocation because commuters repeatedly connect the same populations. Anupriya, Bansal and Graham (2022) showed that aggregate origin-destination matrices can support infectious-disease propagation models even when detailed individual traces are unavailable. Their work is methodologically important because many transport agencies routinely collect origin-destination data, creating opportunities for public-health applications

without requiring continuous individual surveillance. Li, Xiang and He (2021), reviewing epidemic models in transportation systems, likewise highlighted the importance of behavioural response, dynamic travel demand and the distinction between infection occurring during travel and infection enabled by travel between communities.

Aviation has received substantial attention because it compresses long-distance travel into periods shorter than the incubation time of many infections. During the early COVID-19 epidemic, Chinazzi et al. (2020) used a global metapopulation model to assess travel restrictions and found that the Wuhan travel quarantine changed the timing and pattern of dissemination but could not by itself prevent international spread. Kraemer et al. (2020) found that movement from Wuhan was strongly associated with the early spatial distribution of cases across China; as local transmission became established, local control measures and within-location dynamics became increasingly important. Together, these studies support a temporal interpretation: mobility may have high explanatory value during epidemic seeding, but its relative importance changes after a pathogen becomes widely established.

More recent aviation research has added caution about the use of static passenger data. Wardle et al. (2024) examined temporal variation in international air travel and showed that historical passenger matrices may not adequately represent contemporary travel patterns in all settings. This matters because risk models often use older aviation data when real-time commercial data are unavailable. Klamser et al. (2024) similarly demonstrated that importation risk depends on the architecture of connecting routes rather than direct flight counts alone. The emerging literature therefore treats the global air network as dynamic: seasonality, route changes, connecting itineraries and changes in travel behaviour can alter epidemiological connectivity even when physical airport locations remain unchanged.

Migration scholarship adds another dimension because migration is socially structured and often recurrent. Lee et al. (2021) combined district-day COVID-19 case data with migration measures for Bangladesh, India and Pakistan. They found that prior international out-migration was associated with subsequent case patterns in India and Pakistan, while domestic out-migration predicted diffusion in India. The study is significant not because it identifies migrants as inherently risky, but because established migration linkages can act as indicators of where return movement is likely to connect outbreak locations with home districts. Rajan, Sivakumar and Srinivasan (2020) documented the severe disruption experienced by internal migrant workers during India's pandemic lockdown and described the period as a crisis of mobility. Read together, these studies reveal an important policy tension: restrictions intended to reduce movement can also produce sudden, concentrated return migration if livelihoods collapse, thereby redistributing mobility rather than simply eliminating it.

Vector-borne disease research provides an important corrective to respiratory-disease generalisation. Wesolowski et al. (2012) combined mobile-phone mobility data with malaria information in Kenya to identify routes through which infected people could move parasites between regions. The study showed that human mobility can connect malaria source and sink areas over distances beyond normal mosquito dispersal. In India, Enduri and Jolad (2018) modelled dengue transmission with human and vector mobility and demonstrated that movement changes spatial dynamics, although model outcomes depend on assumptions regarding vector density and host movement. Ospina-Aguirre et al. (2023) later examined dengue mobility in Caldas, Colombia, using a mobility-informed framework that further demonstrated how human movement reshapes local and regional transmission patterns.

Recent Indian malaria evidence illustrates the elimination-stage relevance of mobile populations. Lata et al. (2024) screened walking pilgrims travelling towards the Ramdevra pilgrimage in western

Rajasthan and identified malaria parasite infections among the mobile population studied. Their public-health argument was that movement from endemic towards low-transmission areas can create reintroduction risk and that surveillance along pilgrimage routes may provide earlier detection. The study is valuable because it shifts surveillance away from residence alone and towards corridors. It also demonstrates why mobility analysis must remain pathogen-specific: malaria importation is epidemiologically meaningful only where vectors and environmental conditions make onward transmission possible.

