Virology 617 (2026) 110825

Contents lists available at ScienceDirect

Virology

journal homepage: www.elsevier.com/locate/virology

Mosquito-borne viruses in Australia: An emerging trend of increasing prevalence in Northern Queensland

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ARTICLE INFO

Keywords:
Mosquito-borne viruses (MBVs)
Northern Queensland
Wolbachia-based control
Public health

ABSTRACT

Mosquito-borne viruses (MBVs) remain a significant public health concern in Northern Queensland, Australia, with dengue virus (DENV), Ross River virus (RRV), and Barmah Forest virus (BFV) representing the most common pathogens. *Wolbachia*-based biological control programs have made notable contributions to reducing dengue transmission by suppressing *Aedes aegypti* vector competence. Recent surveillance data indicates increased MBV activity, with national case numbers nearly doubling between 2023 and 2024 and early 2025 data suggesting sustained transmission during seasonal peak. Traditional surveillance approaches, while highly valuable for disease monitoring, have limitations in detecting novel or divergent viral strains in real time. Over the past decades, more than 919 unclassified flaviviruses have been reported nationwide, including 117 in Queensland. The advent of metagenomic and metatranscriptomic approaches now enable enhanced, field-based detection of both known and emerging arboviruses. Strengthening mosquito control programs through continued *Wolbachia* releases, alongside integrated genomic surveillance, predictive modelling, and community engagement will enhance early detection, guide targeted interventions, and reduce the MBV burden in Northern Queensland. This integrated framework provides a strategic pathway to sustains and expand vector control effectiveness while safeguarding public health in high-risk regions.

1. Introduction

Mosquitoes, though diminutive in size, serve as highly effective reservoirs and vectors of a broad range of viruses (Wang et al., 2022). MBVs remain among the most pressing public health threats worldwide, causing recurrent epidemics, persistent endemic circulation, and significant morbidity and mortality (Mbaoma et al., 2025; Naik et al., 2023). Among them, dengue virus (DENV), chikungunya virus (CHIKV), Zika virus, Ross River virus (RRV), Barmah Forest virus (BFV), Japanese encephalitis virus (JEV), and West Nile virus (WNV) represent one of the most formidable and escalating public health threats of the 21st century (Girard et al., 2020; Madzokere et al., 2022b; Viennet et al., 2024). Collectively, these pathogens threaten nearly half of the world's population, with an estimated four billion people living in regions at risk of dengue transmission. Dengue alone exemplifies the scale of this threat with 390 million infections annually (Anasir et al., 2023; Ong et al., 2021a). Now endemic in more than 125 countries across the tropics and subtropics of Asia-Pacific, the Americas, Africa, and the Middle East, DENV underscores both the global scale and accelerating pace of MBV-related public health threats (de Almeida et al., 2025).

The intensification of MBV transmission reflects the convergence of multiple drivers. Climate change is lengthening and intensifying transmission seasons, while rapid urbanisation provides abundant breeding habitats for mosquito vectors (Franklinos et al., 2019; Wang et al., 2020). Globalisation and human mobility accelerate the cross-border spread of both viruses and vectors, and surveillance limitations in resource-limited settings exacerbate under detection and delayed response. These factors have fuelled outbreaks that are increasingly frequent, intense, and geographically widespread, placing immense strain on public health systems (Duval et al., 2023; Franklinos et al., 2019; Ortiz et al., 2021; Wang et al., 2020). Traditional vector control methods, primarily reliant on insecticides and environmental

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https://doi.org/10.1016/j.virol.2026.110825
Received 24 November 2025; Received in revised form 26 January 2026; Accepted 3 February 2026
Available online 3 February 2026

management have achieved only temporary success (Wilson et al., 2020). Their longer-term effectiveness is often undermined by insecticide resistance, difficulties in sustaining community engagement, and environmental concerns (Tiffin et al., 2025; Wilson et al., 2020). Even integrated strategies such as the IMS-dengue framework, implemented in the Americas to combine patient care, communication, surveillance, and environmental interventions, remain insufficient on their own to reverse global transmission trends (Allen, 2013; Sisay et al., 2025).

In this context, innovative, nature-based strategies are being implemented as promising alternatives. Among these, the *Wolbachia* method has shown transformative potential. Introducing the *Wolbachia* endosymbiotic bacterium into *Aedes aegypti* mosquitoes reduces their capacity to transmit viruses such as DENV, CHIKV, and ZIKV (Moreira et al., 2009; Walker et al., 2011). The World Mosquito Program has implemented this approach in 14 countries, protecting more than 13 million people (Poinsignon et al., 2025; World Mosquito Program, 2024). Field evidence from Yogyakarta, Indonesia, demonstrated a 63% reduction in dengue incidence in *Wolbachia*-treated areas (Indriani et al., 2020), while large-scale release in Townsville and Cairns achieved approximately a 95% reduction in DENV up to 2020 (O'Neill et al., 2019; Ryan et al., 2020). Beyond releases conducted under the World Mosquito Program, *Wolbachia*-based vector control has also been implemented with notable success. In Malaysia, large-scale field releases of *Aedes aegypti* carrying the wAlbB strain of *Wolbachia*, a locally adapted strain distinct from the commonly deployed wMel resulted in stable population replacement and substantial reductions in dengue incidence (Hoffmann et al., 2024; Nazni et al., 2019). These results underscore *Wolbachia* as one of the most effective and sustainable public health interventions for dengue control to date, providing a model for global vector-borne disease management. However, sustained monitoring remains important to ensure long-term population stability and effectiveness under varying ecological conditions.

Northern Queensland exemplifies the convergence of ecological, climatic, and demographic vulnerabilities that heighten MBV risk. Competent vectors such as *Aedes aegypti* and *Culex annulirostris* thrive in the region, while urbanisation, tropical climate, and proximity to Southeast Asia increase exposure to both endemic viruses like RRV and BFV and epidemic incursions such as DENV and JEV (Ong et al., 2021a). Although *Wolbachia*-based control has successfully reduced dengue transmission, recent surveillance data indicate that broader MBV activity continues to rise, reflecting the influence of multiple factors and likely circulating diverse viruses (Department of Health, D.a.A. Australian Government, 2025; Health, 2018). This highlights the need to complement *Wolbachia* with additional approaches that address other arboviruses beyond dengue.

