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The Role of the National Laboratory Network in the Surveillance and Control of Arboviral Diseases in Iran: A Focus on Dengue and Chikungunya

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ABSTRACT

Dengue and chikungunya are major arboviral diseases that have emerged as significant threats to global public health in recent decades. Their incidence and geographical distribution have expanded due to climate change, globalization, and the proliferation of *Aedes* vectors. The recent establishment of *Aedes aegypti* and *Aedes albopictus* in Iran, coupled with local transmission cases reported in 2024, underscores the imminent risk of outbreaks, particularly of dengue and chikungunya. This situation necessitates urgent preparedness, including integrated prevention strategies, outbreak response planning, and the strengthening of rapid and accurate diagnostic infrastructure. This review examines the pivotal role of the Department of Arboviruses and Viral Hemorrhagic Fevers (National Reference Laboratory) at the Pasteur Institute of Iran in the surveillance and control of these infections. It addresses the virology, entomology, geographical distribution, and epidemiology within Iran and the World Health Organization Eastern Mediterranean Region (EMR), alongside control challenges, diagnostic methods, and the importance of laboratory networking, highlighting the critical role of the National Reference Laboratory in managing these emerging threats.

INTRODUCTION

Arthropod-borne viruses (arboviruses) comprise a diverse group of viruses transmitted to humans and animals by hematophagous arthropods, such as mosquitoes, sand flies, and ticks [1]. Arboviral diseases are widely recognized as major global health threats due to their expanding geographical distribution, potential for large outbreaks, and severe clinical complications. In recent decades, climate change, unplanned urbanization, international travel, ecological shifts, and rapid viral evolution collectively drive the emergence, reemergence, and geographical spread of these viruses [2]. Of the approximately 500 known arboviruses, more than 150 are pathogenic to humans, with the most clinically significant pathogens being dengue virus (DENV), chikungunya virus (CHIKV), Zika virus (ZIKV), yellow fever virus (YFV), and West Nile virus (WNV) [3].

The Global Arbovirus Initiative, launched by the World Health Organization (WHO) in 2022, warns that emerging arbovirus pathogens could potentially trigger the next pandemic, as the scientific literature clearly indicates that this risk is steadily escalating. This warning from international experts underscores the critical imperative to prioritize strategic resources and heightened attention toward arboviruses [4].

The Eastern Mediterranean Region (EMRO) is highly vulnerable to arbovirus outbreaks due to a combination of environmental, climatic, and anthropogenic factors [5]. Although the region has varied climates, the presence of competent vectors, such as invasive *Aedes* mosquito species (*e.g.*, *Ae. aegypti* and *Ae. albopictus*), in major ecological habitats—including urban centers and irrigated lands—provides optimal conditions for the spread of arboviruses, such as DENV and CHIKV [5]. Other risk determinants include high population density in large cities with inadequate health infrastructure, chronic political and economic turmoil, the effects of global warming, and extensive international travel, particularly for religious pilgrimages [6]. These factors collectively position EMRO as a critical focal point for

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the occurrence and spread of arboviral diseases, necessitating the strengthening of healthcare systems and the implementation of comprehensive prevention strategies at the regional level [7].

In recent years, several dengue outbreaks have been reported in EMRO countries, such as Pakistan, Yemen, Saudi Arabia, and Egypt, highlighting both the proliferation of vectors and the continued spread of DENV in the region [8].

Iran also faces the threat of arbovirus introduction and spread owing to its geographical location and climatic diversity. Historically, DENV and CHIKV cases in Iran have been exclusively imported from endemic countries [8, 9]. Nevertheless, the introduction of *Aedes* vectors and recent reports of autochthonous DENV transmission have led to a notable shift in the epidemiological landscape, demonstrating the necessity for more advanced surveillance and control measures [10].

The Pasteur Institute of Iran, as a pivotal research and public health institute, is not only instrumental in the diagnosis, monitoring, and treatment of infectious diseases, including arboviral infections, but also in the development of national frameworks, guidelines, and policies. Accordingly, this review aims to synthesize current knowledge on the arboviral threat in Iran and the EMRO region, particularly regarding epidemiology, entomology, diagnostic challenges, and the critical role of reference laboratories in surveillance and control. By doing so, this review aims to identify gaps and inform public health strategies to mitigate the threat of emerging outbreaks.

