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Spatio-temporal clustering of respiratory syncytial virus in Sakon Nakhon Province, Thailand, across the COVID-19 pandemic: A retrospective space–time scan analysis, 2019–2024

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Abstract

Respiratory syncytial virus (RSV) is a leading cause of acute respiratory infections in young children and older adults. The COVID-19 pandemic and the implementation of non-pharmaceutical interventions (NPIs) profoundly altered the transmission dynamics of RSV worldwide. However, evidence describing how RSV spatio-temporal patterns evolved across pandemic-related phases at fine geographic resolution remains limited in Thailand. We conducted a retrospective spatio-temporal cluster analysis of RSV cases reported in Sakon Nakhon Province, northeastern Thailand, between January 2019 and December 2024. Monthly RSV case counts from 125 sub-districts were analyzed using Kulldorff's space–time scan statistic implemented in SaTScan, applying a space–time permutation model. The analysis was structured into three epidemiological phases: the pre-pandemic (January 2019–March 2020), NPI-associated suppression (April 2020–December 2021), and the post-pandemic resurgence (January 2022–December 2024). Nineteen space–time clusters were identified, eleven of which were statistically significant ($p < 0.05$). During the pre-pandemic phase, the primary cluster occurred between February 2019 and August 2020, encompassing nine sub-districts and exhibiting more than a sixfold excess of cases (relative risk [RR] = 6.08). Only one moderate-intensity cluster was detected during the suppression phase (RR = 2.71), reflecting markedly reduced RSV activity. Following relaxation of NPIs, RSV transmission rebounded sharply, with a large primary cluster between March and May 2022 involving 15 sub-districts and 1,059 cases (RR = 1.98), followed by multiple significant clusters persisting through 2024. RSV transmission in Sakon Nakhon Province showed marked spatio-temporal shifts across the COVID-19 pandemic, transitioning from localized pre-pandemic clustering to suppressed circulation during NPIs and subsequent widespread resurgence. These findings highlight the influence of pandemic-related interventions on RSV epidemiology and the importance of sub-district–level surveillance for preparedness and response in the post-pandemic era.

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1. Introduction

Respiratory syncytial virus (RSV) is a major global cause of acute lower respiratory infections in young children, resulting in an estimated 33 million episodes, 3.6 million hospital admissions, and up to 100,000 deaths annually [1]. Although severe disease predominantly affects infants, RSV also contributes substantially to morbidity in older adults, particularly those with underlying cardiopulmonary disease or compromised immunity [2, 3]. The substantial healthcare burden associated with RSV underscores the importance of understanding its transmission dynamics across diverse epidemiological settings.

Epidemiologically, RSV demonstrates characteristic person–time–place patterns. The burden of disease disproportionately affects children under five years of age, particularly infants younger than one year, who account for most severe cases and hospital admissions [4]. Temporally, RSV transmission exhibits marked seasonality. In tropical climates, epidemics are often aligned with fluctuations in rainfall, humidity, and ambient temperature, producing annual peaks with variable timing and magnitude. Spatially, transmission is heterogeneous, with higher case densities frequently observed in urban and peri-urban areas compared with sparsely populated rural regions. Such heterogeneity reflects differences in population density, childcare attendance, household crowding, healthcare access, and local environmental conditions [4, 5].

The COVID-19 pandemic markedly altered global RSV circulation patterns. Following widespread implementation of NPIs, RSV incidence dramatically decreased in 2020, followed by atypical, off-season rebounds in 2021–2023 across multiple countries [6-9]. Similar trends were observed in Thailand, where RSV transmission resurged after pandemic restrictions were relaxed, raising questions regarding changes in population immunity and potential shifts in the climatic and seasonal drivers of RSV transmission [10-12].

Despite the recognized public health burden of RSV, spatially resolved analyses remain scarce in Thailand. Most existing studies focus on clinical patterns, viral genotyping, or national-level seasonality [12, 13]. However, RSV transmission is influenced by heterogeneous population densities, childcare settings, healthcare access, and local climate variability—all of which vary substantially within provinces. Understanding these finer-scale dynamics requires analytical tools that can identify local outbreaks in transmission across space and time.