The methodological literature nevertheless identifies important limitations. Mobile-phone data may exclude people without consistent device access and can measure location without capturing exposure. Google-type mobility indicators describe changes relative to baselines but generally do not identify the full origin-destination chain. Transport ticketing records may capture passenger journeys while omitting unregistered road travel or informal migration. Disease surveillance is itself geographically uneven because testing access, reporting quality and case definitions differ. Lessani et al. (2024) therefore identified four broad gaps: limited use of big data outside COVID-19, incomplete integration of multiple mobility sources, limited global-scale work and insufficient methodological standardisation. Cheng et al. (2025) additionally argued that mobility, contact and social networks are often analysed separately despite their interdependence. The unresolved issue is thus not whether mobility matters, but how network structure, behaviour and pathogen biology interact across scales. This study addresses that problem through a structured comparative synthesis rather than attempting to pool heterogeneous numerical effect estimates.

Research Methodology

This study employs a qualitative, analytical, comparative and secondary-data-based research design. It does not claim to generate new case counts, mobility estimates, survey responses or causal effect sizes. No primary interviews, questionnaires, field observations or experiments were undertaken. This design is appropriate because the research questions concern the mechanisms through which mobility networks reorganise epidemiological space and the conditions under which these mechanisms differ across transport modes and disease types. A comparative synthesis also avoids the false precision that would result from combining effect estimates derived from incompatible pathogens, spatial units and mobility measures.

The evidence base consists of three categories. The first is peer-reviewed scholarship on spatial epidemiology, transport-network modelling, migration and communicable diseases. Priority was given to publications from 2020-2026, particularly systematic or scoping reviews and empirical studies using mobility or network information, while foundational studies were retained where they established concepts that remain central. The second category is official statistical and policy material used for contextual evidence. This includes UN DESA international migrant-stock estimates, the Government of India's PLFS migration report, Ministry of Railways reporting and the World Health Organization's International Health Regulations framework. Numerical statements are tied to their reporting years to avoid presenting older evidence as current. The third category consists of disease-specific studies selected to compare respiratory and vector-borne transmission mechanisms, with particular attention to South Asia and India where suitable evidence was available.

Source selection followed four criteria: relevance to human mobility or transportation; methodological transparency; identifiable publication or institutional provenance; and direct usefulness for one or more research questions. Peer-reviewed sources were verified through journal, PubMed, PMC or publisher records, and DOI information was retained only where it could be verified. Official

documents were used for migration, transport and regulatory facts rather than substituting secondary commentary. Where the latest available official dataset referred to an earlier survey period, that period is stated explicitly. For example, India's dedicated PLFS migration report covers July 2020-June 2021, whereas railway passenger figures used here refer to financial year 2025-26.

The analytical framework separates mobility-related disease diffusion into three stages. The first is importation: an infected traveller or pathogen reaches a new geographical unit. The second is redistribution: mobility networks move infection among connected locations before or alongside local amplification. The third is local amplification: transmission becomes sustained within the destination through contacts, vectors or environmental pathways. Four dimensions are examined within these stages - connectivity, flow intensity, spatial scale and temporal regularity. Connectivity captures whether places are linked directly or through hubs; flow intensity reflects the volume of movement; spatial scale distinguishes international, national, regional and urban processes; and temporal regularity differentiates recurrent commuting from episodic displacement, pilgrimage or one-time migration.

Analysis proceeded through thematic comparison rather than formal meta-analysis. Evidence was grouped around effective distance and network structure, aviation and long-distance importation, internal migration and recurrent mobility, multimodal transport in India, vector-borne disease, and surveillance implications. Findings reported by original studies are distinguished from interpretations advanced in this paper. When previous work demonstrates statistical association, the present study does not convert that association into a causal claim unless the original design justifies such interpretation. This distinction is especially important for COVID-19 because mobility restrictions, behavioural change, testing intensity and epidemic severity often changed simultaneously.

Reliability was strengthened through source triangulation. General propositions were checked against both review literature and disease-specific empirical studies; current contextual statistics were drawn from official sources; and claims about the International Health Regulations were checked against WHO material. The study nevertheless has limitations. The mobility literature remains heavily weighted towards COVID-19, mobile-phone datasets are not socially representative in all settings, and published research is concentrated in locations with better digital data. Transport use cannot be equated with exposure, and recorded residence may differ from where transmission occurred. These constraints mean that the paper provides a network-sensitive explanatory framework rather than a universal numerical estimate of the effect of mobility on communicable-disease incidence.