Conventional hospital-based surveillance remains a cornerstone for arboviral detection and has provided the backbone of national MBV reporting. However, its reliance on symptomatic cases means it is best complemented by modern tools that can capture early or atypical viral activity. High-throughput genome sequencing approaches such as metagenomics and metatranscriptomics are particularly valuable in this regard, enabling proactive field-based detection of both known and novel arboviruses (Bikel et al., 2015; Jamiu and Chaguza, 2024; Ko et al., 2022b; Shi et al., 2017a). Despite decades of arbovirus surveillance in Australia, a substantial proportion of detected flaviviruses remain incompletely characterised, (Health, 2018), reflecting inherent limitations of conventional surveillance approaches rather than comprehensive genomic resolution. This hidden viral diversity underscores the need for more advanced genomic methods to fully define the spectrum of mosquito-borne flaviviruses circulating nationally. Framing MBV control within an integrated approach that combines the proven success of *Wolbachia* releases, used in Australia to reduce dengue virus transmission by *Aedes aegypti* with genomic surveillance, predictive modelling, and community engagement is therefore essential. While recognising that *Wolbachia*-based strategy is currently species-specific and not applicable to MBVs transmitted by other mosquito vectors. Such integration may strengthen early warning capacity, inform timely interventions, and mitigate the escalating arboviral burden in Northern Queensland.

This review aims to analyse MBV activity in Australia, with a particular focus on Northern Queensland, using routinely collected hospital-based and laboratory-confirmed surveillance data. We synthesise data from the Queensland Health surveillance system and national notifiable disease surveillance databases, covering the period 1991 to July 2025. These data are used to characterise long-term and recent temporal trends in MBV notifications, assess evidence for changing transmission intensity, and identify emerging public health risks. The surveillance findings are systematically interpreted alongside published entomological and virological studies, allowing triangulation of epidemiological patterns with vector ecology, virus circulation, and environmental drivers. Finally, the review explores how integrating *Wolbachia*-based vector control, genomic surveillance technologies, and coordinated surveillance frameworks could strengthen early detection, outbreak attribution, and public health preparedness in Northern Australia.

2. Drivers of mosquito-borne virus intensification in Australia

Mosquito-borne viruses in Australia are driven by a complex interplay of climatic, environmental, ecological and anthropogenic factors that influence vector abundance, virus replication, and transmission dynamics (de Souza and Weaver, 2024; Shocket et al., 2020a; Stratton et al., 2017). Climatic conditions, particularly temperature and rainfall patterns associated with La Niña and climate change, remains the strongest determinant of arbovirus transmission. La Niña–associated hot and wet conditions in Australia during 2023–24 was directly linked to an upsurge in RRV, BFV and DENV transmission by creating extensive mosquito breeding habitats and shortening the extrinsic incubation period of viruses in vectors. These conditions facilitated higher transmission potential at the height of the 2024 outbreak in Queensland (Qian et al., 2025; Sanders, 2025; Stratton et al., 2017; Viennet et al., 2024). Elevated temperatures have been consistently linked to increased RRV and BFV risk across coastal and inland Australia, with infection spikes when temperatures range between ~17 and 31 °C, and particularly near ~26 °C, as mosquito development and survival are optimized at these ranges (Varghese et al., 2025). Although mosquito biting rates increase with rising temperatures (Shocket et al., 2018), RRV notifications in Queensland were observed to decline when temperatures exceeded 35 °C, likely reflecting reduced mosquito survival and population densities at extreme heat (Gatton et al., 2005). Rainfall and flooding further amplify risk by inundating wetlands, creeks, and artificial containers, producing extensive larval habitats. Study in South-eastern Tasmania and South Australia has quantified significant lagged effects of rainfall and temperature on mosquito larvae abundance and subsequent RRV notifications, supporting mechanistic links between environmental conditions and vector population dynamics (Werner et al., 2012). Environmental and ecological factors further modulate transmission risk by shaping habitat suitability for mosquito vectors (Chandrasegaran et al., 2020; Shocket et al., 2020a). Wetlands, estuarine systems and flood-prone landscapes provide persistent larval habitats for key vectors such as *Aedes* and *Culex* species, which in turn amplify virus transmission. Analyses of landscape characteristics have linked the distribution of BFV to wetland extent and climatic zones within Queensland, reflecting habitat disease associations that vary by virus and vector ecology (Naish et al., 2012).

Anthropogenic factors, including international travel and urbanisation, also contribute to intensification by facilitating the introduction and local seeding of DENV and other flaviviruses into receptive regions such as Northern Queensland (Akter et al., 2019; Warrilow et al., 2012). Although endemic BFV and RRV maintain enzootic cycles within Australia, frequent importation of DENV via infected travellers into areas with established *Aedes aegypti* populations has repeatedly triggered local transmission (Sohail et al., 2024). Urban expansion, changing land use patterns, and socio-environmental behaviours that increase human–vector contact further heighten transmission risk and extend spatial opportunities for outbreaks (Alqassim, 2024; Kolimenakis et al., 2021). So, long-term climate change projections indicate an expansion of suitable vector habitats and lengthened seasons for mosquito activity, which will likely broaden the geographic range and duration of arbovirus transmission beyond historical patterns. This integrated evidence underscores that MBV intensification in Australia is not driven by a single factor, but by cascading interactions among climatic variability, environmental change, vector ecology, and human behaviour, requiring adaptive surveillance and control strategies that reflect this multi-dimensional risk landscape.

3. Historical and recent trends in mosquito-borne virus activity

3.1. National overview

The national notifiable disease data from 1991- July 2025 reveals fluctuating but persistent MBV activity, punctuated by pronounced epidemic peaks (Department of HealthD.a.A.Australian Government, 2025). Queensland has remained the national hotspot, with 95,356 hospital-reported cases more than twice the burden observed in New South Wales (40,220) or Western Australia (30,402) (Fig. 1a–c, & Supplementary file). This geographic concentration aligns with previous studies identifying Northern Queensland as Australia's most permissive region for arbovirus transmission due to favourable climate, vector abundance, and historical endemicity (Adekunle et al., 2019; Ong et al., 2021b; Viennet et al., 2024). Recurrent peaks were observed in the mid-1990s, mid-2000s, around 2015, and again in 2024, reflecting sharp boom–bust epidemic cycles. More recently, national MBV cases nearly doubled between 2023 and 2024 (3258 to 6161), largely driven by a threefold increase in Queensland (1043 to 3082), with marked increases also observed in NSW, Victoria, and WA. In 2025, ABC news also reported that MBV almost triple in Queensland due to rises in RRV and DENV infections possibly driven by La Niña condition that facilitates mosquito breeding (Sanders, 2025). Remarkably, by mid-2025, national case numbers (3,024) had already approached the total reported for 2023, suggesting another potential surge (Fig. 1b).

