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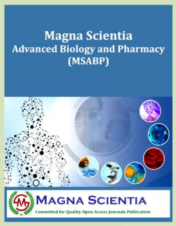

(Review Article)

Dengue in South Asia: Emerging epidemiological patterns and surveillance obstacles

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Abstract

This systematic review synthesizes current knowledge on dengue epidemiology, serotype distribution, and surveillance systems across four South Asian countries: India, Bangladesh, Sri Lanka, and Bhutan. Through analysis of peer-reviewed literature (2000-2024) and official health reports, the study examines the historical progression from sporadic outbreaks to hyperendemic circulation of multiple dengue virus serotypes (DENV-1 through DENV-4). The findings reveal significant epidemiological shifts across the region, with all countries experiencing increasing case numbers, expanding geographic distribution, and evolving viral genetics. India demonstrates remarkable serotype diversity with all four serotypes circulating nationwide. Bangladesh has transitioned from epidemic to endemic transmission with sequential serotype dominance. Sri Lanka exhibits bimodal seasonal patterns with record outbreaks despite improved case fatality rates. Bhutan presents a unique case study of recent dengue establishment with concerning altitudinal expansion exceeding 1,800 meters. The review identifies critical surveillance challenges, including entomological indices with limited predictive value, significant under-reporting, diagnostic inconsistencies, and fragmented data management systems. Climate change and urbanization emerge as key drivers of transmission, extending vector ranges to previously non-endemic regions and creating abundant breeding habitats in rapidly developing urban centers. The study evaluates emerging approaches such as genomic surveillance, novel vector control technologies, digital reporting systems, and integrated surveillance frameworks. Recommendations include enhancing laboratory capacity, implementing climate-informed early warning systems, strengthening cross-border collaboration, expanding community engagement, evaluating novel control technologies, and establishing regional knowledge-sharing platforms. These findings provide evidence-based guidance for policymakers and public health practitioners to address the growing dengue burden in South Asia through improved surveillance and targeted interventions.

Keywords: Dengue Virus; Epidemiology; Serotype Distribution; Surveillance Systems; South Asia; Climate Change; Urbanization; Vector Control; Genomic Surveillance; Public Health

1. Introduction

Dengue fever represents one of the most significant mosquito-borne viral diseases globally, with an estimated 390 million infections occurring annually, of which approximately 96 million manifest clinically (Bhatt et al., 2013; WHO, 2022a). The World Health Organization (WHO) recognizes dengue as a major international public health concern, particularly in tropical and subtropical regions where ecological conditions favor vector proliferation (WHO, 2020). The geographic distribution of dengue has expanded dramatically in recent decades, with the disease now endemic in over 129 countries and threatening approximately 3.9 billion people worldwide (Brady et al., 2012; Wilder-Smith et al., 2019).

The dengue virus (DENV), a member of the Flaviviridae family, consists of four antigenically distinct serotypes (DENV-1 through DENV-4), each capable of causing the full spectrum of disease manifestations ranging from asymptomatic

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infection to severe, potentially fatal outcomes (Guzman et al., 2010; Muller et al., 2017). Transmission occurs primarily through the bite of infected female Aedes aegypti mosquitoes and secondarily by Aedes albopictus mosquitoes, with urbanization, climate change, and globalization significantly contributing to the expanding range of these vectors (Kraemer et al., 2015; Liu-Helmersson et al., 2016).

The WHO South-East Asia Region (SEAR) bears a disproportionate burden of dengue, accounting for approximately 70% of the global disease burden, with hyperendemicity of multiple DENV serotypes leading to frequent outbreaks and severe disease manifestations (Bhatt et al., 2013; WHO, 2022b). The co-circulation of multiple serotypes increases the risk of sequential infections, which have been associated with higher rates of severe dengue through antibody-dependent enhancement (ADE) (Halstead, 2014; Katzelnick et al., 2017). Within this region, India, Bangladesh, Sri Lanka, and Bhutan have experienced significant dengue transmission patterns with unique epidemiological characteristics and control challenges (Mutheneni et al., 2017; NVBDCP, 2021).

These countries represent diverse geographical, climatic, and socioeconomic contexts within which dengue transmission dynamics have evolved over time. India, with its vast population and diverse ecosystems, has reported increasingly larger outbreaks since the 1990s, with all four serotypes now circulating in various regions (Chakravarti et al., 2012; Ganeshkumar et al., 2018). Bangladesh has witnessed a similar trend, with regular outbreaks since 2000 and a concerning increase in the geographic spread of cases beyond traditional urban centers (Rahman et al., 2019; Salje et al., 2019). Sri Lanka's dengue burden has intensified significantly following the end of its civil conflict in 2009, with record-breaking outbreaks in recent years (Sirisena & Noordeen, 2014; Tissera et al., 2020). Meanwhile, Bhutan, despite its high-altitude terrain historically considered unsuitable for dengue vectors, has reported increasing cases since its first outbreak in 2004, highlighting the role of climate change in expanding dengue's reach (Dorji et al., 2009; Wangchuk et al., 2013).

This review aims to synthesize current knowledge regarding dengue epidemiology, serotype distribution, and surveillance systems in these four South Asian countries. By examining the historical progression of dengue, current trends, and surveillance challenges, this paper provides a comprehensive analysis of factors influencing dengue transmission and control. The review explores the impact of urbanization, population mobility, and climate variability on vector ecology and viral transmission dynamics (Messina et al., 2019; Racloz et al., 2012). Furthermore, it evaluates the effectiveness of existing surveillance frameworks in capturing the true disease burden, considering limitations such as underreporting, variable diagnostic capabilities, and inconsistent case definitions across different healthcare settings (Beatty et al., 2010; Shepard et al., 2016).

Additionally, the review highlights gaps in existing surveillance methodologies and proposes integrated approaches to enhance dengue prevention and management strategies. This includes the application of novel technologies such as geographic information systems (GIS), remote sensing, and predictive modeling to strengthen early warning systems and targeted interventions (Louis et al., 2014; Racloz et al., 2012). The potential impact of recent developments in dengue prevention, including vaccination programs and innovative vector control strategies such as Wolbachia-infected mosquitoes and genetic modification approaches, is also assessed within the context of these countries' healthcare infrastructures and resources (Achee et al., 2015; Ferguson et al., 2016).

Understanding the complex interplay between viral evolution, vector ecology, and human factors is essential for developing effective dengue control programs, particularly as climate change threatens to further expand the geographic range of vectors and extend transmission seasons (Ebi & Nealon, 2016; Messina et al., 2019). This review contributes to this understanding by analyzing country-specific experiences and identifying common challenges and opportunities for regional collaboration in dengue surveillance and control. By synthesizing evidence from these four diverse yet geographically connected countries, this paper provides valuable insights for policymakers, healthcare professionals, and researchers working to mitigate the growing public health threat posed by dengue in South Asia and beyond.

2. Methodology

This comprehensive review employed a systematic approach to gather and analyze information on dengue epidemiology and surveillance in India, Bangladesh, Sri Lanka, and Bhutan. Additional data were obtained from national health ministry reports, WHO publications, and regional surveillance network documents. The review prioritized peer-reviewed literature published between 2000 and 2024 but included seminal papers from earlier periods to establish historical context. Gray literature, including government reports and technical documents from international health organizations, supplemented peer-reviewed sources to provide up-to-date epidemiological data.

Data extraction focused on the following categories: (1) historical progression of dengue in each country; (2) serotype and genotype distribution; (3) epidemiological trends including incidence, mortality, and case fatality rates; (4) entomological surveillance methods and findings; (5) disease surveillance systems; and (6) challenges and innovations in dengue control. The analysis synthesized findings to identify patterns, trends, and gaps in current knowledge and practice. Comparative analysis across the four countries highlighted common challenges and unique contextual factors influencing dengue transmission and control efforts.