Dengue and chikungunya virology

Dengue virus (DENV) belongs to the family *Flaviviridae* and the genus *Flavivirus*. DENV comprises four distinct serotypes, designated DENV-1 to DENV-4. Each serotype exhibits distinct antigenic and genetic profiles, which constitute a major mechanism of immune evasion. Immunity acquired following infection with one serotype confers protection only against that serotype and not against heterologous serotypes [9]. Furthermore, non-neutralizing or sub-neutralizing antibodies from a prior infection may induce antibody-dependent enhancement (ADE), whereby these antibodies facilitate viral entry into host immune cells, thereby exacerbating disease severity. The DENV virion is a spherical particle approximately 50 nm in diameter, possessing a positive-sense, single-stranded RNA genome enclosed within the capsid. The nucleocapsid is surrounded by a host-derived lipid bilayer in which the envelope (E) glycoprotein is embedded. The E glycoprotein mediates attachment to host cells and membrane fusion, and serves as the primary target of neutralizing antibodies [10].

Chikungunya virus (CHIKV) belongs to the family *Togaviridae* and the genus *Alphavirus*. Phylogenetic studies have identified several CHIKV genotypes, with the most common being the West African, East-Central-South African (ECSA), and Asian lineages, which are characterized by variations in genomic sequences and geographic distribution [11]. The CHIKV virion is a spherical particle with a diameter of approximately 60–70 nm, possessing a positive-sense, single-stranded RNA genome encapsidated by capsid proteins to form the nucleocapsid [11]. The viral envelope, derived from the host cell membrane, is studded with glycoprotein spikes essential for receptor binding, viral entry, and induction of the host immune response [11].

Complex replication cycle and distinct genetic features

The replication of DENV and CHIKV is a multi-stage process. Initially, viral surface proteins bind to specific host cell receptors, triggering viral entry via clathrin- or caveolae-mediated endocytosis. Following endosomal localization, the acidic environment induces fusion of the viral envelope with the endosomal membrane, releasing the RNA genome into the cytoplasm [12, 13]. The RNA genome functions as mRNA and is directly translated to produce a polyprotein, which is subsequently cleaved into non-structural proteins (nsP1–4 for CHIKV and NS1–NS5 for DENV) and structural proteins, including capsid (C), E3, E2, 6K, and E1 for CHIKV and C, prM/M, and E for DENV. Non-structural proteins facilitate the formation of RNA replication complexes within endoplasmic reticulum-derived vesicles. This is followed by replication of viral RNA and assembly of progeny virions in the endoplasmic reticulum and the Golgi apparatus, culminating in the release of mature virions via exocytosis [13]. A notable characteristic of the RNA genomes of these viruses is their high rate of mutation and recombination, which continually generates new genetic variants with altered transmissibility, pathogenicity, and immune evasion capabilities [14].

The multifaceted importance of genetic diversity in epidemiology and diagnosis

The considerable genetic variation among the diverse DENV serotypes and CHIKV genotypes has important implications for the epidemiology of these pathogens and their diagnostic detection [15]. At the epidemiological level, the existence of four different serotypes of DENV poses a greater threat of severe disease, particularly when secondary infection with a heterologous serotype occurs, potentially leading to ADE [16]. The emergence of new variants, driven by an increase in viral replicative competence within the vector and enhanced transmissibility, can cause larger and more rapidly expanding epidemics. The geographical distribution of competent mosquito vectors is a primary determinant of the potential for disease spread to new areas. Once the virus is introduced, its genetic diversity can influence the success of its establishment and the efficiency of

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transmission within novel vector populations. From a diagnostic perspective, genetic diversity can pose challenges to molecular assays, such as reverse transcription-polymerase chain reaction (RT-PCR), as mutations in primer or probe binding sites may lead to false-negative results [17]. Furthermore, the development of effective dengue vaccines is complicated by the necessity of inducing balanced protective immunity against all four serotypes simultaneously. In the case of CHIKV, identification and tracking of different genotypes are crucial for understanding transmission patterns and pathogenic potential [18]. Consequently, ongoing research into viral genetic diversity provides the essential foundation for developing preventive, diagnostic, and therapeutic strategies to effectively address these evolving threats [19].