Over the past three decades, multiple medically important arboviruses have been detected in Australia, including RRV, BFV, DENV, CHIKV, JEV, MVEV, KUNV/WNV, and unclassified flaviviruses (Fig. 1b). RRV dominated the national burden with 142,680 cases, followed by BFV (31,536) and DENV (26,725). Research indicates that RRV is the most widespread arbovirus in Australia, responsible for most human vector-borne infections, followed by BFV, while dengue exhibits notable but more localized transmission dynamics (Madzokere et al., 2022a; Stratton et al., 2017). Moderate activity was recorded for CHIKV (1, 135), while WNV/KUNV (48), JEV (71), and MVEV (72) were comparatively rare. Importantly, although RRV and BFV are the most prevalent endemic arboviruses, DENV poses the significant biosecurity risk in Australia due to its epidemic potential and the widespread presence of competent vectors, particularly *Aedes aegypti,* in Northern Queensland and other tropical regions that facilitate local transmission (Horwood et al., 2018; Silburn and Arndell, 2024). These local outbreaks are strongly influenced by importation of DENV via infected travellers,

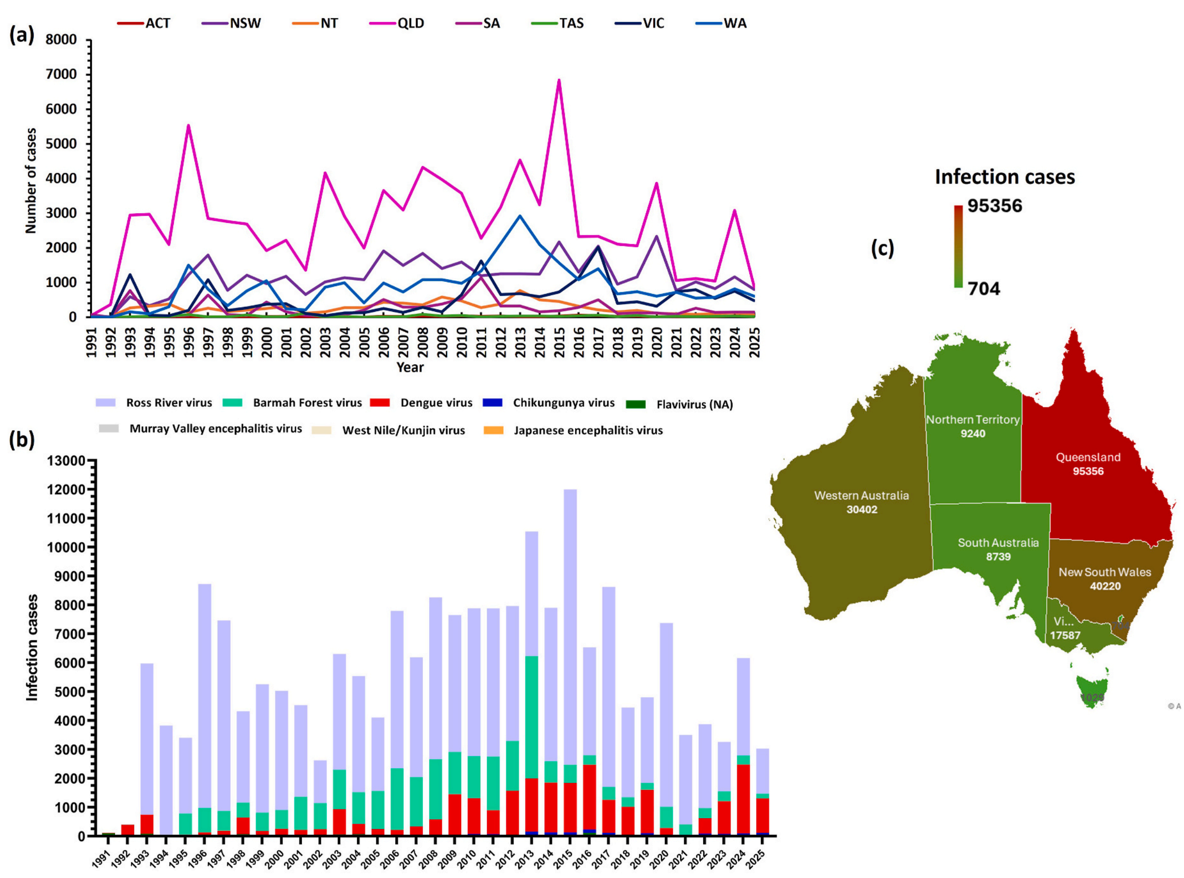

Fig. 1. Spatial and temporal distribution of MBV infections in Australia. (a) Line graph showing annual MBV infection cases reported from 1991 to 2025 across all Australian states and territories, highlighting recurrent peaks in Queensland. (b) Bar graph representing the number of cases of individual MBVs (DENV, RRV, BFV, MVEV, KUNV, JEV, and others) reported in each state and territory. (c) Choropleth map illustrating cumulative MBV cases by state and territory, indicating Queensland as the most affected region with the highest case count (93,556) (**See Supplementary file**).

which can seed transmission in areas where *Aedes aegypti* populations are established (Rowe et al., 2018; Sohail et al., 2024).