Sakon Nakhon Province in northeastern Thailand provides an informative setting for such analysis shaped by its mixture of rural and urban populations, diverse environmental zones, and distinct rainy–cool–hot seasonal cycles. Although routine RSV surveillance is conducted province-wide, no prior study has investigated spatio-temporal clustering of RSV in this area. Identifying high-risk districts and outbreak windows can enhance early warning systems, improve hospital preparedness, and guide targeted public health messaging.

Space–time scan statistics, implemented in SaTScan, offer a robust approach to detecting unusually high clusters of infectious diseases. The space–time permutation model is particularly suitable in surveillance settings where only case data—and not population-at-risk estimates—are available. It adjusts for purely spatial and temporal heterogeneity, enabling accurate detection of outbreak clusters [14, 15].

In this study, we applied spatio-temporal scan statistics to characterize RSV transmission at the sub-district level in Sakon Nakhon Province, northeastern Thailand, from 2019 to 2024. By leveraging the COVID-19 pandemic as a natural experiment, we examined how RSV clustering patterns shifted across the pre-pandemic, suppression, and post-pandemic resurgence phases. To our knowledge, this represents the first application in Thailand of sub-district–level space–time scan statistics to examine RSV transmission across distinct pandemic phases, providing fine-scale spatial insights beyond those captured by hospital-based or province-level analyses.

2. Materials and Methods

Study Area

This study was conducted in Sakon Nakhon Province, located in northeastern Thailand, comprising 18 districts and 125 sub-districts covering about 9,605 km² with a population of ~1.14 million [16], distributed across mixed urban and predominantly rural settings. Sakon Nakhon exhibits diverse topography, and seasonal climatic variation that may influence respiratory virus transmission.

Data Sources

Routine monthly surveillance of RSV was obtained from the Sakon Nakhon Provincial Public Health Office and included all laboratory-confirmed RSV cases reported between January 2019 and December 2024. A total of 2,395 cases from 125 sub-districts were extracted (Fig. 1). Case records contained date of diagnosis, reporting facility, and sub-district code. Each location was assigned geographic coordinates (latitude and longitude) based on the WGS84 reference system. Administrative boundary data at the district level were obtained from DIVA-GIS [17].

Data management

Data cleaning procedures included verification of temporal completeness, removal of duplicate entries, correction of formatting inconsistencies, and assessment of missing geographic information. Records outside the defined study period (1 January 2019–31 December 2024) or outside provincial geographic boundaries were excluded. Location coordinates were cross-checked using open-source Quantum GIS (QGIS) version 3.40.3 [18] to ensure accuracy and consistency with administrative boundaries. All data were anonymized prior to analysis, with no personal identifiers retained.

RSV incidence

To quantify and compare the burden of RSV across sub-districts in Sakon Nakhon Province, cumulative incidence for the entire study period (2019–2024) was calculated by summing all RSV cases reported in each sub-district and dividing this total by the aggregated mid-year population for the corresponding years, obtained from the Official statistics registration systems of Thailand [16]. All incidence estimates were subsequently linked to geospatial boundary files referenced to the WGS84 coordinate system and visualized as incidence maps using ArcGIS Pro (Esri, Redlands, CA, USA).

Spatio-temporal clustering and sensitivity analysis

Spatio-temporal clustering of RSV was assessed using Kulldorff's space–time scan statistic implemented in SaTScan™ software version 10.3.3 (M Kulldorff and Information Management Services Inc., Calverton, MD, USA) [15]. Two datasets were prepared for analysis: (i) geographic coordinates of sub-district centroids in the WGS84 reference system and (ii) monthly RSV case counts for all 125 sub-districts over the six-year study period.