3. Historical Context of Dengue in South Asia

3.1. Early Reports and Recognition

The history of dengue in South Asia reflects the global spread of this arboviral disease throughout the 20th century, with the region witnessing a significant transition from sporadic outbreaks to hyperendemic circulation of multiple serotypes. The earliest documented cases of dengue-like illness in the region date back to the 1780s, with clinical descriptions consistent with dengue reported from Madras (now Chennai) and Calcutta (now Kolkata) in India (Gubler, 1998; Smith, 2012). These early accounts described a "breakbone fever" characterized by severe myalgia, arthralgia, and rash—symptoms that align with contemporary understanding of classic dengue fever (Carey, 1971; Gubler, 2006). Historical medical records from British colonial physicians further document suspected dengue outbreaks throughout the 19th century, particularly in port cities that served as commercial hubs along maritime trade routes (Vasilakis & Weaver, 2008). However, laboratory-confirmed dengue cases were not reported until the mid-20th century, when improved diagnostic capabilities enabled viral identification and serological confirmation. In India, the first virologically confirmed dengue outbreak occurred in 1945 in Calcutta (Sarkar et al., 1964), involving approximately 200,000 cases and representing one of the largest urban epidemics of that era (Chakravarti et al., 2012). This outbreak, caused by DENV-1, marked the beginning of documented dengue surveillance in the Indian subcontinent and highlighted the virus's potential for explosive transmission in densely populated urban environments (Gupta et al., 2006; Sarkar et al., 1964). Subsequent outbreaks were reported in Madras (1956), Visakhapatnam (1964), and multiple locations throughout northern India in the 1960s and 1970s, with DENV-1 and DENV-2 predominating during this period (Karamchandani, 1957; Rodrigues et al., 1972). Similarly, early dengue cases in Bangladesh (then East Pakistan) were reported in the 1960s, with the "Dacca fever" outbreak of 1964 later confirmed as DENV-3 through retrospective serological analysis (Aziz et al., 1967; Russell et al., 1966). This outbreak affected approximately 30,000 individuals in Dhaka and surrounding areas, establishing dengue's presence in what would eventually become an independent Bangladesh (Hossain et al., 2003; Islam et al., 2006). The limited surveillance infrastructure during this period likely resulted in substantial underreporting, with many cases misclassified as influenza or other febrile illnesses due to diagnostic constraints (Mahmood et al., 2013). Figure 1 illustrates the member countries of the WHO South-East Asia Region, highlighting dengue-endemic areas and the year of the first laboratory-confirmed dengue case in each country. Sri Lanka's first documented dengue cases date to 1962, with subsequent outbreaks in 1965-1968 attributed to DENV-1 and DENV-2 based on serological surveys conducted among affected populations (Vitarana et al., 1990; Messer et al., 2002). These early outbreaks primarily affected the southwestern coastal regions, particularly the greater Colombo area, which continues to report the highest incidence rates nationally (Kanakaratne et al., 2009; Sirisena & Noordeen, 2014). Historical records indicate that dengue cases in Sri Lanka during this period typically presented as a self-limited febrile illness, with few reports of severe manifestations or hemorrhagic phenomena (Mendis, 1967; Vitarana & Jayakuru, 1990). In contrast, Bhutan remained relatively free from documented dengue until 2004, when the first official cases were reported in southern districts bordering India (Dorji et al., 2009; Wangchuk et al., 2013). This delayed emergence of dengue in Bhutan is attributed to several factors, including the country's geographical isolation, predominantly high-altitude terrain unsuitable for Aedes mosquito breeding, and limited international travel during much of the 20th century (Dorji et al., 2009; Wangdi et al., 2016). The first outbreak in 2004 involved 52 laboratory-confirmed cases from Phuntsholing, a border town with significant population movement to and from neighboring Indian states where dengue was already endemic (Dorji et al., 2009; Zangmo et al., 2015). The recognition of dengue in South Asia progressed through several distinct phases, reflecting advances in diagnostic techniques, surveillance systems, and clinical awareness (Gubler, 2002; Ooi & Gubler, 2009). Initially identified through clinical symptoms alone, confirmation techniques evolved from mouse inoculation studies in the 1940s-1960s to serological methods such as hemagglutination inhibition and complement fixation tests in the 1970s-1980s (Hammon et al., 1960; Russell et al., 1966). The introduction of enzyme-linked immunosorbent assays (ELISA) for detecting anti-dengue immunoglobulins in the 1980s and 1990s significantly improved diagnostic capabilities throughout the region, though cross-reactivity with other flaviviruses remained a limitation (Innis et al., 1989; Kuno et al., 1991). The advent of reverse transcription polymerase chain reaction (RT-PCR) techniques in the 1990s further enhanced surveillance by enabling serotype-specific diagnosis and phylogenetic analysis (Lanciotti et al., 1992; Morita et al., 1991). Entomological surveys conducted during early outbreaks confirmed Aedes aegypti as the primary vector throughout South Asia, with its distribution initially limited to urban areas with reliable water storage practices (Christopher, 1960; Wattal, 1964).

Historical records indicate that vector control efforts during colonial and early post-colonial periods focused primarily on environmental management and larviciding with oil-based products, with limited success in containing transmission (Karamchandani, 1957; Rahman et al., 2019). Table 1 provides an overview of the first documented laboratory-confirmed dengue cases in South Asian countries, highlighting the transition from early clinical observations to modern diagnostic methodologies.

The genotypic diversity reflected in Table 1 underscores the complex evolutionary history of dengue viruses in South Asia, with multiple introductions occurring over decades (Holmes & Twiddy, 2003; Weaver & Vasilakis, 2009). Phylogenetic analyses suggest that many of these genotypes represent importations from Southeast Asian countries, particularly Thailand, Myanmar, and Indonesia, highlighting the role of human movement in facilitating viral dispersal across national boundaries (Arima et al., 2013; Dash et al., 2015). The early recognition period established fundamental patterns that would characterize dengue epidemiology in South Asia for decades to come: urban predominance, *Aedes aegypti* as the primary vector, seasonal transmission coinciding with monsoon rains, and the gradual introduction and establishment of multiple viral serotypes (Gubler, 1998; Ooi & Gubler, 2009). These historical foundations laid the groundwork for the subsequent transition to hyperendemicity that would dramatically transform the regional dengue landscape in later decades.

Table 1 Dengue Virus Serotypes and Genotypes in Selected Countries

Country	DENV-1	DENV-2	DENV-3	DENV-4
India	I, II, III, V	Asian I, Cosmopolitan	I, II, III	I
Bangladesh	V	Cosmopolitan	I, II	Not subtyped
Sri Lanka	I, IV	Asian I, Cosmopolitan	III	I
Bhutan	V	Cosmopolitan	III	Not reported

Sources: Adapted from Dash et al. (2013), Islam et al. (2015), Kanakaratne et al. (2009), Dorji et al. (2009), and Wangchuk et al. (2013)

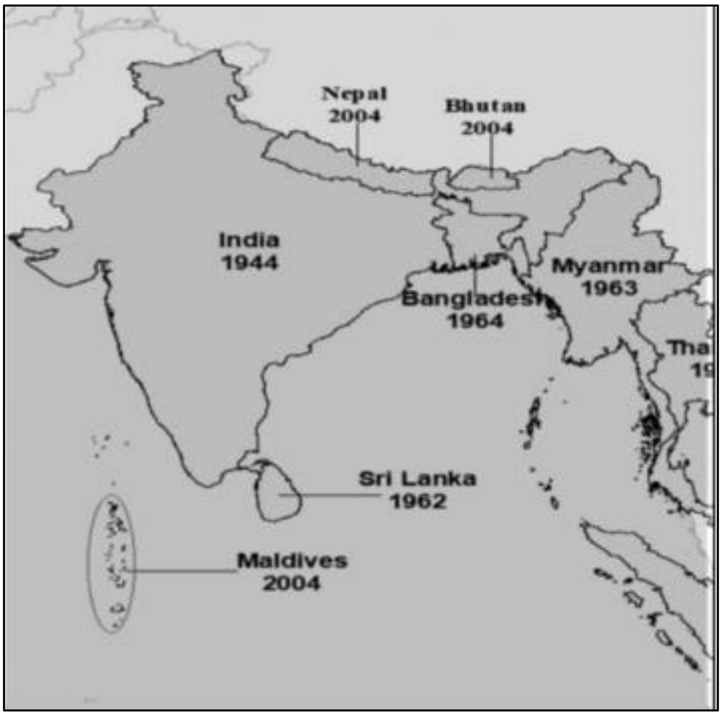

Figure 1 Member Countries of the WHO South-East Asia Region: Dengue Endemic Areas and First Laboratory-Confirmed Reports

3.2. Evolution from Epidemic to Endemic Disease

The epidemiological pattern of dengue in South Asia has transformed dramatically over the past seven decades. Initially manifesting as sporadic, self-limiting outbreaks with extended inter-epidemic periods, dengue has evolved into an endemic disease with yearly transmission cycles and periodic severe epidemics (Hasan et al., 2016). This transition reflects global trends in dengue epidemiology, driven by urbanization, population growth, increased mobility, and ecological changes favorable to vector proliferation.