Recent surveillance data show a marked increase in arboviral detections from 2023 to 2024, with RRV (1710 to 3375) and DENV (1118 to 2375) driving the rise, while BFV remained stable (345 to 316) and JEV emerged with a single case. In early 2025, RRV (1,559) and DENV (1,184) continue to dominate, supported by moderate BFV (164) and rising JEV (8), underscoring the ongoing and evolving arboviral threat in Northern Australia (Fig. 1b). In recent years, JEV has undergone a notable range expansion on the Australian mainland, shifting from a historically northern distribution to widespread detections across multiple states (Australian Department of Agriculture, 2026; Pyke et al.,

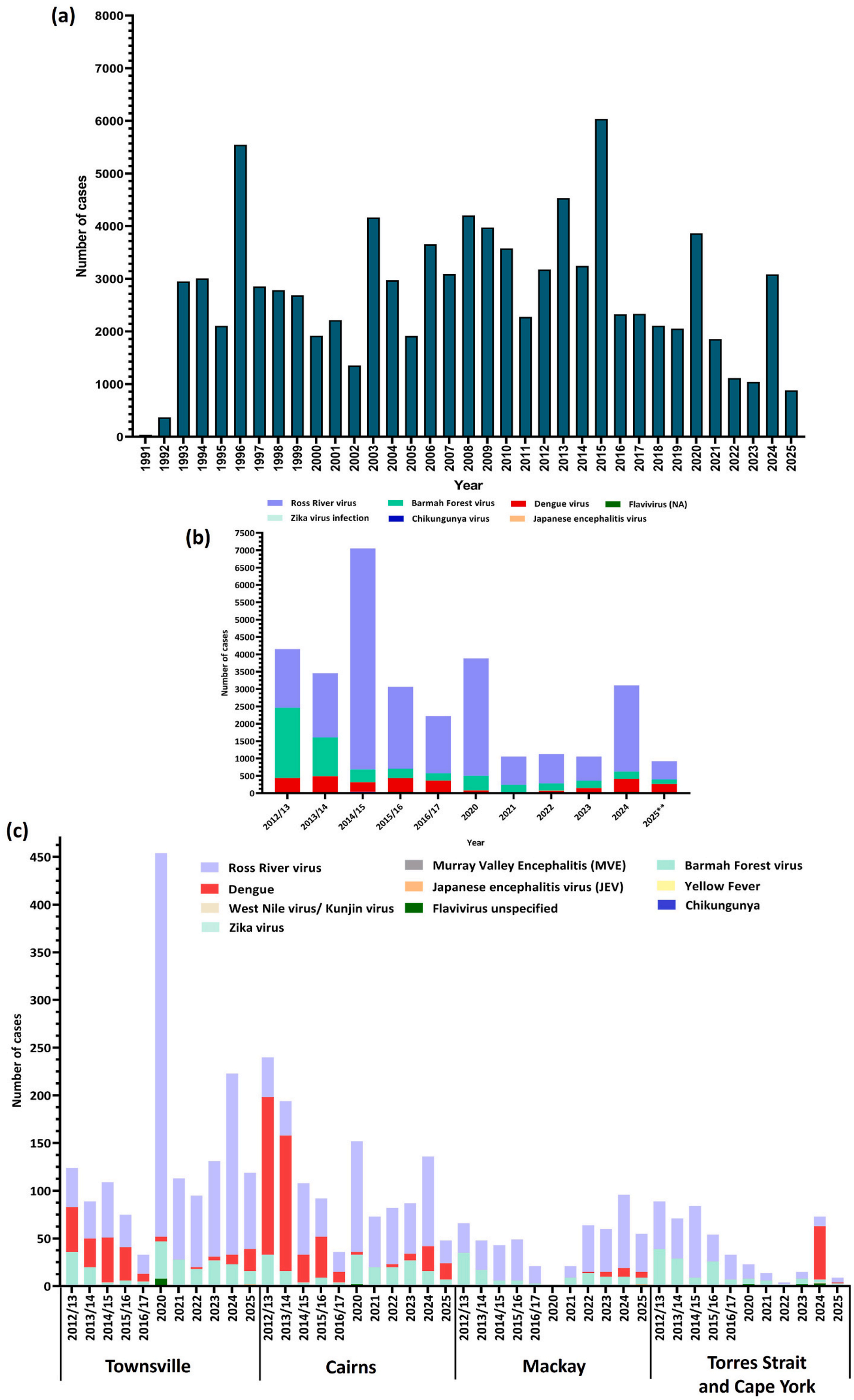

Fig. 2. Distribution of MBVs infections in Queensland. (a) Annual reported MBV cases in Queensland from 1991 to 2025, highlighting periodic spikes corresponding to outbreak years. (b) Cumulative MBV cases by virus type across Queensland, showing the predominance of RRV, DENV, and BFV in most regions. (c) Reported MBV cases in Townsville, Cairns, Mackay, and Torres Strait and Cape York from 2012/13 to 2025 (data for 2017–2019 are unavailable; see **Supplementary file** for details).

2001). In 2022, JEV was first confirmed in more than 80 commercial piggeries in Queensland, New South Wales, Victoria, and South Australia, resulting in reproductive losses in pigs and at least 42 human cases with seven fatalities during that outbreak, demonstrating significant public health and agricultural impact (Mackenzie and Williams, 2022). JEV detection in domestic pigs and feral pig populations has since become more geographically extensive, with continued reports in Queensland and other states, indicating establishment of local transmission cycles involving *Culex mosquito* vectors and amplifying hosts such as pigs and wading birds (Ahmed et al., 2025; Halter, 2025; Shava et al., 2025). The involvement of pigs as amplifying hosts is central to JEV epidemiology. Infected pigs develop high viraemia levels that enhance onward transmission by mosquitoes, increasing infection pressure on humans and other incidental hosts (McLean and Graham, 2022; Park et al., 2022; Ratnamrutha et al., 2025). This expanded enzootic cycle, and the presence of susceptible pig populations underscore the biosecurity implications of pig industry dynamics for JEV emergence and persistence in Australia, necessitating integrated animal health surveillance alongside human arbovirus monitoring.