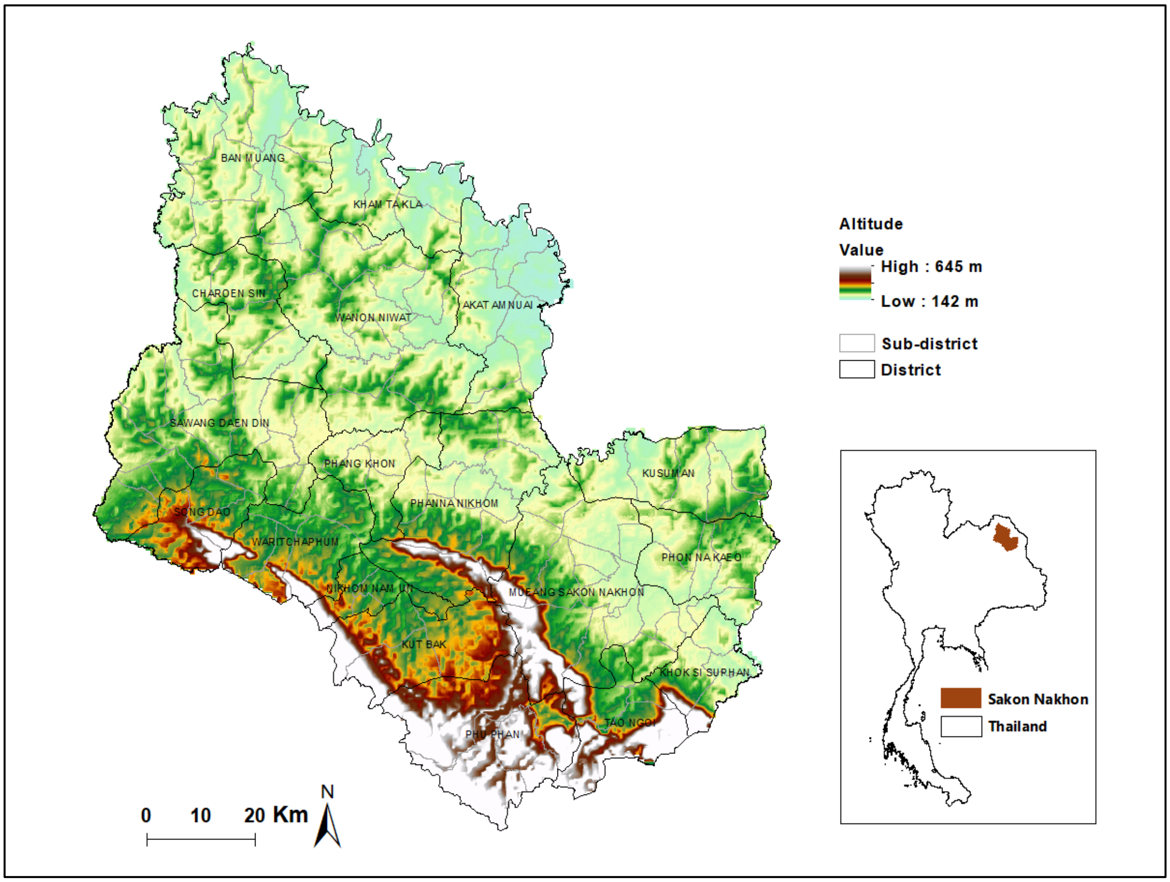

Fig. 1 Map of the study area showing the district and sub-district boundaries in Sakon Nakhon Province, northeastern Thailand.

A retrospective space–time permutation model was applied to detect clusters of RSV. This model is appropriate for surveillance-based analyses where the primary objective is outbreak detection, as it adjusts for purely spatial and temporal heterogeneity using the internal distribution of cases and does not require population denominators. The scanning window was defined as a cylindrical structure with a circular spatial base and a temporal height. Spatial windows were allowed to expand to a maximum of 50% of the population at risk to avoid overly large or epidemiologically diffuse clusters, while the temporal window ranged from a minimum of one month to a maximum of 50% of the study duration, enabling detection of both short-term outbreaks and extended seasonal patterns. To evaluate potential spatial oversmoothing at the sub-district level, a sensitivity analysis was conducted using a reduced maximum spatial window of 25% of the population at risk.