In India, dengue transitioned from causing isolated urban outbreaks to becoming endemic in most states, with rural expansion noted since the 1990s (Chakravarti et al., 2012). Bangladesh witnessed a similar pattern, with dengue initially confined to Dhaka but gradually expanding to other urban centers and, more recently, to rural areas (Sharmin et al., 2015). Sri Lanka's experience mirrors this trend, with dengue evolving from sporadic outbreaks to endemic circulation across the island, accompanied by increasing case numbers and expanding geographic distribution (Sirisena & Noordeen, 2014). Bhutan represents the most recent country in this group to experience dengue establishment, with rapid geographic expansion from a single southern district in 2004 to 19 districts by 2019, including areas at higher altitudes previously considered non-endemic (Dorji et al., 2016). This historical progression from epidemic to endemic disease underscores the adaptability of both the dengue virus and its primary vectors, as well as the challenges in implementing effective control measures in the context of rapid environmental and social changes across South Asia.

4. Epidemiology of Dengue in South Asian Countries

4.1. India

4.1.1. Serotype Distribution and Evolution

India exhibits remarkable diversity in DENV serotypes and genotypes, with all four serotypes (DENV-1 to DENV-4) circulating throughout the country. This hyperendemicity creates a complex epidemiological landscape characterized by frequent serotype shifts that often precede major outbreaks (Murhekar et al., 2019). Molecular epidemiological studies have revealed significant genotypic diversity within these serotypes, reflecting both local evolution and international importation of viral strains.

DENV-1 circulation in India has been characterized by the predominance of Genotype III until 2005, after which Genotype I emerged as the dominant lineage (Cecilia et al., 2011). This genotype replacement coincided with increased dengue activity in several states, suggesting potential fitness advantages of the emerging genotype. Simultaneously, Genotypes II and V have been detected in different regions, highlighting the complex viral population structure (Sharma et al., 2015).

DENV-2 has historically been associated with severe outbreaks in India, particularly the Cosmopolitan genotype which caused the devastating 1996 Delhi epidemic that resulted in 8,900 reported cases and 374 deaths (Dar et al., 1999). The Asian I genotype of DENV-2 has also been detected in various regions, contributing to the genetic diversity of this serotype in the Indian subcontinent (Anoop et al., 2010).

DENV-3 emerged as a significant public health concern in India in 2003, with Genotype III causing severe outbreaks in northern and central regions (Dash et al., 2006). This emergence represented a serotype shift that coincided with increased disease severity, supporting the hypothesis that serotype switches can enhance epidemic potential through population susceptibility patterns (Chakravarti et al., 2012).

DENV-4 has historically been the least prevalent serotype in India, with limited circulation reported until its re-emergence in 2003 after decades of absence (Cecilia et al., 2011). Since then, DENV-4 has been detected in various regions, although at lower frequencies compared to other serotypes. Genotype I has been the predominant DENV-4 lineage identified in India (Afreen et al., 2015).

4.1.2. Epidemiological Trends and Disease Burden

The epidemiological landscape of dengue in India has undergone substantial transformation since the first documented outbreak in 1944. The geographic distribution has expanded from urban centers to rural areas, with cases reported from previously non-endemic regions, including higher altitude locations (Chakravarti et al., 2012). This expansion reflects both improved surveillance and actual disease spread due to changing ecological conditions and human mobility patterns.

National surveillance data indicate a dramatic increase in reported dengue cases, from 18,860 in 1996 to 101,192 in 2018 (National Vector Borne Disease Control Programme [NVBDCP], 2019). This upward trend likely reflects both increased transmission and improved reporting systems, although significant underreporting persists. A community-based study in Chennai estimated that only 2.8% of all DENV infections were captured by passive surveillance systems, suggesting the true burden is substantially higher than official figures indicate (Joshua et al., 2016).

Despite increasing case numbers, the case fatality rate (CFR) has shown a favorable trend, declining from 3.3% during the 1996 Delhi epidemic to approximately 0.2% in recent years (NVBDCP, 2019). This reduction in mortality likely reflects improved clinical management protocols, enhanced awareness among healthcare providers, and earlier patient presentation for treatment. The seasonal pattern of dengue in India typically follows monsoon rainfall, with peak transmission occurring between July and November in most regions. However, regional variations exist, with year-round transmission reported in southern states and distinctive seasonal patterns in different geographical zones (Chakravarti et al., 2012). Recent years have seen a concerning trend of extended transmission seasons, possibly related to changing climatic conditions and vector adaptation (Mutheneni et al., 2017).

4.2. Bangladesh

4.2.1. Serotype Dynamics and Molecular Epidemiology

Bangladesh's dengue serotype landscape has been characterized by sequential dominance of different serotypes, with substantial implications for disease severity and outbreak potential. The earliest documented dengue outbreak in 1964, known as "Dacca fever," was retrospectively identified as caused by DENV-3 (Genotype II) (Aziz et al., 1967). This serotype remained predominant until the turn of the century, when significant epidemiological shifts occurred.

The landmark 2000 epidemic marked a turning point in Bangladesh's dengue history, with over 5,500 reported cases and the first documented concurrent circulation of all four serotypes (Rahman et al., 2002). This event coincided with the introduction of DENV-3 Genotype I, which partially replaced the previously circulating Genotype II. The genetic diversity of circulating viruses increased substantially following this epidemic, suggesting multiple importation events and local evolution (Islam et al., 2015).

From 2013 to 2016, DENV-2 (Cosmopolitan genotype) emerged as the dominant serotype in Bangladesh, associated with increased case numbers and geographic expansion of transmission (Shirin et al., 2019). This serotype shift aligned with regional trends in DENV-2 circulation across South Asia during this period. DENV-1 (predominantly Genotype V) has been consistently detected throughout Bangladesh, while DENV-4 has been reported but not extensively genotyped (Islam et al., 2015). Recent molecular surveillance has identified the introduction of novel genetic lineages, including DENV-2 Cosmopolitan genotype variants with distinctive mutation patterns (Shirin et al., 2019). These findings highlight the dynamic nature of DENV evolution in Bangladesh and the importance of continued genomic surveillance for outbreak prediction and response.

4.2.2. Spatial Distribution and Temporal Trends

Dengue in Bangladesh exhibits marked spatial concentration, with Dhaka city bearing a disproportionate burden of cases. This urban focus reflects the ecological preferences of *Aedes aegypti*, the primary vector, which thrives in densely populated areas with inadequate waste management and water storage practices (Hasan et al., 2016). However, recent surveillance data indicate gradual geographic expansion to other urban centers and some rural areas, suggesting changing transmission dynamics (Mutsuddy et al., 2019).

The temporal pattern of dengue in Bangladesh is characterized by seasonal transmission, typically peaking during the monsoon months of July to October when vector breeding conditions are optimal. However, interannual variability is substantial, with explosive epidemics interspersed with years of lower transmission (Mutsuddy et al., 2019). The 2019 epidemic represented an unprecedented surge in case numbers, with over 112,000 reported infections and 129 deaths, dwarfing all previous outbreaks since systematic surveillance began (Rahman et al., 2021). Analysis of long-term trends reveals increasing incidence rates and expanding seasonal transmission windows. Reported cases rose from sporadic outbreaks in the 1960s-1990s to thousands of annual cases since 2000, with substantial spikes during epidemic years (Hasan et al., 2016). This upward trajectory is likely influenced by multiple factors, including urbanization, climate change, evolving viral characteristics, and improved surveillance systems. Despite the increasing case numbers, the case fatality rate has shown improvement, declining from approximately 1.6% during the 2000 epidemic to 0.1% in 2019 (Rahman et al., 2021). This reduction reflects advances in clinical management protocols, improved diagnostic capabilities, and greater awareness among healthcare providers and the general public.