3.2. Regional dynamics in Queensland

Queensland has reported highly variable but persistent MBV activity, ranging from 41 cases in 1991 to 6039 in 2015, with multiple years exceeding 3000 notifications (Fig. 2a & Supplementary file). RRV remains the dominant endemic pathogen, peaking at over 6300 cases in 2014/15 and showing recurrent surges, including 1701 cases in 2024 whereas BFV contributed substantially to earlier decades (2025 cases in 2012/13) but has since declined. During the past decade, intermittent dengue outbreaks were observed, with major peaks in 2012/13 (422 cases) and 2015/16 (398 cases) (Health, 2018). Queensland surveillance data for July 1, 2012 to June 30, 2017, where both locally acquired and overseas-acquired cases were recorded, show that dengue locally acquired cases ranged from 3 (2015) to 207 (2012) per year, while overseas-acquired cases were consistently higher, ranging from 215 (2012) to 364 (2015). Locally acquired dengue cases represented only 30–49% of total notifications, highlighting the substantial contribution of imported cases to overall incidence (Table 1). In contrast, RRV and BFV were predominantly locally acquired, while CHIKV and ZIKV cases were mainly imported, for example, in 2012, 100% of CHIKV cases (12/12) and in 2014, all ZIKV cases (3/3) were overseas acquired. No locally acquired JEV cases were reported during this period. The most recent three years illustrate a sharp escalation in MBV notifications. In 2023, Queensland recorded 1043 MBV cases, which tripled in 2024 (3083), driven by increases in dengue, BFV, and RRV across multiple regions. Dengue cases rose threefold from 125 in 2023 to 378 in 2024; data for this period do not distinguish between locally acquired and imported infections, as only total case notifications were reported by Queensland Health. By mid-2025, a further 236 dengue cases had already been reported, alongside detections of CHIKV, ZIKV, and JEV, underscoring the persistence of MBV regional risk.

A major public health success story in this context has been the *Wolbachia* release program, which has fundamentally changed the trajectory of dengue control in Northern Queensland. Deployment of the wMel strain into *Aedes aegypti* populations in Cairns and Townsville was associated with substantial reductions in locally acquired dengue, with modelling estimating a 96% reduction in Cairns (95% CI: 84–99%) (Ryan et al., 2020) and a >95% reduction in Townsville in the two years following *Wolbachia* establishment (Ogunlade et al., 2023). Table 1 shows that 28% of dengue notifications in this period were locally acquired, majority of cases occurring in the Cairns and Hinterland (76.8%) and Townsville (17.3%) Hospital and Health Service area, coinciding with areas where *Wolbachia* releases were conducted. While locally acquired cases remained relatively low compared to imported cases, causality cannot be directly inferred from the available data. More recent notifications (2023–2025) report only total dengue cases, without distinguishing locally acquired from imported infections, highlighting the need for continued surveillance to evaluate the long-term impact of *Wolbachia* on local dengue transmission. These data indicate that *Wolbachia* may contribute to limiting community transmission, although imported cases continue to drive overall dengue notifications. Notably, detections of unclassified flaviviruses have risen in recent years, with 22 cases recorded in 2024 nearly double that of 2023 (13) and 14 cases already reported in the first half of 2025 (Fig. 2b). Over the last decade, more than 117 unclassified flaviviruses have been detected in Queensland alone, highlighting both the diversity of circulating viruses and the critical importance of maintaining robust surveillance systems.

Regional MBV surveillance in Queensland reveals heterogeneity in arboviral activity across Townsville, Cairns, Mackay, and Torres Strait and Cape York (Fig. 2c). RRV remains the predominant contributor to case burden, with major peaks in Townsville (402 cases in 2020), Cairns (116 in 2020), and sustained detections in Mackay and Torres Strait and Cape York. Dengue has exhibited intermittent outbreaks, particularly in Cairns (165 cases in 2012/13) and Torres Strait and Cape York, which experienced a notable resurgence in 2024 (56 cases). BFV contributes consistently at lower levels across regions, with higher historical burdens (e.g., >30 cases in Cairns and Mackay in 2012/13) followed by a gradual decline. Sporadic detections of CHIKV, flavivirus of uncertain origin, and more recently JEV (1 case each in Mackay and Townsville in 2025) highlight the dynamic and expanding arboviral landscape.

Hospital-based diagnostic reporting remains the cornerstone of MBV surveillance in Queensland, providing essential data that guide public health responses. Recent notifications highlight a sharp rise in MBV activity, with 2024 marking a major escalation compared to 2022 and 2023. The three main contributors such as DENV, BFV, and RRV, all recorded significant increases across multiple regions. In Townsville, dengue rose to 10 cases in 2024 (vs. 4 in 2023 and 2 in 2022), BFV to 22 (vs. 27 in 2023 and 18 in 2022), and RRV surged to 190 (vs. 100 in 2023 and 75 in 2022). Similar trends were observed in Cairns, where dengue climbed to 26 cases in 2024 (vs. 7 in 2023 and 3 in 2022), BFV to 16 (vs. 27 in 2023 and 20 in 2022), and RRV to 94 (vs. 53 in 2023 and 59 in 2022). Torres Strait and Cape York experienced a striking dengue outbreak in 2024 (56 cases, absent in the two preceding years), accompanied by BFV and RRV increases. Importantly, data from only the first half of 2025 report multiple DENV, BFV, and RRV cases across Northern Queensland, with Townsville reporting 23 dengue, 14 BFV, and 80 RRV cases, Cairns 17, 7, and 24 cases respectively, and Mackay and Torres Strait and Cape York also detecting multiple infections. These notifications represent total cases, without distinction between locally acquired and overseas-acquired infections. However, patterns indicate

Table 1
Mosquito-borne virus cases in Queensland, categorized by locally and overseas-acquired infections. Data available only from July 1, 2012 to June 30, 2017.

Year	Japanese encephalitis virus	Chikungunya virus	Zika virus	Dengue virus	Barmah Forest virus	Ross River virus
	Locally/Overseas	Locally/Overseas	Locally/Overseas	Locally/Overseas	Locally/Overseas	Locally/Overseas
2012/13	0/0	0/12	0/0	207/215	2025/0	1690/0
2013/14	0/2	0/8	0/7	203/259	1116/0	1847/0
2014/15	0/0	0/37	0/3	70/207	366/0	6371/0
2015/16	0/1	0/3	0/28	33/364	268/0	2362/0
2016/17	0/0	0/5	0/12	18/315	211/0	1651/0

not only to year-on-year growth but also early evidence that 2025 may continue the upward trajectory.