To reflect the impact of COVID-19 control measures on RSV epidemiology, the analysis was structured around three epidemiological phases: a pre-pandemic period (January 2019–March 2020), a suppression period characterized by widespread NPIs (April 2020–December 2021), and a resurgence period following the relaxation of these interventions (January 2022–December 2024). Phase boundaries were defined *a priori* based on national COVID-19 policy milestones in Thailand, including the implementation of nationwide school closures and mobility restrictions in April 2020 and the subsequent large-scale relaxation of NPIs, with reopening of schools and public venues, in January 2022 [19, 20]. Because SaTScan detects clusters across the full study period, some clusters extended beyond phase boundaries; therefore, phases were used for interpretative purposes only. Although SaTScan identifies a single most-likely (primary) cluster for the entire dataset, phase-based interpretation enabled assessment of how cluster magnitude, duration, and spatial extent varied across these distinct epidemiological contexts.

Temporal precision was set to the monthly level. Statistical significance was evaluated using 999 Monte Carlo replications, and the analysis focused on identifying clusters with higher-than-expected case counts. For each detected cluster, SaTScan generated detailed metrics including the spatial radius, temporal span, number of locations involved, observed and expected case counts, the observed-to-expected (O/E) ratio, reported as relative risk (RR) under the permutation framework, log-likelihood ratio (LLR), and Monte Carlo p-value. Because the space–time permutation model does not incorporate population denominators, the reported O/E ratios represent relative excess of cases rather than population-based incidence risk. Clusters with $p < 0.05$ were considered statistically significant. Significant clusters and sub-district centroids were subsequently visualized using ArcGIS Pro (ESRI, Redlands, CA, USA).

3. Results and Discussion

RSV case distribution

A total of 2,395 laboratory-confirmed RSV cases were included in the analysis, reported from 125 sub-districts in Sakon Nakhon Province between January 2019 and December 2024 (Fig. 2). RSV transmission was detected throughout the study period but marked interannual variability was observed. Case counts were relatively low during 2019–2021, followed by a pronounced increase during 2022–2024, with monthly case numbers exceeding pre-pandemic levels.

Clear seasonal patterns were evident, with RSV transmission peaking predominantly during the cool season (October–February) and the early rainy season (May–July). These seasonal peaks were especially pronounced during the post-pandemic period, when several months in 2022 and 2023 showed substantial surges in case counts. In contrast, RSV transmission during 2020–2021 was notably suppressed, consistent with the period of COVID-19–related NPIs, including mobility restrictions and enhanced hygiene practices.

Spatial distribution of RSV incidence

The cumulative incidence map for 2019–2024 demonstrates substantial geographic heterogeneity in RSV incidence across sub-districts in Sakon Nakhon Province (Fig. 3). The highest incidence levels (approximately 100–227 cases per 100,000 population) were observed in several contiguous sub-districts in the central and south-central regions of the province. Adjacent sub-districts showed moderate incidence (50–100 cases per 100,000 population), forming a continuous zone of elevated RSV burden. In contrast, the majority of sub-districts in the northern, eastern, and western regions exhibited low incidence (0–50 cases per 100,000 population). Overall, RSV incidence was unevenly distributed across the province, with clear spatial clustering evident at the sub-district level. The spatial patterns observed in the cumulative incidence map (Fig 3) were consistent with the locations of the primary and secondary space–time clusters identified by SaTScan (Table 1; Fig. 4).

Spatio-temporal clustering and sensitivity analysis

SaTScan identified 19 space–time clusters of RSV across the six-year study period, of which 11 were statistically significant ($p < 0.05$) (Table 1). These clusters varied considerably in spatial extent, duration, and transmission intensity, indicating persistent but heterogeneous RSV circulation across Sakon Nakhon Province. Distinct patterns emerged when clusters were examined across the three epidemiological phases corresponding to pre-pandemic activity, RSV suppression during COVID-19 NPIs, and the post-pandemic resurgence (Fig. 4).