4.3. Sri Lanka

4.3.1. Serotype Circulation and Genetic Diversity

Sri Lanka's experience with dengue serotypes illustrates the complex relationship between serotype shifts and epidemic patterns. The earliest documented outbreaks (1965-1968) were attributed to DENV-1 and DENV-2, establishing endemic transmission on the island (Vitarana et al., 1990). However, the emergence of DENV-3 (Genotype III) in 1989 marked a significant epidemiological shift, leading to severe epidemics with increased morbidity and mortality (Messer et al., 2002).

Genotype IIIB of DENV-3 has been particularly significant in Sri Lanka's dengue history, causing widespread outbreaks and becoming established as the predominant serotype throughout the 1990s and early 2000s (Kanakaratne et al., 2009). Phylogenetic analysis suggests this genotype was introduced from India or other parts of South Asia, highlighting regional viral circulation patterns (Messer et al., 2002). Recent decades have witnessed increasing genotypic diversity across all serotypes in Sri Lanka. DENV-1 genotypes I and IV have been detected, with fluctuating prevalence over time (Ocwieja et al., 2014). DENV-2 shows similar diversity, with both Asian I and Cosmopolitan genotypes circulating in different regions and time periods. The Cosmopolitan genotype of DENV-2 was implicated in the largest recorded outbreak in 2017, which resulted in 185,688 cases and 250 deaths (Tissera et al., 2020). DENV-4 (Genotype I) has been sporadically detected in Sri Lanka since the 1990s but has not achieved sustained dominance (Ocwieja et al., 2014). This serotype appears to circulate at low levels, occasionally causing localized outbreaks but generally overshadowed by the more prevalent DENV-1, DENV-2, and DENV-3.

4.3.2. Epidemiological Patterns and Disease Impact

Sri Lanka has experienced a profound transformation in dengue epidemiology, evolving from sporadic outbreaks to endemic transmission with regular epidemic cycles. The disease is now reported from all districts of the island, though with notable spatial heterogeneity in incidence rates (Sirisena & Noordeen, 2014). Urban areas, particularly Colombo and other coastal cities, consistently report higher case numbers, reflecting vector ecology and population density factors.

The temporal pattern of dengue in Sri Lanka is characterized by bimodal annual peaks corresponding to the southwest (May-July) and northeast (October-December) monsoon seasons, when vector breeding conditions are optimal (Sirisena & Noordeen, 2014). These seasonal patterns show geographical variation across the island, reflecting regional differences in rainfall patterns. Long-term trends indicate increasing case numbers and expanding geographic distribution. The annual reported cases have risen from hundreds in the 1990s to tens of thousands in recent years, with the 2017 epidemic representing an unprecedented surge with 185,688 confirmed cases (Tissera et al., 2020). While improved surveillance partially explains this increase, ecological, viral, and immunological factors have also contributed to genuine increases in transmission intensity. Despite rising case numbers, disease outcomes have improved substantially. The case fatality rate decreased from 9.90 per thousand cases in 1989 to 0.24 per thousand in 2017, reflecting advances in clinical management protocols and healthcare provider awareness (Tissera et al., 2020). This improvement has occurred despite periodic increases in severe dengue manifestations associated with serotype shifts, highlighting the importance of adaptive clinical management approaches.

4.4. Bhutan

4.4.1. Recent Introduction and Serotype Patterns

Bhutan represents a unique case study of recent dengue establishment in a previously non-endemic Himalayan country. The first officially reported dengue cases occurred in 2004, with 2,579 confirmed infections in the southern district of Phuentsholing bordering India (Dorji et al., 2009). Molecular analysis identified DENV-2 (Cosmopolitan genotype) as the causative agent of this initial outbreak, suggesting importation from neighboring endemic countries (Dorji et al., 2009).

Subsequent surveillance documented the introduction and circulation of additional serotypes. DENV-3 (Genotype III) emerged during the 2005-2006 period, causing localized outbreaks in southern districts (Zangmo et al., 2015). DENV-1 (Genotype V) became the predominant serotype during the 2013-2014 and 2016-2017 outbreaks, indicating a serotype shift that may have contributed to increased case numbers during these periods (Zangmo et al., 2015). While DENV-4 has not been officially reported from Bhutan as of current literature, the country's proximity to regions where all four serotypes circulate suggests potential for future introduction. The observed pattern of sequential serotype introductions mirrors the historical experience of other South Asian countries and raises concerns about increasing epidemic potential as population immunity patterns evolve.

4.4.2. Geographic Expansion and Altitudinal Trends

The most striking aspect of Bhutan's dengue epidemiology is its rapid geographic expansion within a mountainous country previously considered largely unsuitable for *Aedes* mosquito establishment. From the initial confined outbreak in one southern subdistrict in 2004, dengue had expanded to 19 of Bhutan's 20 districts by 2019 (Tenzin et al., 2020).

Particularly notable is the altitudinal expansion of transmission. While initial outbreaks were confined to southern districts below 700 meters above sea level, recent cases have been reported from locations exceeding 1,800 meters, including the capital city of Thimphu (Tenzin et al., 2020). This altitudinal shift aligns with global observations of vector range expansion due to climate change and raises significant public health concerns for mountainous regions previously considered protected from dengue transmission.

The temporal pattern in Bhutan follows a distinct seasonal cycle, with cases predominantly occurring during the monsoon months of June to September. However, interannual variability is substantial, with major outbreaks reported in 2004, 2013-2014, 2016-2017, and 2019 (Tenzin et al., 2020). The 2019 outbreak was particularly significant, with 53,929 suspected cases representing an unprecedented surge in this small country of approximately 750,000 people. Despite the increasing case numbers and geographic expansion, Bhutan has maintained a relatively low case fatality rate, with no deaths reported during the initial outbreaks. This favorable outcome likely reflects both the relatively recent introduction of dengue (limiting the potential for antibody-dependent enhancement) and the country's responsive healthcare system (Dorji et al., 2016).

5. Surveillance Challenges and Limitations

5.1. Entomological Surveillance

5.1.1. Methodological Approaches and Limitations

Entomological surveillance forms a critical component of dengue control programs across South Asia, yet substantial methodological challenges limit its effectiveness for outbreak prediction and response. Current approaches rely predominantly on larval indices, which measure immature mosquito populations but have limited correlation with adult vector abundance and dengue transmission risk (Bowman et al., 2014).

In India, entomological surveillance primarily employs the House Index (HI, percentage of houses infested with larvae/pupae) and Breteau Index (BI, number of positive containers per 100 houses) as standard metrics (Srivastava et al., 2012). However, multiple studies have demonstrated the limited predictive value of these indices. For example, high HI and BI values were recorded in Kerala without subsequent epidemics, while areas with relatively low indices experienced significant outbreaks (Srivastava et al., 2012). This inconsistency highlights the complex relationship between vector abundance, human immunity, and viral factors in determining transmission dynamics.

Bangladesh faces similar challenges, with entomological surveillance focused on larval indices that show inconsistent correlation with dengue incidence (Dhar-Chowdhury et al., 2016). The limited implementation of adult mosquito sampling methods restricts the ability to assess vector density and infection rates, which are more directly related to transmission risk. Additionally, the focus on *Aedes aegypti* potentially underestimates the contribution of *Aedes albopictus*, which has been implicated in rural transmission cycles (Hasan et al., 2016).

Sri Lanka employs the Breteau Index as the primary entomological indicator for vector control decisions (Tissera et al., 2016). However, a significant limitation is the combined reporting of indices for *Ae. aegypti* and *Ae. albopictus*, despite their different ecological niches and vectorial capacities. This aggregation complicates risk assessment and targeted intervention planning. Furthermore, the threshold values used for control decisions lack local validation, potentially leading to misallocation of resources (Tissera et al., 2016).