Analysis and Discussion

Network connectivity and the compression of epidemiological distance

The first research question concerns the mechanism through which transport and migration alter disease geography. The evidence consistently indicates that connectivity transforms the relationship between physical and epidemiological distance. In a conventional map, Delhi and London are separated by thousands of kilometres, while two neighbouring districts may share a boundary. In a mobility network, however, a high-volume direct or connecting route can make the distant pair epidemiologically accessible, whereas the adjacent districts may have limited interaction. Effective-distance theory captures this principle formally (Brockmann & Helbing, 2013), and subsequent air-network work shows that import risk is influenced by multi-step route structure as well as direct connections (Klamser et al., 2024). The implication is not that geography becomes irrelevant; rather, transport infrastructure reorganises geographical accessibility.

This reorganisation produces a nested sequence of mobility scales. International aviation is capable of seeding infections into major gateway cities. Domestic aviation, intercity rail and long-distance roads redistribute travellers among urban regions. Buses, secondary roads and local rail extend movement towards smaller towns and rural areas. Within cities, metro systems, buses, informal transport and commuting repeatedly connect residential and employment zones. The epidemiological significance of each layer depends on the disease stage. During initial introduction, identifying international and national gateways may be crucial. After widespread community transmission, local contact structures and neighbourhood conditions may become more informative than border crossings.

This temporal transition is visible in COVID-19 research. Kraemer et al. (2020) found that mobility from Wuhan was highly informative in explaining the early distribution of cases across China, but the relationship changed after control measures and local transmission became established. Chinazzi et al. (2020) similarly showed that travel restrictions changed the timing of dissemination without being sufficient to prevent global spread in the absence of effective local transmission control. These findings caution against interpreting transport interventions as binary successes or failures. Their value depends on when they are introduced, what they are intended to accomplish and whether the time gained is used to strengthen surveillance, testing, clinical readiness or other measures.

Table 1. Mobility systems and their principal geographical roles in disease diffusion

Mobility system	Principal scale	Primary geographical function	Key analytical caution
International aviation	Global/intercontinental	Rapid long-distance importation	Passenger connectivity indicates importation opportunity, not transmission.
Domestic aviation	National/regional	Inter-metropolitan redistribution	Seasonal and connecting routes can change effective accessibility.
Railways	National/regional	High-volume corridor movement	Fixed routes are measurable, but passenger counts do not reveal infection status.
Road transport	Regional/local	Broad spatial penetration and last-mile redistribution	Informal and private travel is often poorly captured.
Urban transit/commuting	Metropolitan	Recurrent daily mixing between activity zones	Local contact and ventilation conditions affect transmission opportunity.
Migration/pilgrimage corridors	Multi-scalar	Repeated or episodic origin-destination linkage	Migration status is not a biological risk factor; recent movement and exposure are the relevant variables.

Source: Author's analytical synthesis of the verified literature reviewed in this study.

Transport modes, scale and the distinction between travel and transmission

The second research question asks how transport modes differ. Aviation has a distinctive role because it allows infected travellers to cross large distances during incubation or pre-symptomatic periods. Yet aviation risk is not constant through time. Wardle et al. (2024) demonstrated that international passenger patterns vary sufficiently for historical travel matrices to become less accurate for some

disease-importation models. This is important for operational surveillance: an airport's relevance depends not only on its long-term centrality but also on seasonal routes and contemporary passenger flows. Klamser et al. (2024) further show that connecting itineraries matter, so surveillance focused only on direct routes from an outbreak origin may overlook pathways through intermediary hubs.

Surface transportation operates differently. Railways combine high passenger volumes with fixed corridors and identifiable stations, which can make them valuable for network-based analysis. Roads provide wider spatial penetration but are often harder to measure because private vehicles, informal buses and unregistered movement are poorly captured. In India, the magnitude of rail mobility is particularly notable: official reporting states that Indian Railways carried 741 crore passenger journeys in 2025-26, compared with 716 crore in 2024-25 (PIB, 2026). This statistic should be interpreted as a measure of mobility opportunity, not disease exposure. Still, the fixed architecture of the rail network creates repeatable connections that can be incorporated into origin-destination or hub-based surveillance if appropriately anonymised and aggregated.