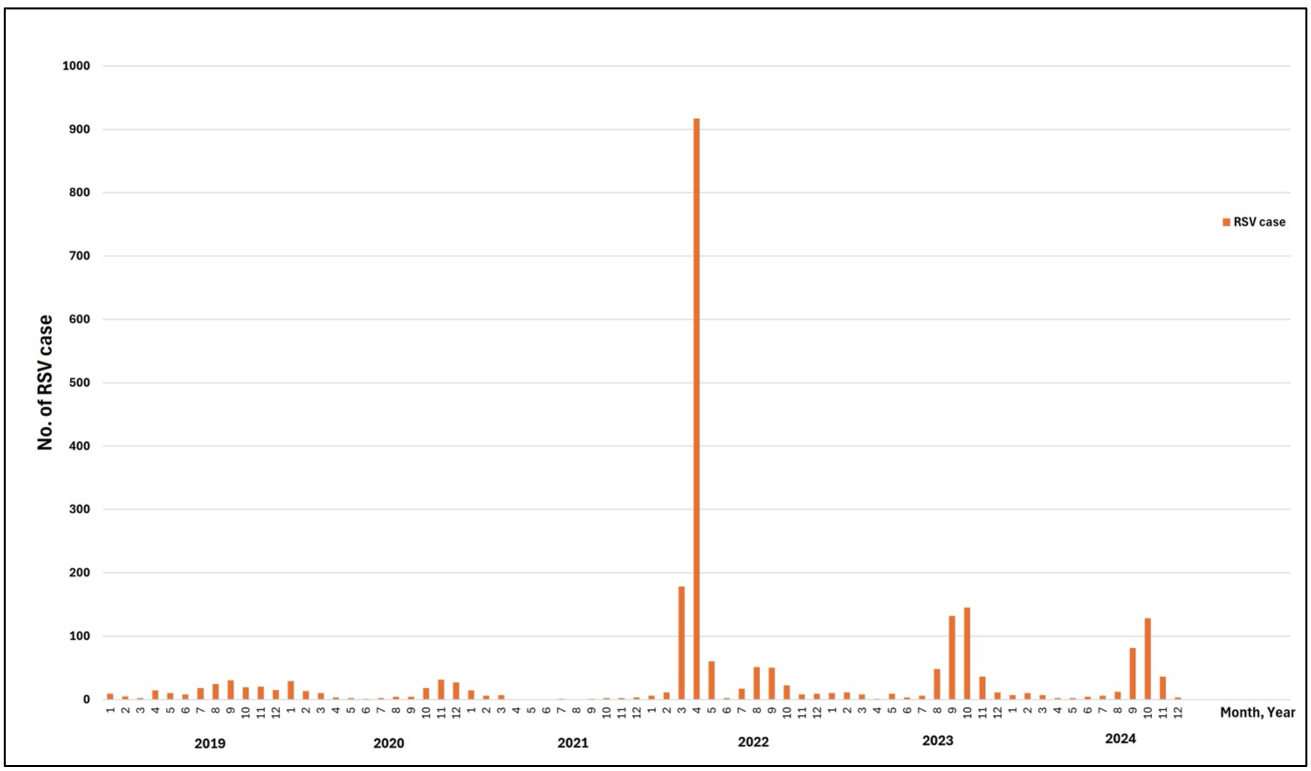

Fig. 2 Monthly and yearly distribution of RSV cases in Sakon Nakhon Province, 2019-2024.