Bhutan's relatively recent experience with dengue has led to less developed entomological surveillance systems compared to neighboring countries. The country lacks routine adult mosquito surveillance, relying primarily on larval surveys during outbreak investigations (Dorji et al., 2016). This reactive approach limits the potential for early warning and proactive vector control interventions.

5.1.2. Emerging Approaches and Innovations

Recognizing the limitations of traditional indices, several innovative approaches to entomological surveillance have emerged in South Asian countries. Adult mosquito sampling methods, including BG-Sentinel traps, CDC light traps, and gravid traps, are increasingly being incorporated into surveillance programs in urban centers of India and Sri Lanka (Ramaiah et al., 2021). These methods provide more direct measures of the epidemiologically relevant adult vector population and enable assessment of infection rates through molecular testing. Pupal demographic surveys, which quantify the productivity of different container types, represent another methodological advance being piloted in selected sites across the region (Weeraratne et al., 2013). This approach enables targeted control efforts focused on the most productive breeding sites, potentially improving cost-effectiveness of vector control interventions.

Mobile technology has facilitated community-based entomological surveillance in several countries. India has piloted the Mobile-based Surveillance Quest using IT (MoSQuIT) system in selected cities, enabling real-time reporting of vector breeding sites through smartphone applications (Ramaiah et al., 2021). Similarly, Sri Lanka has implemented the Mo-Buzz system, which combines public reporting of breeding sites with predictive analytics for risk mapping (Lwin et al., 2016). Drone technology for identifying breeding sites in inaccessible locations has been piloted in urban areas of India, with promising results for large-scale surveillance (Ramaiah et al., 2021). This approach may be particularly valuable for monitoring construction sites, rooftops, and other elevated locations that traditional ground-based surveys often miss. Despite these innovations, significant challenges remain in scaling effective entomological surveillance across diverse ecological and socioeconomic contexts. Limited resources, technical capacity constraints, and coordination difficulties between research institutions and control programs hamper the widespread adoption of advanced surveillance methods (Bowman et al., 2014).

5.2. Disease Surveillance

5.2.1. Passive Surveillance Systems and Under-reporting

Disease surveillance for dengue in South Asia relies predominantly on passive reporting systems, which capture only a fraction of actual cases and provide limited real-time data for outbreak response. These systems depend on healthcare provider reporting, which is influenced by diagnostic capacity, awareness, and compliance with reporting requirements (Hasan et al., 2016).

In India, the National Vector Borne Disease Control Programme (NVBDCP) coordinates dengue surveillance, collecting data from government healthcare facilities and selected private hospitals (NVBDCP, 2019). However, significant under-reporting occurs due to several factors. A community-based study in Chennai estimated that only 2.8% of all dengue infections were captured by the passive surveillance system (Joshua et al., 2016). Private hospitals and clinics, which manage the majority of dengue cases in many urban areas, are often excluded from routine reporting networks. Additionally, mild or atypical cases frequently remain undiagnosed or unreported, leading to systematic underestimation of disease burden (Chakravarti et al., 2012).

Bangladesh's disease surveillance system faces similar challenges, with laboratory-based reporting capturing only serologically confirmed cases (Mutsuddy et al., 2019). The Directorate General of Health Services (DGHS) coordinates surveillance through designated hospitals, but private healthcare providers are inconsistently integrated into the reporting system. Rural areas with limited diagnostic capacity experience particularly severe under-reporting, creating geographical biases in surveillance data (Hasan et al., 2016).

Sri Lanka has developed a relatively robust surveillance system compared to neighboring countries, with mandatory case reporting from all healthcare institutions (Tissera et al., 2020). However, challenges persist, particularly regarding the timeliness of reporting and the integration of data from different sources. Paper-based reporting in some regions introduces delays and potential data entry errors, limiting the system's utility for real-time response (Tissera et al., 2016).

Bhutan implemented a web-based reporting system in 2015, facilitating more efficient data collection and analysis (Dorji et al., 2016). However, under-reporting remains a significant issue due to limited awareness among health professionals and diagnostic challenges in remote areas. Additionally, the reliance on clinical diagnosis without laboratory confirmation in some settings reduces the specificity of surveillance data (Tenzin et al., 2020).

5.2.2. Laboratory Capacity and Diagnostic Challenges

Laboratory capacity for dengue diagnosis varies substantially across and within countries, affecting the quality and completeness of surveillance data. Diagnostic approaches range from clinical assessment and rapid diagnostic tests (RDTs) to more sophisticated serological, molecular, and virus isolation methods (Guzman et al., 2010).

In India, the laboratory network for dengue diagnosis has expanded significantly, with 646 sentinel surveillance hospitals and 16 apex referral laboratories as of 2018 (NVBDCP, 2019). However, quality assurance remains a challenge, with variable performance of RDTs and limited molecular testing capacity in many regions. Serotype-specific surveillance is predominantly conducted in research settings rather than as part of routine public health surveillance, limiting the ability to monitor serotype shifts and their implications for disease severity (Chakravarti et al., 2012).

Bangladesh exhibits significant urban-rural disparities in diagnostic capacity. While major hospitals in Dhaka have access to ELISA-based serological testing, peripheral healthcare facilities often rely on clinical diagnosis or RDTs with variable sensitivity and specificity (Mutsuddy et al., 2019). The Institute of Epidemiology, Disease Control and Research (IEDCR) provides reference laboratory services, including RT-PCR for serotyping, but capacity limitations restrict comprehensive molecular surveillance (Shirin et al., 2019).

Sri Lanka has developed a tiered laboratory network, with enhanced sentinel surveillance in Colombo providing detailed serotype data through molecular methods (Tissera et al., 2016). This system enables comprehensive monitoring of circulating serotypes and early detection of shifts that may precede epidemics. However, regional disparities persist, with limited molecular diagnostic capacity in peripheral laboratories affecting the completeness of national serotype data (Sirisena & Noordeen, 2014).

Bhutan faces substantial laboratory constraints, with limited in-country capacity for confirmatory testing and serotyping (Dorji et al., 2016). The country relies on reference laboratories in neighboring countries for molecular characterization of circulating viruses, introducing delays in obtaining crucial epidemiological information. Recent efforts to establish RT-PCR capacity at the Royal Centre for Disease Control represent significant progress but require further strengthening for comprehensive surveillance (Tenzin et al., 2020). Across all four countries, differentiating dengue from other co-circulating arboviruses, particularly chikungunya and Zika, presents a diagnostic challenge due to overlapping clinical presentations and serological cross-reactivity (Mardekian & Roberts, 2015). This challenge has implications for the accuracy of surveillance data and appropriate clinical management of cases.

6. Impact of Climate Change and Urbanization

6.1. Climatic Factors and Dengue Transmission

Climate variables significantly influence dengue transmission dynamics through their effects on vector biology, viral replication, and human behavior. Temperature affects multiple aspects of the vector life cycle, including development rates, survival, reproduction, and biting behavior, while precipitation creates breeding habitats and influences relative humidity, which affects mosquito survival (Morin et al., 2013).

Research across South Asia has demonstrated strong associations between climatic factors and dengue incidence. In India, time-series analyses have identified significant correlations between rainfall, temperature, and dengue cases, with optimal conditions for transmission occurring at temperatures between 25°C and 30°C and rainfall between a specific threshold amount (Mutheneni et al., 2017). Notably, the relationship is not always linear, as excessive rainfall can flush out breeding sites, temporarily reducing vector populations. Climate change projections indicate potential expansion of dengue transmission zones in all four countries. Rising temperatures are expected to extend the geographic range of *Aedes* mosquitoes to higher elevations and latitudes, as already observed in Bhutan and northern India (Dhimal et al., 2015). Additionally, changing precipitation patterns may alter seasonal transmission dynamics, potentially extending transmission seasons and increasing epidemic potential in previously low-risk areas. The El Niño Southern Oscillation (ENSO) has been linked to dengue outbreaks across South Asia, with El Niño events associated with increased case numbers in Sri Lanka and parts of India (Sirisena & Noordeen, 2014). This relationship highlights the importance of including macro-climatic factors in predictive models for dengue outbreaks. Climate-based early warning systems have been piloted in several South Asian locations. Sri Lanka has implemented a climate-informed forecasting system that incorporates temperature and rainfall data to predict high-risk periods up to six months in advance (Lowe et al., 2018). Similarly, India has developed district-level models integrating climate variables with vector indices to enhance predictive capacity (Ramaiah et al., 2021).