A practical distinction is necessary between transmission during travel and transmission enabled by travel. Crowded vehicles or terminals may create contact opportunities for some respiratory infections, but a transport system can affect disease geography even when no infection occurs aboard the vehicle. An infected person may travel while non-infectious, become infectious after arrival and transmit in a household or workplace. Conversely, a person may acquire infection at a destination and carry it back along the same recurrent route. Transport network analysis therefore needs to be linked to pathogen natural history. Li et al. (2021) emphasised this modelling challenge in their review of epidemic spread in transportation systems, where assumptions about travel behaviour and contact during movement substantially influence estimated outcomes.

Migration corridors and recurrent mobility in India

The third research question concerns migration and recurrent mobility. Migration is distinct from one-time travel because it creates durable social connections between origins and destinations. Seasonal workers, circular migrants and students may return repeatedly; family members may travel in both directions; and social networks can channel new migrants along established routes. These pathways can become epidemiologically relevant when infection prevalence differs between connected areas. Lee et al. (2021) showed that pre-existing international and domestic out-migration measures predicted aspects of early COVID-19 diffusion in South Asia, including domestic diffusion in India. The appropriate interpretation is relational: migration data can reveal which districts are strongly connected to external labour markets or urban destinations, not that migrants constitute a biologically distinct risk group.

India's 2020 lockdown illustrates why this distinction matters. Sudden restrictions disrupted employment and transport while many migrant workers sought to return to home regions. Rajan et al. (2020) described the resulting crisis as one of mobility and social protection. From a disease-geography perspective, the episode demonstrates that policies intended to suppress movement can alter its timing and composition. When normal movement is interrupted without adequate livelihood and transport planning, travel may reappear as concentrated and less manageable flows. This reinforces a general principle: epidemiological models should not treat mobility as an exogenous quantity that can simply be switched off. Human movement responds to policy, employment, fear, family obligations and access to services.

Official migration data provide further context but also illustrate measurement constraints. MoSPI's Migration in India, 2020-21 report estimated a migration rate of 28.9 per cent during July 2020-June

2021 using a usual-place-of-residence definition (MoSPI, 2022). The rate varied sharply by sex, reflecting the importance of marriage-related migration as well as labour and other reasons. For disease surveillance, therefore, a broad migrant/non-migrant classification is insufficient. Epidemiologically relevant dimensions include recent travel, frequency of return, route, duration of stay, origin prevalence and destination conditions. A person classified as a migrant may not have travelled recently, while a non-migrant commuter may cross administrative boundaries every day.

Vector-borne diseases: mobility, receptivity and reintroduction

Vector-borne infections provide an even clearer demonstration that movement is necessary in some diffusion processes but insufficient for local transmission. In malaria, infected humans can transport parasites between regions, yet onward transmission requires competent mosquitoes and suitable environmental conditions. Wesolowski et al. (2012) used mobility and malaria data to identify source-sink relationships that could not be explained by mosquito movement alone. Their work supports a two-part geographical assessment: first identify where infected humans are likely to travel; then determine which destinations are receptive to onward transmission.

The Rajasthan pilgrimage study by Lata et al. (2024) gives this logic a contemporary Indian application. By detecting malaria infections among walking pilgrims, the study highlighted the possibility that large mobile populations can connect endemic and low-transmission areas. Its recommendation for sentinel surveillance along pilgrimage routes is particularly relevant to geographical epidemiology because the unit of attention becomes a corridor rather than a residential district. Such corridor-based surveillance could be proportionate: testing and awareness can be intensified during predictable high-mobility periods without labelling an entire migrant or pilgrim population as hazardous.

Dengue demonstrates similar but not identical dynamics. Enduri and Jolad (2018), modelling human and vector mobility, showed that human movement changes the speed and pattern of spread, while Ospina-Aguirre et al. (2023) demonstrated the importance of mobility in regional dengue dynamics in Colombia. Yet dengue importation leads to sustained transmission only where competent *Aedes* vectors and environmental conditions are suitable. Transport corridors therefore interact with climate, urban water storage, housing, vector control and population immunity. This interaction explains why the same volume of human movement can have very different epidemiological consequences in different destinations.

These disease-specific differences lead to a broader analytical conclusion: network centrality is not equivalent to epidemic vulnerability. A highly connected city may have a high probability of receiving imported cases but strong surveillance, vaccination or vector control may limit amplification. Conversely, a less connected destination may receive fewer introductions but be highly vulnerable once introduction occurs. Public-health geography should therefore distinguish importation risk from amplification risk. The former is strongly influenced by mobility networks; the latter depends more heavily on local susceptibility, contact structure, environmental receptivity and health-system performance. Risk maps that collapse these components into a single score may obscure the mechanism that an intervention needs to address.