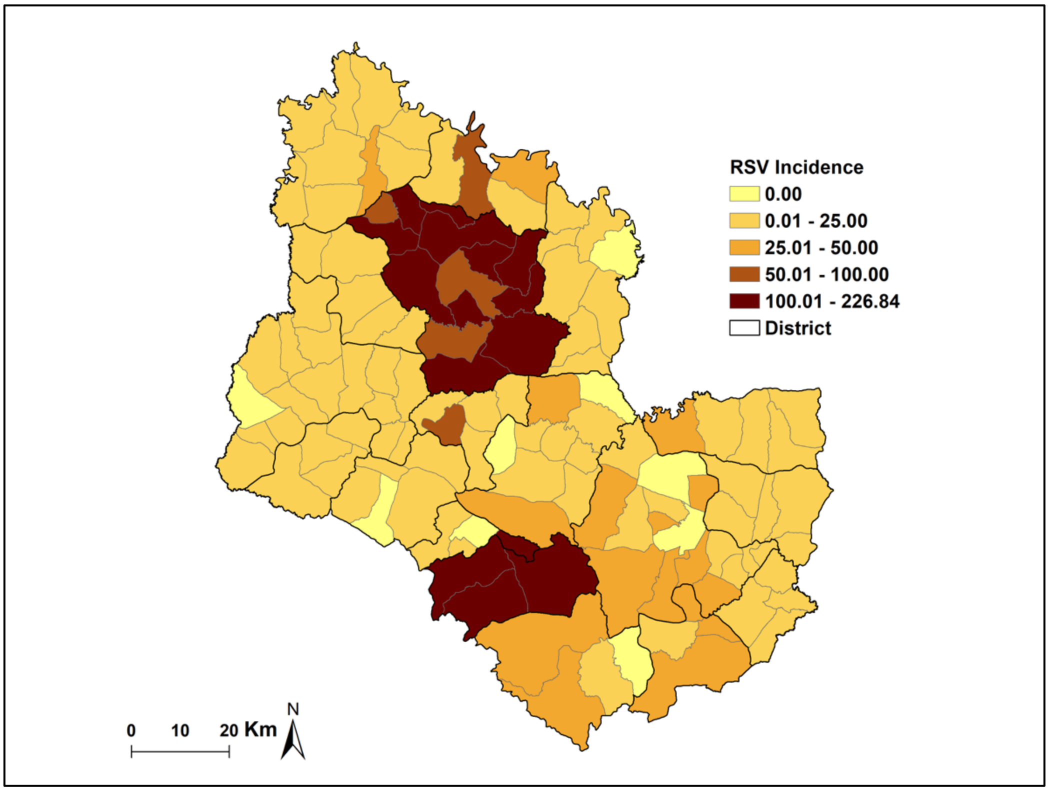

Fig. 3 Cumulative incidence of RSV by sub-district in Sakon Nakhon Province, 2019–2024 (cases per 100,000 population).

During the pre-pandemic phase (January 2019–March 2020), three significant clusters were detected. The primary cluster, spanning February 2019 to August 2020, encompassed nine sub-districts in the southern part of the province and exhibited markedly elevated transmission (RR = 6.08, LLR = 155.94, $p < 0.001$). Two smaller secondary clusters were observed in early and late 2019: a micro-cluster (March–June 2019) confined to a single northern sub-district with an exceptionally high RR (44.03, $p = 0.0012$), and a three-location cluster (July–October 2019) in the same region (RR = 7.64, $p = 0.049$). These clusters were spatially distinct and reflect localized but recurrent RSV transmission before the onset of COVID-19 control measures (Fig. 4A).

In the suppression phase (April 2020–December 2021), only one significant cluster was identified. This cluster, detected from November 2020 to February 2021, involved 41 sub-districts concentrated in the central and eastern regions (RR = 2.71, LLR = 21.07, $p < 0.001$) (Table 1, Fig. 4B).

In contrast, the resurgence phase (January 2022–December 2024) was characterized by numerous and more geographically diffuse clusters. The primary resurgence cluster, detected between March and May 2022, consisted of 15 sub-districts and accounted for 1,059 cases—nearly twice the expected count (RR = 1.98, LLR = 280.54, $p < 0.001$). Several secondary clusters emerged throughout the province during 2022–2024, including a large cluster from July to October 2022 (RR = 1.92), a prolonged cluster from December 2022 to June 2023 (RR = 3.58), and additional clusters extending into late 2023 and 2024 (RR range: 3.55–4.85). These clusters were spatially dispersed across northern, western, central, and southern districts, with overlapping scanning windows indicating widespread, multi-focal transmission (Fig. 4C).

To evaluate the robustness of cluster detection, a sensitivity analysis was conducted using a reduced maximum spatial window of 25% of the population at risk. The primary clusters identified under the default 50% specification demonstrated strong spatial concordance under the reduced window, with minimal changes in temporal span and comparable observed-to-expected ratios. Although smaller window sizes yielded modest reductions in cluster radius and increased spatial localization, the overall cluster configuration and temporal structure remained consistent (Supplementary Table 1).

This study provides the first detailed characterization of RSV spatio-temporal clustering in Sakon Nakhon Province across three epidemiologically distinct periods shaped by the COVID-19 pandemic: the pre-pandemic, suppression, and resurgence phases. Using Kulldorff's space–time scan statistic, we identified 11 statistically significant clusters between 2019 and 2024, revealing substantial shifts in the magnitude, duration, and geographic distribution of RSV transmission in relation to changes in population mixing and NPIs. These findings complement emerging global evidence showing that COVID-19 had a profound and unprecedented impact on RSV epidemiology [1, 21, 22].