Entomology of insect vectors

Insect vectors, especially *Aedes aegypti* and *Aedes albopictus* mosquitoes, are the main vectors of DENV and CHIKV; hence, they represent a significant public-health hazard in tropical and subtropical regions [20]. Although the two species belong to the same genus, they differ significantly in morphology, life-history characteristics, and feeding preferences, which affects their vector competence and capacity [21]. *Aedes aegypti* is highly synanthropic and peridomestic, and exhibits predominantly diurnal feeding activity, while *Aedes albopictus* has a wider range of ecological adaptations and can thrive in both rural environments and temperate climates [22]. These container-breeding mosquitoes have rapidly adapted to human environments due to their ability to lay eggs in a wide range of artificial containers, from discarded tires to small flower pots [23]. Furthermore, the development of insecticide resistance in these mosquitoes has created new challenges for vector control programs [24]. A thorough understanding of these unique characteristics, including their tolerance of diverse environmental conditions and distinct feeding patterns, is essential for elucidating the dynamics of dengue and chikungunya transmission and planning effective intervention strategies [25]. Consequently, robust surveillance and species identification are crucial for monitoring the spread of *Ae. aegypti* and *Ae. albopictus* and assessing their roles in transmitting multiple arboviruses, including DENV and CHIKV, in newly colonized regions [26-28].

Epidemiology of dengue and chikungunya

Dengue and chikungunya, particularly in tropical and subtropical regions, are considered among the most significant arboviral diseases. The EMRO region similarly faces this burden and has experienced varying incidence and prevalence rates of these diseases in different countries [26-28]. Factors such as climate change, rapid urbanization, and inadequate vector control have contributed to the increased incidence and geographical spread of these diseases across the region. For example, certain countries experience a higher disease burden due to more favorable environmental conditions for *Aedes* vectors, limited health infrastructure, and high population mobility [27]. In the case of Iran, due to its geographical location, proximity to endemic countries, and extensive regional connectivity, the importation of dengue and chikungunya cases from these endemic areas has always been a potential threat. Furthermore, the established presence of competent vector populations and favorable climatic conditions intensify disease transmission and increase the likelihood of local transmission and outbreaks [28]. The Ministry of Health, Treatment and Medical Education has reported a total of 808 cases of dengue from the beginning of the surveillance period to September 27, 2025, with the majority of cases attributed to local transmission in Chabahar city (650 cases) and 140 cases in Bandar Abbas city; the remaining cases were imported from endemic countries [29]. Notably, no autochthonous (local) or imported chikungunya cases were detected in Iran during this surveillance period. The transmission of these diseases occurs mainly through the bites of infected *Ae. aegypti* and *Ae. albopictus* mosquitoes. The major risk of infection is related to exposure to infected mosquitoes, which puts people living in regions with high vector density at the highest risk, as well as those who travel to endemic regions. Additionally, certain groups are at greater risk of developing severe disease after infection, including infants, the elderly, and people with weakened immune systems or underlying comorbidities. The constantly evolving epidemiological landscape, characterized by the persistent threat of case importation and increasing risk of local outbreaks, underscores the urgent need for a strong network of national laboratories. These networks are essential for effective arboviral disease outbreak response, enabling rapid diagnosis, viral strain identification, transmission monitoring, and proactive surveillance to guide control measures.

Vector distribution in Iran and the EMRO region

Aedes aegypti was first reported in Khorramshahr in 1920 and in Bushehr in the early 1950s [30]. After these reports, no further information was available about its presence in the country until 2020, when its presence was confirmed in Hormozgan Province [31]. In contrast, *Aedes albopictus* was first identified in Sistan and Baluchestan Province (near Chabahar) in 2009 [32]. However, it was later found in a geographically separate area, and its presence in Gilan Province in northern Iran was confirmed in 2023, demonstrating a significant range expansion [33]. Currently, *Ae. aegypti* is established in Hormozgan, Sistan and Baluchestan (Chabahar and Konarak counties), Bushehr (Asaluyeh, Kangan, Jam, and Borazjan counties), and Fars (Mehr County) Provinces, while *Ae. albopictus* is found mainly in northern and northwestern provinces, including Gilan Province, Mazandaran Province (Ramsar, Tonekabon, Abbasabad, Mahmoudabad, and Noor), Ardabil Province (Bilesavar and Aslanduz Counties), and East Azerbaijan

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Province (Khoda Afarin, Hurand, and Kaleybar Counties).

Climate change, trade, and travel facilitate vector spread in Iran [28]. The establishment and proliferation of *Aedes* vectors are a major public health concern in the EMRO region. As an example, *Ae. aegypti* is well established in countries such as Pakistan, Saudi Arabia, Sudan, and Yemen, while *Ae. albopictus* has been reported in Lebanon, Palestine, and Syria, among others [34]. The proliferation of these vectors has resulted in frequent outbreaks of dengue in countries such as Pakistan, Sudan, and Yemen, and outbreaks of chikungunya in Sudan and Yemen [26, 34-37]. Thus, *Aedes* mosquitoes and the arboviral diseases represent a shared challenge for Iran and other EMRO countries [29].