To assess the impact of *Wolbachia* interventions, DENV case data were analysed separately for regions with and without *Wolbachia* releases. In *Wolbachia*-treated areas, *Wolbachia*-infected *Aedes aegypti* were progressively released and established in Cairns from 2011 and in onwards (O'Neill et al., 2019; Ryan et al., 2020). Prior to widespread *Wolbachia* deployment, both regions experienced substantial locally acquired DENV incidence, with particularly large outbreaks in Cairns (165 cases in 2012/13 and 142 cases in 2013/14) and recurrent high case numbers in Townsville (30–47 cases annually between 2012/13 and 2015/16) (Fig. 3a). Following *Wolbachia* releases and establishment, DENV notifications declined sharply and remained low for several years, with zero or near-zero cases recorded in 2021 across both regions. Although modest increases were observed between 2022 and 2025 (Townsville: 2–27 cases; Cairns: 3–26 cases annually), remaining substantially below pre-release or during release levels (Fig. 3a). In contrast, DENV notifications from Queensland regions outside *Wolbachia* release areas demonstrates sustained, and in some regions, increasing DENV activity between 2020 and 2025 (however, data on the timing of releases are not available for these regions). Metropolitan and peri-urban regions reported the highest burdens, with Metro South (81 cases), Metro North (65 cases), and the Gold Coast (60 cases) recording substantial case numbers in 2025, following similarly elevated notifications in 2024. The Sunshine Coast and West Moreton also showed consistent increases, reaching 52 and 31 cases respectively in 2025. In contrast, northern and inland regions such as Northwest Queensland reported no dengue cases throughout the study period. Torres Strait and Cape York exhibited episodic transmission, with a notable spike in 2024 (56 cases), but minimal activity otherwise (Fig. 3b). This separation of DENV trends highlights the profound and sustained suppression of DENV transmission in *Wolbachia*-treated areas relative to non-intervention regions. Together with the proven success of *Wolbachia* releases, these findings reinforce the urgency of strengthening Queensland's biosecurity through integrated strategies that combine community-based biological control, hospital-based diagnostics, and genomic surveillance to ensure early detection and rapid response.

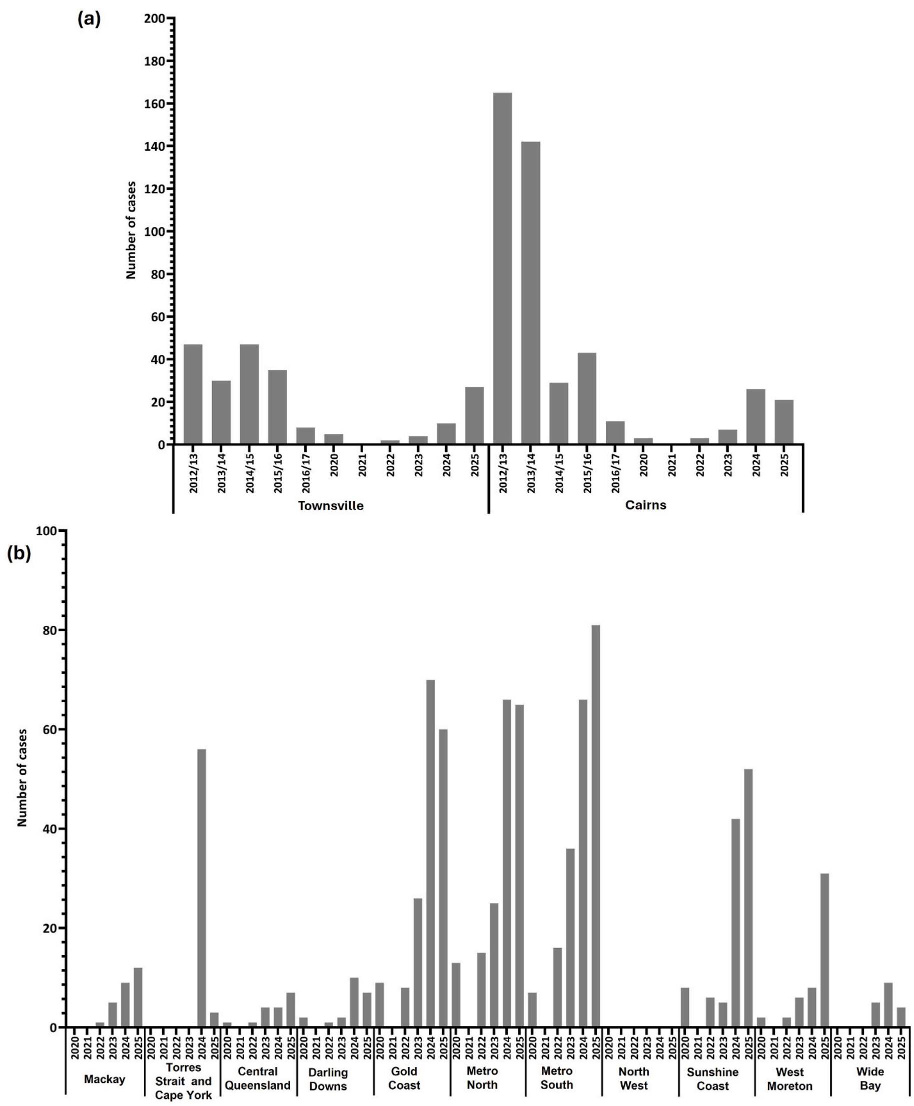

Fig. 3. Dengue notifications within and outside *Wolbachia* release areas in Queensland, Australia. (a) Dengue case notifications from *Wolbachia*-treated regions (Townsville and Cairns), compiled from Queensland Health Public Health Unit (PHU) annual reports. Data are shown for the *Wolbachia* release period (2012/13–2016/17), during which all reported cases were locally acquired, and the post-release period (2020–2025). Data for 2017–2019 were unavailable. (b) Dengue case notifications from Queensland regions without *Wolbachia* releases, shown for 2020–2025 due to earlier data unavailability. These data illustrate the sustained reduction in dengue case numbers in *Wolbachia*-treated regions compared with non-intervention areas (Supplementary file for details).