6.2. Urbanization and Socioeconomic Factors

Rapid and often unplanned urbanization across South Asia has created ideal conditions for dengue transmission by increasing vector breeding sites, population density, and human-vector contact. Inadequate water supply leading to household water storage, poor waste management creating water-holding containers, and suboptimal housing conditions all contribute to the urban concentration of dengue observed across the region (Hasan et al., 2016).

In India, studies have demonstrated significant associations between urban infrastructure characteristics and dengue risk. Irregular water supply, forcing residents to store water in containers that become potential breeding sites, has been identified as a major risk factor in Delhi and other metropolitan areas (Chakravarti et al., 2012). Similarly, construction sites, which proliferate in rapidly developing cities, often create abundant breeding habitats for *Aedes* mosquitoes through improper water storage and accumulated debris (Sharma et al., 2015).

Bangladesh's experience, particularly in Dhaka, illustrates how socioeconomic factors interact with environmental conditions to influence dengue transmission. Informal settlements with limited access to piped water and waste management services report higher vector densities and dengue incidence compared to planned residential areas (Dhar-Chowdhury et al., 2016). However, the relationship between socioeconomic status and dengue risk is complex, as wealthier households may also maintain gardens and ornamental containers that provide suitable breeding habitats (Hasan et al., 2016).

Sri Lanka's urbanization patterns have similarly influenced dengue epidemiology, with the Western Province, which includes the capital Colombo, consistently reporting the highest incidence rates (Sirisena & Noordeen, 2014). Urban ecological factors, including land use patterns, vegetation cover, and surface water distribution, have been associated with spatial heterogeneity in dengue risk within cities (Tissera et al., 2020). Recent studies have employed geographic information systems (GIS) and remote sensing to identify high-risk urban microenvironments based on these ecological characteristics (Sirisena et al., 2017).

Bhutan presents a unique case study of urbanization in a predominantly rural, mountainous country. The growing urban centers in southern districts and the capital Thimphu have experienced increased dengue transmission, associated with changing housing patterns, water storage practices, and waste management challenges (Tenzin et al., 2020). The recent detection of *Aedes aegypti* in urban areas at elevations above 1,800 meters represents a concerning trend potentially linked to both climate change and urban development patterns (Dorji et al., 2016). Across all four countries, certain occupations and activities associated with urbanization carry elevated dengue risk. Construction workers, waste collectors, and market vendors experience higher exposure to vector breeding environments, while educational institutions and healthcare facilities can serve as transmission hubs during outbreaks (Mutheneni et al., 2017). These occupation-specific risks highlight the need for targeted interventions in high-risk urban settings. The growing popularity of urban container gardening, rainwater harvesting, and ornamental water features introduces additional breeding habitats in residential areas across socioeconomic strata. These practices, while environmentally beneficial in many respects, require appropriate design and maintenance to minimize vector breeding potential (Dhiman et al., 2014).

7. Integrated Surveillance Approaches and Innovations

7.1. Combined Entomological and Epidemiological Surveillance

Integrated surveillance systems that combine entomological and epidemiological data offer greater predictive power for dengue outbreaks compared to single-domain approaches. These integrated systems enable the identification of spatiotemporal associations between vector indices and disease incidence, potentially allowing for more targeted and timely interventions (Bowman et al., 2014).

In India, the National Centre for Disease Control (NCDC) has piloted integrated surveillance models in selected urban centers, combining traditional entomological indices with clinical reporting and laboratory confirmation (Ramaiah et al., 2021). This approach has demonstrated improved sensitivity for early outbreak detection compared to either system alone. The integration of adult mosquito sampling methods, including ovitrap networks and BG-Sentinel traps, has further enhanced the predictive capacity of these systems (Srivastava et al., 2012).

Sri Lanka has implemented one of the most comprehensive integrated surveillance systems in the region through its National Dengue Control Unit (NDCU). This system coordinates entomological and epidemiological data collection, analysis, and response across all districts (Tissera et al., 2016). Regular review meetings at district and national levels facilitate data integration and coordinated decision-making for resource allocation and intervention planning. The system's effectiveness was demonstrated during the 2017 epidemic, when early warning signals triggered enhanced vector control measures in high-risk areas (Tissera et al., 2020).

Bangladesh has initiated steps toward integrated surveillance through the Directorate General of Health Services (DGHS), with joint collection and analysis of vector and case data during epidemic periods (Mutsuddy et al., 2019).

However, challenges persist in maintaining routine integrated surveillance during inter-epidemic periods and in establishing clear thresholds for action based on combined indicators.

Bhutan's emerging dengue control program has adopted integrated surveillance principles from the outset, with the Vector-borne Disease Control Programme coordinating both entomological surveys and clinical case reporting (Dorji et al., 2016). This integrated approach, while still developing, provides a foundation for comprehensive monitoring of transmission dynamics in this recently endemic country.

7.2. Technological Innovations and Digital Solutions

Digital technologies have transformed surveillance capabilities across South Asia, enabling more efficient data collection, analysis, and dissemination for dengue prevention and control. Mobile applications, geographic information systems (GIS), remote sensing, and artificial intelligence offer promising tools to enhance traditional surveillance approaches (Lwin et al., 2016). Mobile technology has facilitated real-time reporting and spatial visualization of both vector breeding sites and dengue cases. India has implemented the Mobile-based Surveillance Quest using IT (MoSQuIT) system in selected cities, enabling field workers to upload geotagged data on vector breeding sites directly to central databases (Ramaiah et al., 2021). This system reduces reporting delays and provides accurate spatial information for targeted interventions. Similarly, the Dengue Case Information System (DCIS) mobile application has streamlined clinical case reporting from healthcare facilities, improving the timeliness and completeness of surveillance data (NVBDCP, 2019).

In Sri Lanka, the Mo-Buzz system represents a comprehensive digital solution combining public reporting, predictive analytics, and health communication functions (Lwin et al., 2016). The system enables citizens to report vector breeding sites through a mobile application, which feeds into a predictive algorithm incorporating meteorological data and historical case patterns to generate real-time risk maps. These maps guide both public health interventions and individual preventive behaviors through targeted messaging (Lwin et al., 2016).

Bangladesh has implemented the District Health Information Software 2 (DHIS2) platform to integrate dengue reporting within the broader health information system (Mutsuddy et al., 2019). This web-based system facilitates standardized data collection, analysis, and visualization across different administrative levels, improving the utility of surveillance data for decision-making. However, challenges persist in ensuring consistent reporting from all healthcare providers, particularly in the private sector (Hasan et al., 2016).

Bhutan's web-based reporting system, implemented in 2015, represents a significant advancement in surveillance capacity for this small country with challenging geography (Dorji et al., 2016). The system enables rapid case notification from district hospitals to the national level, facilitating timely response to emerging outbreaks. Mobile applications for community-based reporting are being piloted to complement this formal surveillance system, particularly in remote areas with limited healthcare access (Tenzin et al., 2020). Geographic information systems and remote sensing technologies have enhanced spatial analysis of dengue risk factors across South Asia. In India, satellite imagery has been used to identify environmental risk factors associated with dengue transmission, including vegetation indices, surface temperature, and urban land use patterns (Ramaiah et al., 2021). These analyses enable the development of risk maps at various spatial scales, from city neighborhoods to regional landscapes, guiding resource allocation for prevention and control activities. Artificial intelligence and machine learning approaches are emerging as powerful tools for dengue prediction and risk assessment. Studies in Sri Lanka and India have demonstrated the potential of neural networks and other advanced analytics to improve forecasting accuracy by integrating diverse data streams, including climatic variables, vector indices, population immunity patterns, and historical case data (Sirisena et al., 2017). While these approaches require further validation and optimization, they represent promising avenues for enhancing predictive capacity in complex transmission environments.