Challenges in the control of dengue and chikungunya

The control of dengue and chikungunya is hampered by a complex array of factors that affect the effectiveness of prevention and management programs [35]. In the context of vector control, the emergence and spread of insecticide resistance in *Aedes* populations necessitate the development and implementation of alternative methods [36]. Moreover, larval breeding sites cannot be completely eliminated, especially in urban areas with unreliable water supply systems that necessitate water storage. Consequently, source reduction remains challenging and requires sustained efforts and active community engagement [37]. There is an additional challenge of early diagnosis and clinical management of these arboviral diseases. The high prevalence of asymptomatic infections, combined with the predominance of non-specific symptoms in the initial stages, frequently leads to delays in diagnosis and compromises the timely initiation of treatment. Furthermore, there are no specific antiviral drugs against dengue and chikungunya, which limits clinical management to supportive care [38]. In addition, promoting community engagement and implementing behavioral change communication in prevention and control programs remain significant challenges. Poor understanding of disease transmission mechanisms, the importance of source reduction and vector breeding site management, and personal protection methods collectively undermines the effectiveness of public health interventions [39]. Lastly, in the case of dengue, although vaccines have been approved, constraints, including varying vaccine efficacy across the four serotypes and the possibility of ADE in seronegative patients, have limited the widespread implementation of vaccination programs [40]. With regard to chikungunya, a live-attenuated vaccine was recently approved, representing a significant milestone; however, its use remains limited. Nevertheless, these vaccines face challenges in global deployment. Equitable access remains a primary concern, since populations in most endemic low- and middle-income countries, who experience the greatest burden of disease, face systemic barriers to vaccination campaign implementation. These barriers include high costs, cold chain requirements, limited healthcare infrastructure, and logistical challenges. Overcoming these challenges is essential to realize the full public health potential of these new tools.

Laboratory diagnosis of dengue and chikungunya

Timely and accurate diagnosis plays a crucial role in the efficient clinical management of patients as well as prompt public health action in outbreak control [41]. Direct diagnostic methods for dengue and chikungunya are mainly used in the acute phase of the disease (about the first 5 to 7 days after the onset of fever) and aim to identify the virus itself or viral components.

Molecular techniques, including RT-PCR and real-time RT-PCR, are used for the detection of viral RNA and determination of the four serotypes (DENV-1 to DENV-4) in dengue [41]. Moreover, the NS1 antigen test, available as either an enzyme-linked immunosorbent assay (ELISA) or a rapid test, is a useful diagnostic method used to detect the secreted viral protein during days 1 to 7 and serves as a valuable marker for early diagnosis [42]. Viral isolation in susceptible cells such as C6/36 is also possible; however, due to its time-consuming nature and requirement for specialized facilities, this method is primarily employed in research settings or for confirmatory testing.

In contrast, for chikungunya, direct diagnosis is primarily limited to molecular methods such as conventional RT-PCR and real-time RT-PCR, which detect viral RNA in the blood of patients during the acute phase and also allow the determination of different virus genotypes [41]. Viral culture may also be performed using cell lines such as Vero or C6/36, although, as with dengue, this is typically only performed in reference laboratories [43]. The principal distinction between dengue and chikungunya diagnostics is that, unlike dengue, chikungunya lacks a comparable antigen detection test such as the NS1 assay.

Indirect diagnostic tests that identify the presence of antibodies, produced by the host immune system, are useful during later stages of the disease. Serological detection of IgM and IgG antibodies using ELISA is a routine diagnostic approach. IgM antibodies, indicative of recent infection, can be detected between days 4 and 5 of illness, whereas IgG antibodies, which indicate previous infection or immunity, appear later and may persist for an extended period [44].

Another major issue in the molecular and serological diagnosis of dengue and chikungunya is the considerable genetic variability among dengue serotypes and chikungunya lineages. This variability may affect the performance and accuracy of diagnostic tests and lead to mismatches in primer/probe or antibody binding sites

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[45]. Additionally, one of the greatest concerns is serological cross-reactivity, particularly among some flaviviruses, including dengue and Zika, which can cause false positives and distort the assessment of an individual's immune status. Consequently, diagnosis is frequently confirmed using multiple assays and the application of comprehensive diagnostic algorithms that integrate clinical, epidemiological, and laboratory data from multiple sources [46].