4. Surveillance strategies: Foundations and opportunities

The re-emergence of MBV reflects not only the persistence endemic transmission but also the influence of climate variability, urban expansion, and increased human–vector contact in tropical and subtropical regions (de Souza and Weaver, 2024; Eder et al., 2018). Effective surveillance is therefore the keystone of MBV control, yet current systems in Northern Queensland remain largely hospital-based. These approaches, which depends on serological and PCR diagnostic, provide reliable confirmation of infections but mainly capture cases after clinical onset, offering a reactive rather than proactive view of transmission dynamics. Traditional diagnostic methods such as serology and PCR, continue to be invaluable for confirming known viruses or variants. However, they are inherently limited by their targeted nature (Chong et al., 2019; Dias et al., 2023; Madere et al., 2025). For instance, serological assays can encounter cross-reactivity among antigenically related flaviviruses like DENV, ZIKV, and JEV, while PCR requires prior knowledge of viral genome sequences, constraining detection of novel or highly divergent strains (Houldcroft et al., 2017; Musso and Desprès, 2020). Consequently, long-term surveillance in Australia has recorded a substantial number of flavivirus detections without full genomic resolution, including more than 919 unclassified flaviviruses nationally, highlighting persistent gaps in virus characterisation rather than true absence of diversity.

Next-generation sequencing (NGS) approaches, particularly shotgun metagenomics and metatranscriptomics, address key gaps in arbovirus surveillance by enabling untargeted, high-resolution profiling of viral communities within mosquito populations (Bikel et al., 2015; Kumar and Yadav, 2024). In current practice, metagenomic sequencing of total nucleic acids allows the simultaneous detection of DNA and RNA viruses following reverse transcription, providing a comprehensive overview of the mosquito virome, including insect-specific viruses and low-abundance arboviruses (Pan et al., 2024; Ramírez et al., 2020). In contrast, metatranscriptomic approaches, sequence total or ribosomal RNA–depleted RNA, preferentially capture actively transcribed viral genomes and replicative intermediates, thereby enriching for replication-competent RNA viruses and enabling insights into viral activity, co-infections, and temporal dynamics (Ko et al., 2022b; Shi et al., 2017a). Several sequencing platforms and methodological refinements are currently in use or emerging for vector surveillance. Short-read platforms (e.g., Illumina) remain the dominant technology due to their high accuracy and depth, supporting sensitive detection of low-prevalence viruses and robust comparative analyses across sites and time points (Chin et al., 2025; Tan et al., 2024a). Long-read sequencing technologies (e.g., Oxford Nanopore) are increasingly applied for rapid field-deployable surveillance, enabling near–real-time detection and improved assembly of complete viral genomes, including structurally complex or divergent arboviruses (Ko et al., 2022a; Oehler et al., 2025; Patiño et al., 2024). Hybrid strategies combining short- and long-read data are likely to be most informative for surveillance applications, balancing sensitivity, resolution, and turnaround time (Patiño et al., 2024; Torma et al., 2021).

Sampling strategies underpinning these approaches typically involve systematic trapping of adult mosquitoes, followed by pooling of specimens by species, location, and collection date (Russell et al., 2022). Surveillance programs have demonstrated the value of longitudinal sampling across ecological gradients, including urban, peri-urban, and rural sentinel sites, with repeated collections during peak vector activity or transmission seasons to capture viral persistence, introduction events, and amplification dynamics (Agha et al., 2017; Hermanns et al., 2023; Koh et al., 2025; McMillan et al., 2023; Osalla et al., 2025). While adult mosquitoes are the primary targets, blood-fed individuals or immature stages may also be sampled in specific contexts, depending on surveillance objectives and logistical constraints (Oguzie et al., 2022; Pan et al., 2024; Vieira et al., 2024). Metagenomic and metatranscriptomic sequencing can be applied at scales ranging from local sentinel surveillance to regional, state-wide, or national monitoring programs, enabling both fine-scale early detection of emerging viruses and broader assessments of viral circulation and temporal trends.

So, integrating routine vector surveillance with genomic sequencing at sentinel sites provides early warning of arbovirus emergence and persistence. Sequencing-based approaches have transitioned from research contexts to real-world applications, including clinical viral diagnostics, where institutions such as UCSF Medical Center (USA), Guy's and St Thomas' Hospital and the UK Health Security Agency, the Institut Pasteur (France), and hospitals across South Korea, Japan, China, and Germany have successfully implemented NGS for pathogen detection (Charalampous et al., 2023; Fourgeaud et al., 2024; Obermeier et al., 2024; Seydel, 2022; Tang et al., 2025; Venkatesan, 2025). These programs demonstrate the feasibility and reliability of metagenomic approaches when paired with robust laboratory validation, including assessments of sensitivity, specificity, reproducibility, and robustness against interfering substances (Tan et al., 2024b). Australia already applied NGS for MBV detection. However a similar framework (international) could build on existing mosquito trapping and diagnostic infrastructure by incorporating periodic or event-driven metagenomic and metatranscriptomic sequencing in high-risk regions, including tropical Northern Australia and major population centres. Experiences from international vector surveillance initiatives indicate that integrating field-based mosquito sampling with NGS-driven virome analysis can provide early warning of arbovirus emergence well before increases in human case notifications are observed. Given that arboviruses are maintained in complex enzootic cycles involving diverse mosquito species and wildlife reservoirs and can circulate silently for extended periods prior to spillover into human populations (Guth et al., 2020). Proactive mosquito-based surveillance using metagenomic and metatranscriptomic sequencing offers a scalable and adaptable framework for early detection. Pilot evaluations of these approaches in Australian research and public health laboratories indicate feasibility and provide benchmarks for operational deployment. Despite ongoing challenges related to cost, data interpretation, and the requirement for specialised bioinformatics expertise (Kumar and Yadav, 2024; Shakya et al., 2019), these technologies are increasingly recognised as critical components of integrated public health, veterinary, and biosecurity surveillance systems. These approaches combine targeted detection of known arboviruses with untargeted discovery of emerging or cryptic viruses.

5. Vector control strategies in Northern Queensland

Vector control strategies in Northern Queensland have evolved into a comprehensive, multi-layered program that integrates biological, chemical, and community-led interventions. Among these, the introduction of *wMel-Wolbachia*–infected *Aedes aegypti* mosquitoes in Townsville (2014 – 2019) and Cairns (from 2011) represents some of the most successful biological control initiatives against dengue globally. In both locations, *Wolbachia* replacement of wild-type mosquito populations initially suppressed local dengue transmission (Hoffmann et al., 2011; O'Neill et al., 2019). Subsequent studies have demonstrated that this protection has been sustained for over a decade (Huang et al., 2020; Ross et al., 2022; Ryan et al., 2020). Empirical data from field releases indicate substantial reductions in dengue transmission following *Wolbachia* establishment in *Aedes aegypti* populations. Complementary mathematical modelling supports these observations, showing that *Wolbachia* can reduce mosquito transmission capacity by approximately 20-fold relative to wild-type vectors, contributing to the observed reductions in dengue incidence during and after the release period (Ogunlade et al., 2023).