8. Challenges and Opportunities in Dengue Prevention and Control

8.1. Diagnostic and Reporting Challenges

Accurate diagnosis and comprehensive reporting remain fundamental challenges for dengue surveillance and control across South Asia. Several key issues require attention to strengthen these essential components of effective response systems.

8.1.1. Laboratory Diagnostic Capacity

Limited laboratory capacity for confirmatory testing continues to hamper surveillance efforts, particularly in rural and resource-constrained settings. While rapid diagnostic tests (RDTs) have improved point-of-care diagnosis, their variable sensitivity and specificity, especially during the early phase of infection, affect the reliability of surveillance data (Mardekian & Roberts, 2015). The cross-reactivity between dengue and other flaviviruses, including Zika and Japanese encephalitis, further complicates accurate diagnosis in areas where multiple arboviruses co-circulate (Guzman et al., 2010). Molecular diagnostic methods, particularly RT-PCR for serotype identification, remain concentrated in reference laboratories with limited geographic coverage (Chakravarti et al., 2012). This centralization creates delays in obtaining crucial serotype data, which has implications for both clinical management and public health response. Strengthening peripheral laboratory capacity through equipment provision, personnel training, and quality assurance programs represents a critical need across all four countries (WHO, 2020). The development and validation of multiplex diagnostic platforms capable of simultaneously detecting multiple arboviruses could enhance efficiency and cost-effectiveness in resource-limited settings (Mardekian & Roberts, 2015). Similarly, innovative point-of-care molecular testing platforms that combine the accuracy of nucleic acid detection with the field applicability of RDTs offer promising solutions for improving diagnostic capability in remote areas (Guzman et al., 2010).

8.1.2. Reporting Systems and Integration

Under-reporting remains a significant challenge across all four countries, with estimated reporting rates as low as 2.8% in some regions of India (Joshua et al., 2016). This under-reporting creates a distorted picture of disease burden, complicating resource allocation and intervention planning. Several factors contribute to this gap, including limited healthcare access, reliance on clinical diagnosis without laboratory confirmation, and incomplete integration of private healthcare providers into national reporting systems (Hasan et al., 2016).

The fragmentation of reporting systems, with separate channels for clinical cases, laboratory results, and entomological data, impedes integrated analysis and response. While digital platforms have improved data management capabilities, challenges persist in interoperability between different systems and standardization of data formats across programs and administrative levels (WHO, 2020). Public-private partnerships represent a crucial opportunity to enhance reporting completeness. Engaging private healthcare providers through simplified reporting mechanisms, incentive structures, and feedback loops has shown promising results in pilot projects across the region (Ramaiah et al., 2021). Similarly, community-based reporting through mobile applications and social media monitoring can complement formal surveillance systems, particularly for detecting early outbreak signals (Lwin et al., 2016).

8.2. Vector Control Strategies and Limitations

Effective vector control remains elusive despite decades of experience, with several challenges limiting the impact of current approaches across South Asia.

8.2.1. Insecticide Resistance

The emergence and spread of insecticide resistance in *Aedes* populations represent significant threats to chemical control strategies. Studies in India have documented resistance to multiple insecticide classes, including organophosphates, pyrethroids, and carbamates, among *Aedes aegypti* populations in various regions (Dhiman et al., 2014). Similarly, Bangladesh and Sri Lanka have reported increasing resistance to commonly used insecticides, particularly pyrethroids, which form the basis for both larvicidal and adulticidal interventions (Karunaratne et al., 2013).

The limited availability of alternative insecticides with different modes of action constrains resistance management strategies. Rotation schedules, mosaic applications, and combination approaches require multiple effective compounds, which may not be available or affordable in many settings (Dhiman et al., 2014). This situation highlights the need for integrated vector management approaches that reduce reliance on chemical control and incorporate biological, environmental, and community-based interventions. Monitoring programs for insecticide resistance remain inconsistent across the region, with limited standardization of methods and reporting formats. Establishing comprehensive resistance monitoring networks, with regular testing using standardized protocols, would enable more effective insecticide selection and resistance management planning (Karunaratne et al., 2013).

8.2.2. Community Engagement and Sustainable Interventions

Sustainable vector control requires active community participation, yet engaging communities effectively remains challenging across diverse socioeconomic and cultural contexts. Top-down approaches often fail to address local perceptions, priorities, and behavioral determinants related to vector breeding and personal protection measures (Arunachalam et al., 2012). Promising community-based approaches have emerged in various settings, including the Community Effectiveness Trial for Dengue (COMDENG) in Sri Lanka, which demonstrated significant reductions in vector indices through participatory interventions (Tissera et al., 2016). Similarly, the Communication for Behavioral Impact (COMBI) approach has shown effectiveness in mobilizing communities for sustained vector control in selected sites across India and Bangladesh (Arunachalam et al., 2012). Integration of vector control with broader urban development and environmental management represents another promising avenue. Improved water supply systems that reduce the need for household water storage, waste management programs that eliminate container habitats, and housing improvements that decrease vector entry can provide sustainable solutions to vector proliferation (Bowman et al., 2014).

8.3. Emerging Approaches and Future Directions

8.3.1. Genomic Surveillance and Phylodynamics

Advanced genomic surveillance offers new opportunities for understanding dengue transmission dynamics and predicting epidemic potential. Whole-genome sequencing of DENV strains provides high-resolution data on viral evolution, enabling the detection of emerging variants with altered virulence, transmissibility, or immune escape potential (Islam et al., 2015; Faria et al., 2017). These genomic approaches have revealed important insights into the microevolution of dengue viruses during epidemic cycles, identifying mutations associated with fitness advantages that may drive outbreak dynamics (Sim & Hibberd, 2016; Sasmono et al., 2018).

Phylodynamic analysis, which integrates evolutionary and epidemiological data, has demonstrated utility for reconstructing transmission chains and identifying factors driving viral spread within and between countries (Ocwieja et al., 2014; Tian et al., 2021). Recent studies have employed Bayesian evolutionary analysis to track the movement of specific DENV genotypes across Southeast Asia, revealing patterns of viral traffic that correspond with human mobility networks (Pyke et al., 2016; Grubaugh et al., 2019). These approaches can potentially identify specific viral lineages associated with enhanced epidemic potential, guiding targeted interventions before widespread transmission occurs. Real-time genomic surveillance has proven particularly valuable during outbreaks, allowing public health officials to distinguish between endemic transmission and imported cases, while also monitoring for signs of selective pressure that might indicate changes in virulence (Schmidt et al., 2021; Chua et al., 2019). The integration of genomic data with traditional epidemiological surveillance significantly enhances outbreak investigations and improves the precision of response efforts (Dengue Vaccine Initiative, 2018; Shepard et al., 2016). Capacity building for genomic surveillance represents a priority area for regional collaboration. Establishing sequencing hubs with standardized protocols, bioinformatics capabilities, and data-sharing mechanisms would enhance the regional understanding of DENV evolution and spread (WHO, 2020; Luo et al., 2022). Successful implementations in Brazil and Singapore demonstrate how sustained investment in genomic infrastructure can strengthen dengue preparedness and response (Faria et al., 2018; Hapuarachchi et al., 2019). Initiatives such as the Global Initiative on Sharing All Influenza Data (GISAID) provide models for collaborative platforms that could be adapted for dengue genomic surveillance (Shu & McCauley, 2017; Ramakrishnan et al., 2021). The Southeast Asia Infectious Disease Clinical Research Network (SEAICRN) has already made significant strides in implementing shared genomic resources across the region (Ong et al., 2020; Aaskov et al., 2017).