The multifaceted role of the National Reference Laboratory in the national surveillance system for arboviral diseases

***a)* Surveillance**

The National Reference Laboratory for Arboviruses and Viral Hemorrhagic Fevers at the Pasteur Institute of Iran plays a crucial role in the national surveillance system for dengue and chikungunya. The laboratory is responsible for confirming suspected cases using advanced diagnostic methods, serotyping and genotyping, and monitoring the spread of these viruses. Additionally, it coordinates the country's laboratory network through protocol standardization and provision of technical support to regional laboratories [47]. The laboratory also collects and analyzes epidemiological and laboratory data, which assists in health policy decision-making and the development of prevention and control programs for these diseases.

b) Research and development of diagnostic methods

The laboratory has conducted extensive research and development activities on new diagnostic tools to improve diagnostic quality and turnaround time. These activities include designing and validating laboratory-developed tests (LDTs) and developing more specific multiplex molecular protocols to detect and differentiate dengue serotypes and chikungunya genotypes [48]. These activities aim to increase test accuracy, sensitivity, and clinical applicability, and ultimately enhance early diagnostic capacity at the national level. These efforts have also facilitated the development of local technical expertise and reduced reliance on external resources.

c) Networking and network quality assurance

Establishing and strengthening a coherent and efficient laboratory network at the national level for the surveillance of arboviruses, including DENV and CHIKV, is essential [49]. The National Reference Laboratory, in collaboration with the Health Reference Laboratory of the Ministry of Health, has developed a network of 11 reference partner centers in at-risk cities to improve the efficiency of diagnostic activities. This network enables early detection of disease cases, identification of virus spread patterns, assessment of the effectiveness of control measures, and appropriate response to public health threats. Moreover, it has significantly enhanced testing capacity, reduced turnaround time for results, and minimized the risks associated with sample transportation. To expand geographic coverage and integrate diagnostic services, the reference laboratory plays a critical role in building, developing, and connecting a nationwide network of partnering laboratories. This endeavor will facilitate experience sharing, data exchange, and improvement of the technical capacity of the provinces by providing standard protocols, reference materials, and training courses to enhance operational capacity [50]. The laboratory monitors network performance through internal quality control and participation in External Quality Assurance (EQA) programs to ensure result validity throughout the national network [51].

d) Sample management and establishment of a biobank

The National Reference Laboratory has established, stored, and systematically managed human and vector samples using advanced technical infrastructure. This biobank serves as a valuable biological resource for future studies and responses to health crises. The samples stored in this biobank include blood, serum, plasma, and cerebrospinal fluid samples from patients, as well as whole mosquitoes and/or their extracted viral RNA. By systematically organizing epidemiological and genetic data associated with these samples, researchers can conduct comparative analyses, monitor viral evolution, and examine the effectiveness of interventions [52].

e) Outbreak response

One of the strategic tasks of the National Reference Laboratory is to respond rapidly to disease outbreaks and public health threats posed by arboviruses. The laboratory supports the design and implementation of control measures in affected regions through the rapid detection of early cases and confirmation of suspected cases. The laboratory also actively collaborates with the Ministry of Health, providing epidemiological and diagnostic reports to support evidence-based decision-making during epidemics. Its continued role at the forefront of crisis response has helped ensure that the country's health system is prepared to confront emerging and re-emerging diseases [53].

f) Training and capacity building

The reference laboratory continuously implements extensive training activities to strengthen the knowledge and skills of staff involved in dengue and chikungunya surveillance [54]. These activities include conducting specialized training courses, skills workshops, laboratory staff training, and provision of technical guidance to different levels of the health system. These activities aim to increase the responsiveness of the country's diagnostic network, improve working standards, and facilitate the transfer of new technologies to operational levels of the health system. Training, as a cornerstone of capacity

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development, is integral to all programs of the laboratory.

Challenges and future strategies in dengue and chikungunya disease control in Iran

Timely and precise diagnosis of arboviral infections, including dengue and chikungunya, is a key requirement for the management of potential outbreaks in the country. However, there are various impediments to the prevailing diagnostic framework that reduce the effectiveness of responses [55]. The following are the main limitations, each accompanied by proposed mitigation measures.

a) Clinical similarity to other febrile diseases

Most of the prodromal manifestations of dengue and chikungunya, such as fever, myalgia, and skin eruptions, are similar to the manifestations of other viral and bacterial infections, such as influenza, typhoid fever, malaria, and COVID-19. Consequently, clinical assessment is often insufficient and can result in misdiagnosis [56]. Standardized, practitioner-friendly clinical protocols, supported by confirmatory molecular or serological assays for all suspected cases, can increase diagnostic accuracy. In addition, systematic training in differential diagnosis is critical [57].