The Queensland experience has since become a global benchmark, with *Wolbachia* releases now deployed in multiple high-burden countries. While environmental factors, particularly temperature, can influence the long-term stability of *Wolbachia* in mosquito populations (Hien et al., 2022; Ross et al., 2020), the Australian program remains a leading example of how biological control can reshape arbovirus epidemiology. Importantly, although outcomes of *Wolbachia* releases vary between locations, there is currently no evidence that differences in dengue transmission intensity directly affect the efficacy of *Wolbachia* in reducing virus transmission. Dengue incidence in Townsville and Cairns has fluctuated in recent years, reflecting ongoing challenges from virus importation, human mobility, and environmental factors (Fig. 2c). While overall case numbers have varied, these trends cannot be used to assess the impact of *Wolbachia* interventions, which are primarily effective in reducing local transmission by *Aedes aegypti*. Nevertheless, *Wolbachia* remains a robust component of local dengue control strategies.

Therefore, complementary measures, including targeted insecticide spraying, larval habitat reduction, and community engagement remain critical components of the broader control framework (Okumu et al., 2025; Wilson et al., 2020). These strategies may help address challenges not fully covered by *Wolbachia*, such as the presence of other mosquito species, incomplete release coverage, imported cases, and local environmental variability, ensuring a more robust and resilient arbovirus control program. Despite these layers of protection, recent surveillance indicates a resurgence of DENV and CHIKV, along with sporadic detections of JEV and unclassified flaviviruses. Given the demonstrated successes of *Wolbachia*, and the ongoing emergence of other arboviruses, future strategies should prioritise maintaining and, where appropriate, expanding *Wolbachia* coverage in *Aedes aegypti* populations, as well as exploring the potential development of *Wolbachia* interventions in additional mosquito species. These efforts should be coupled with the integration of next-generation genomic surveillance to guide and monitor control programs. Such combined approaches will strengthen long-term resilience against the dynamic arboviral landscape in Northern Queensland.

6. Future prospects

Looking ahead, Northern Queensland is well placed to lead arboviral control by integrating its demonstrated *Wolbachia* success with cutting-edge genomic surveillance and predictive modelling, globally. The long-term impact of *Wolbachia* in suppressing dengue transmission has been documented over more than a decade (Huang et al., 2020; Ross et al., 2022; Ryan et al., 2020), providing a strong biological foundation for future interventions. Scaling up field-based mosquito and reservoir sampling programs, coupled with metagenomic and metatranscriptomic sequencing will enable early detection of emerging or divergent viruses before human outbreaks occur (Guth et al., 2020; Shi et al., 2017b; Torres Montaguth et al., 2026). Predictive modelling that incorporates entomological, climatic, and epidemiological data will be critical to forecasting transmission risk and guiding targeted interventions. Both mechanistic transmission models (e.g., Ross–Macdonald or SEIR-based compartmental models) and agent-based models have been useful for forecasting arbovirus transmission by incorporating key parameters such as vector abundance and species composition, biting rates, *Wolbachia* prevalence, extrinsic incubation period, human population density and movement, and climatic variables (temperature, rainfall, humidity) have been shown to improve forecasting of transmission risk and guide targeted control measures (Huber et al., 2018; Perkins et al., 2019; Reiner et al., 2013; Shocket et al., 2020b; Smith et al., 2012). Complementary vector control strategies, including environmental modification, larviciding, and judicious insecticide use, strengthen long-term control (O'Neill et al., 2019; Ryan et al., 2020), while active community engagement remains essential for public awareness, adherence to preventive measures, and timely reporting of unusual events. By uniting *Wolbachia's* enduring success with next-generation genomic surveillance and strong community partnerships, Northern Queensland can not only safeguard its own population but also establish a scalable blueprint for global arboviral preparedness. This integrated, forward-looking approach positions the region at the forefront of innovation in mosquito-borne disease control, offering both immediate benefits and long-term resilience.

7. Conclusions

Northern Queensland faces an increasingly complex arboviral landscape, with RRV and BFV accounting for the highest endemic burdens, while DENV continues to pose the greatest epidemic threat. Recent surveillance highlights sharp increases in RRV (1701 cases in 2024) and DENV (378 cases in 2024), along with emerging detections of chikungunya, Japanese encephalitis, and over 117 unclassified flaviviruses. Large-scale deployments of *Wolbachia*-infected *Aedes aegypti* have achieved sustained reductions in dengue transmission over more than a decade, establishing an international benchmark for biological control. Building on this success, strengthening surveillance through field-based mosquito and reservoir monitoring, next-generation sequencing, and predictive modelling has been shown internationally to enable early detection of emerging viruses and guide targeted interventions. Complementary vector control measures and active community engagement further enhance intervention effectiveness. These observations suggest that an integrated framework combining *Wolbachia* expansion, genomic surveillance, predictive modelling, and community participation may represent a promising, evidence-informed strategy to mitigate the rising arboviral burden and safeguard public health in Northern Queensland.

CRediT authorship contribution statement

Md. Eram Hosen: Writing – original draft, Visualization, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Scott Dunsdon:** Writing – review & editing, Validation. **Subir Sarker:** Writing – review & editing, Validation, Supervision, Resources, Project administration, Funding acquisition, Conceptualization.

Funding

This research received no external funding.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

The authors acknowledge the Townsville City Council for their assistance with mosquito collection for the ongoing study investigating mosquito-borne viruses in the tropics. We also thank Mr. Scott Lyons, Senior Medical Entomologist at the Townsville Public Health Unit, for his valuable support in mosquito collection for MBVs surveillance project. Subir Sarker is the recipient of an Australian Research Council Discovery Early Career Researcher Award (grant number DE200100367) funded by the Australian Government. The Australian Government had no role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.virol.2026.110825.

Data availability

This study used publicly available aggregated surveillance data from Australian and Queensland Government health websites, including the Queensland Health Notifiable Conditions Dashboard and national notifiable diseases reports. No ethics approval was required as no individual or sensitive health information was accessed.

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