8.3.2. Novel Vector Control Approaches

Innovative vector control technologies offer promising alternatives to conventional methods facing insecticide resistance and sustainability challenges. The release of *Wolbachia*-infected mosquitoes, which reduce viral transmission through cytoplasmic incompatibility and pathogen interference mechanisms, has shown effectiveness in pilot studies in other dengue-endemic regions (Tantowijoyo et al., 2020; O'Neill et al., 2018). In field trials in Yogyakarta, Indonesia, areas with established *Wolbachia* infections demonstrated a 77% reduction in dengue incidence compared to control areas (Utarini et al., 2021). The World Mosquito Program has successfully implemented this approach in multiple countries including Australia, Brazil, and Vietnam, with sustained impact over several years (Ryan et al., 2020). While not yet implemented at scale in South Asia, this approach holds significant potential for sustainable dengue reduction in urban settings, particularly given the region's high population density and year-round transmission patterns (Jeffery et al., 2022).

Similarly, sterile insect technique (SIT) and related genetic approaches, including Release of Insects carrying Dominant Lethals (RIDL), offer species-specific control methods that could complement conventional approaches (Carvalho et al., 2015; Zheng et al., 2019). These technologies have advanced significantly in recent years, with field trials demonstrating feasibility and effectiveness in various contexts. A large-scale field trial in Brazil using transgenic *Aedes aegypti* resulted in an 81-95% suppression of wild mosquito populations (Crawford et al., 2020). The International Atomic Energy Agency (IAEA) has supported SIT implementation in over 20 countries globally, demonstrating the scalability of this approach when properly adapted to local conditions (Bouyer et al., 2020). Their application in South Asian settings requires careful assessment of local ecological factors, including species distribution and seasonal dynamics, as well as regulatory frameworks and social considerations regarding the release of modified organisms (Ramchurn et al., 2021; Bartumeus et al., 2019). Lethal ovitraps and other attract-and-kill technologies represent less complex but potentially effective additions to the vector control toolkit. These approaches target gravid female mosquitoes seeking oviposition sites, reducing both the adult population and subsequent larval emergence (Eiras et al., 2018; Johnson et al., 2020). Field studies in Thailand demonstrated that high-density deployment of lethal ovitraps reduced adult *Aedes aegypti* populations by up to 79% and maintained this suppression for extended periods (Suwannapong et al., 2022). Additionally, the CDC Autocidal Gravid Ovitrap (AGO) demonstrated 53-70% reduction in adult *Aedes* populations in Puerto Rico over a three-year deployment period (Barrera et al., 2019). Their relative simplicity and targeted nature make them suitable for community-based implementation, potentially enhancing sustainable vector control efforts, particularly in resource-limited settings common throughout South Asia (Ritchie et al., 2022; Das et al., 2021). The integration of these novel approaches with established methods offers particular promise within an Integrated Vector Management (IVM) framework. Recent models suggest that combining *Wolbachia* releases with targeted insecticide application could reduce dengue transmission by over 90% in endemic settings, compared to 40-60% for either approach alone (Ferguson et al., 2021). Furthermore, cost-effectiveness analyses indicate that while initial implementation costs for novel technologies may be higher than conventional methods, their sustained impact and reduced maintenance requirements often result in greater long-term economic benefits (Brady et al., 2023; Yakob and Walker, 2022).

9. Regional Collaboration and Integration

9.1. Cross-border Surveillance and Response

The interconnected nature of dengue transmission across South Asia necessitates collaborative approaches to surveillance and control. Viral strains frequently move across national borders through human mobility, with introduced strains often associated with subsequent outbreaks (Ocwieja et al., 2014). Despite this reality, cross-border surveillance and response mechanisms remain underdeveloped in the region.

The Association of Southeast Asian Nations (ASEAN) Dengue Network provides a model for regional collaboration that could be adapted for South Asia. This network facilitates standardized case definitions, harmonized reporting formats, and regular data sharing among member countries, enhancing regional early warning capacity (WHO, 2020). A similar network for South Asian countries could strengthen collective preparedness and response capabilities. Border areas often experience enhanced dengue transmission due to frequent population movement, limited healthcare access, and coordination challenges between national health systems. Establishing joint surveillance and response mechanisms in these zones, including shared laboratory resources and coordinated vector control activities, could improve epidemic containment and prevention (Hasan et al., 2016). Regional capacity building initiatives, including training programs, technical exchanges, and shared research projects, can address disparities in surveillance and control capabilities among neighboring countries. The World Health Organization's South-East Asia Regional Office (WHO SEARO) has facilitated some cross-border collaboration, but more structured and sustained mechanisms are needed for effective regional dengue management (WHO, 2020).

9.2. Knowledge Sharing and Capacity Building

Knowledge sharing platforms facilitate the exchange of best practices, lessons learned, and innovative approaches across countries with similar dengue challenges. While academic publications and international conferences provide some avenues for exchange, more accessible and practical platforms are needed for frontline public health practitioners (Bowman et al., 2014). Regional training centers focusing on entomological surveillance, laboratory diagnostics, data management, and integrated vector management could enhance technical capacity across South Asia. These centers could offer standardized curricula, practical field experiences, and ongoing mentorship to build sustainable expertise in dengue prevention and control (WHO, 2020). Implementation research networks, connecting researchers with public health programs across the region, could accelerate the translation of evidence into practice. These networks could address critical operational questions regarding the effectiveness, feasibility, and sustainability of various surveillance and control approaches in different ecological and socioeconomic contexts (Arunachalam et al., 2012).

10. Conclusion

Dengue remains a persistent and evolving public health challenge across South Asia, with India, Bangladesh, Sri Lanka, and Bhutan experiencing different but interconnected epidemiological patterns. This comprehensive review has highlighted several critical aspects of dengue surveillance and control in the region, including serotype dynamics, surveillance challenges, and emerging innovative approaches.

The epidemiological landscape is characterized by increasing case numbers, expanding geographic distribution, and evolving serotype patterns across all four countries. Concurrent circulation of multiple serotypes (hyperendemicity) creates complex immunological interactions that influence disease severity and outbreak potential. Serotype shifts frequently precede major epidemics, underscoring the importance of comprehensive molecular surveillance for early warning and response. Surveillance systems face significant challenges, including under-reporting, limited laboratory capacity, inconsistent entomological monitoring, and fragmented data management. Traditional entomological indices show limited correlation with transmission risk, highlighting the need for more epidemiologically relevant indicators and integrated surveillance approaches. Climate change and urbanization are driving the geographic expansion of dengue, with cases reported from previously non-endemic areas including high-altitude regions of Bhutan and northern India. These environmental and social changes require adaptive surveillance and control strategies that account for changing vector ecology and human-vector interactions.

Recommendations

Based on the findings of this review, the following recommendations are proposed to strengthen dengue surveillance and control in South Asia:

- **Enhance laboratory capacity** for confirmatory diagnosis and serotype identification, particularly in peripheral healthcare facilities, through equipment provision, training programs, and quality assurance mechanisms.
- **Implement integrated surveillance systems** that combine entomological, epidemiological, and environmental data for improved risk assessment and early warning, with standardized indicators and clear thresholds for action.
- **Incorporate genomic surveillance** into routine monitoring programs to detect emerging viral variants with altered transmission or virulence characteristics, establishing regional sequencing hubs and data-sharing platforms.
- **Develop climate-informed early warning systems** that integrate meteorological data with vector and case information to predict high-risk periods and locations for targeted interventions.
- **Strengthen cross-border collaboration** through harmonized case definitions, standardized reporting formats, joint outbreak investigations, and coordinated control measures in border areas.
- **Expand community-based surveillance and control** initiatives that engage local populations in sustained vector management activities, tailored to specific socioeconomic and cultural contexts.
- **Evaluate novel vector control technologies**, including *Wolbachia*-based approaches, sterile insect techniques, and attract-and-kill methods, for potential integration into comprehensive control strategies.
- **Establish regional knowledge-sharing platforms** and training centers to facilitate capacity building, technical exchange, and translation of research into practice across South Asian countries.
- **Address urban environmental factors** through intersectoral collaboration between health, water supply, waste management, and urban planning departments to reduce vector breeding habitats in a sustainable manner.
- **Conduct implementation research** to evaluate the effectiveness, feasibility, and sustainability of different surveillance and control approaches in diverse ecological and socioeconomic settings.

Compliance with ethical standards

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