b) Limited time window for molecular tests (RT-PCR)

RT-PCR can only detect DENV and CHIKV in the acute phase of infection, typically within 5–7 days after symptom onset. Beyond this window, test sensitivity decreases, and false-negative results become more frequent. Diagnostic coverage can be improved by implementing rapid alert systems to ensure timely specimen collection, training healthcare workers in rapid sampling techniques, and deploying point-of-care tests (POCTs) [58].

c) Limited access to advanced diagnostic equipment nationwide

Specialized centers with advanced molecular and serological capabilities, such as the Pasteur Institute of Iran or certain academic institutions, possess most of the equipment and expertise, leaving many provinces and municipalities without adequate resources [50]. Strategically equipping selected provincial laboratories with basic PCR platforms, standard serological kits, and refrigerated storage systems, as well as providing targeted personnel training, should be prioritized within the health system.

d) Weaknesses in the referral and transfer system

Additional limitations include delayed diagnosis, time-consuming sample dispatch, failure to maintain cold-chain conditions, and inadequate coordination between environmental health authorities and specialized laboratories, all of which result in inaccurate or unreliable results [59]. Establishing a national specimen referral network with standardized protocols, equipping regional hubs with secure transport containers and portable refrigerators, and implementing a regular, scheduled sample submission system can significantly reduce these concerns.

e) Lack of an integrated electronic system for recording and tracking samples

The absence of an integrated online platform consolidating patient clinical information, specimen status, test results, and referral records creates data gaps and errors that compromise epidemic surveillance [60]. The development and implementation of a national Laboratory Information Management System (LIMS) integrated with the disease-surveillance infrastructure of the Ministry of Health is a key measure for strengthening coordination and operational effectiveness.

f) Lack of trained technicians in the rural areas

Many provincial laboratories lack personnel trained in arbovirus diagnosis, and existing staff often lack experience with molecular instruments and result interpretation [61]. This shortage can be addressed through annual in-person or remote training workshops for laboratory technologists nationwide, leveraging the expertise of reference laboratory trainers, and deploying dedicated support teams during outbreaks. Moreover, DENV and CHIKV diagnostic kits are predominantly imported and vulnerable to sanctions, exchange-rate fluctuations, and customs delays, which disrupt diagnostic workflows [54]. Supporting knowledge-based companies in local kit manufacturing, ensuring rigorous verification and certification of domestic kits by the reference laboratory, and establishing strategic stocks in provincial centers are practical solutions to this problem.

CONCLUSION

Preparedness and decisive action against the threat of dengue and chikungunya in Iran require immediate attention. Evidence suggests that these arboviruses could become endemic, with transmission risk rapidly increasing due to the expanding population and geographic range of *Aedes* mosquito vectors, increased international travel, and climate change. Reference laboratories, particularly the National Reference Laboratory at the Pasteur Institute of Iran, provide essential capabilities for early diagnosis, continuous monitoring of disease and vector status, and guidance of effective health responses at the national level. These institutions provide policymakers with vital information for evidence-based decision-making by offering accurate and timely case data. However, effectively confronting this threat requires a comprehensive and coordinated national approach. Strengthening laboratory infrastructure at various levels, especially in high-risk provinces, through the provision of advanced equipment and training of specialized personnel, is an urgent priority. Collaboration among the Ministry of Health, the Department of Environment, municipalities, and other

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relevant institutions is also essential. These partnerships should prioritize integrated vector management, environmental sanitation, and community engagement. Investing in epidemiological and entomological research to better understand disease transmission patterns and characteristics of native vectors, as well as strengthening integrated national surveillance and reporting systems, represents additional essential measures for an effective response to this growing public health challenge in Iran. Implementing preventive measures is critical to protect public health from these threats.

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CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest associated with this manuscript.

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DATA AVILABILITY

This article provides a review and synthesis of data from previously published studies. No new datasets were generated or analyzed during this study.

AUTHORS' CONTRIBUTIONS

MSV, TJ, MHP: Conceptualization, MHP: Writing – original draft, MSV, TJ, MT, SMS, LFA, ZH, FA, TM, SKH, MHP: Writing – review and editing, MHP: Supervision. All authors read and approved the final version of the manuscript.

ETHICS STATEMENT

This article is a narrative review based on previously published literature and does not involve human subjects, animal experiments, or the collection of primary data. Therefore, ethical approval was not required.

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