Network-sensitive surveillance and public-health governance

The same distinction helps interpret the International Health Regulations. The 2024 amendments to the IHR generally entered into force on 19 September 2025, strengthening the contemporary international framework for coordinated health-emergency preparedness (World Health Organization [WHO], 2025). The IHR are not a mandate for blanket travel restriction; they are intended to manage

international public-health risks while addressing unnecessary interference with international traffic. A network-sensitive surveillance approach is consistent with this logic because it targets information and preparedness to plausible pathways rather than presuming that all travellers pose equal risk.

From a methodological perspective, origin-destination matrices are particularly promising. Anupriya et al. (2022) showed how aggregate OD flows can be integrated into disease-propagation models. For transport agencies and public-health authorities, this offers a pragmatic middle ground between crude administrative statistics and privacy-intensive individual tracking. An anonymised matrix can indicate how strongly locations are connected without identifying specific travellers. When combined with case incidence at origins, it can help estimate where imported cases are more plausible. When combined with local vulnerability indicators, it can also help prioritise destination surveillance.

However, several safeguards are essential. First, mobility data must be temporally matched to the epidemiological period; Wardle et al. (2024) show why stale passenger data can distort importation analysis. Second, different data sources capture different populations, so results should be triangulated. Third, network models should report uncertainty rather than presenting rankings as deterministic forecasts. Fourth, mobility information should be aggregated wherever possible to protect privacy. Finally, risk communication must avoid stigmatising migrants, pilgrims or residents of high-incidence areas. The epidemiological variable of interest is exposure and connectivity, not identity.

Conclusion

This study set out to explain how migration and transportation networks influence the geographical diffusion of communicable diseases and why their effects differ across spatial scales and disease types. The evidence supports a network-based interpretation of epidemic space. Physical distance remains important, but it is transformed by the structure and intensity of human movement. Highly connected locations can be epidemiologically close even when separated by large physical distances, and fixed transport corridors can create predictable routes of redistribution. This directly addresses the first research question: mobility alters disease geography principally by changing the probability, timing and direction of importation between connected populations.

The second research question concerned variation among modes and scales. Aviation is especially important for rapid long-distance importation and global seeding; rail and road systems support national and regional redistribution; and commuting and circular migration repeatedly reconnect origin and destination communities. These systems are not interchangeable, and their significance changes during an outbreak. Mobility is often most informative during introduction and early spatial spread, whereas local contact structures, susceptibility and control measures become increasingly important after community transmission is established. Transport use should therefore never be equated mechanically with transmission.

The third research question asked what recent international and Indian evidence reveals. COVID-19 studies show strong associations between early mobility and spatial diffusion, including evidence that pre-existing migration linkages helped predict patterns in South Asia. Indian official data confirm the scale of both migration and transport connectivity, but the epidemiological meaning lies in routes and timing rather than aggregate counts. Malaria and dengue research further demonstrates that movement alone is insufficient: imported infection produces sustained transmission only where local ecological and population conditions are receptive. This pathogen-specific interaction is a central finding of the comparative analysis.

For the fourth research question, the study concludes that network information can strengthen surveillance when it is used as contextual evidence alongside epidemiological and environmental data. Origin-destination matrices, transport hubs and recurring migration corridors can help identify where imported cases are plausible and where sentinel surveillance may be efficient. Such approaches should be temporally current, privacy-preserving and non-stigmatising. They should also distinguish importation risk from amplification risk so that interventions are matched to mechanism rather than applied indiscriminately.

The paper integrates transport geography, migration and spatial epidemiology through a three-stage framework of importation, redistribution and local amplification. Its main limitation is reliance on heterogeneous secondary evidence dominated by COVID-19 research. Future studies should integrate multimodal transport flows with communicable-disease surveillance at compatible spatial and temporal scales, examine a wider range of pathogens, and test whether network-informed surveillance improves operational outcomes. The most useful geographical question is therefore not whether mobility spreads disease in the abstract, but which connections matter, at what stage, for which pathogen, and under what destination conditions.

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