During the pre-pandemic phase, RSV clusters were frequent and spatially localized. The primary cluster (February 2019–August 2020) and several secondary clusters were consistent with typical seasonal RSV patterns in tropical regions, where transmission is influenced by climatic and ecological factors [5, 23, 24]. These clusters likely reflect underlying demographic and environmental heterogeneity across the province. Similar spatially clustered RSV patterns have been documented in other low-latitude regions, where local conditions such as humidity, rainfall, and household crowding shape transmission intensity [25-27].

Only one significant cluster occurred during the suppression period (late 2020–2021), aligning with evidence from multiple countries showing near elimination of RSV circulation under stringent COVID-19 NPIs [1, 28, 29]. School closures, mask-wearing, reduced mobility, and enhanced hygiene substantially constrained viral transmission. Numerous studies reported historic drops in RSV incidence during this period in Australia, Europe, the United States, and Asia [28-31]. Our findings demonstrate similar dynamics at the sub-district scale in Thailand, with reduced relative risk and fewer spatial aggregations of cases during periods of restricted social mixing. The broad spatial extent but low intensity of the suppression-period cluster may reflect limited but persistent sporadic transmission within smaller population networks.

Following the relaxation of NPIs, RSV transmission rebounded sharply. The primary resurgence cluster (March–May 2022) was the largest detected in the study, with >1,000 cases—consistent with unusually intense RSV epidemics reported globally after NPIs were eased [1, 32, 33]. This resurgence has been widely attributed to an immunity debt, whereby reduced exposure during 2020–2021 resulted in a larger susceptible population, particularly among young children [34, 35]. Enhanced RSV transmission during 2022–2024 in Sakon Nakhon mirrors post-pandemic patterns observed in Japan, Australia, Europe, and the Americas, where out-of-season RSV peaks and expanded age distributions were documented [31, 32, 34].

The multiple secondary clusters during 2022–2024 also indicate spatially heterogeneous re-emergence, with overlapping hot spots across northern, central, and southern districts. Such widespread cluster formation may reflect the rapid resumption of mobility, increased social mixing, and the accumulation of susceptible cohorts across multiple birth years. Similar spatial diffusion of post-pandemic RSV resurgence has been observed in both temperate and tropical settings [32, 36, 37].

Table 1 Statistically significant space–time clusters of RSV by epidemiological phase (2019–2024)

Cluster	Time Frame	No. of sub-districts	Observed Cases	Expected Cases	RR	LLR	Radius (km)	p-value
Pre-pandemic phase (January 2019 – March 2020)								
Primary cluster*	Feb 2019–Aug 2020	9	157	25.82	6.08	155.940	18.43	<0.001
Secondary cluster	Mar–Jun 2019	1	5	0.11	44.03	14.042	0	0.001
Secondary cluster	Jul–Oct 2019	3	9	1.18	7.64	10.492	8.57	0.049
Suppression phase (April 2020 – December 2021)								
Primary cluster*	Nov 2020–Feb 2021	41	57	21.07	2.71	21.067	50.85	<0.001
Resurgence (January 2022 – December 2024)								
Primary cluster*	Mar–May 2022	15	1,059	535.39	1.98	280.535	19.26	<0.001
Secondary cluster	Jul–Oct 2022	39	70	36.53	1.92	12.290	49.86	<0.001
Secondary cluster	Dec 2022–Jun 2023	28	29	8.09	3.58	16.200	31.98	<0.001
Secondary cluster	Aug 2022–Feb 2023	9	18	3.90	4.62	13.475	23.07	<0.001
Secondary cluster	Oct 2023–Mar 2024	12	21	4.33	4.85	16.550	16.09	<0.001
Secondary cluster	Aug–Nov 2024	3	17	4.17	4.08	11.099	7.18	0.028

Note: * Primary cluster refers to the most-likely cluster identified by SaTScan within each epidemiological phase for interpretative purposes, RR = Relative risk; under the permutation model, RR represents the observed-to-expected ratio. LLR = Log-Likelihood Ratio

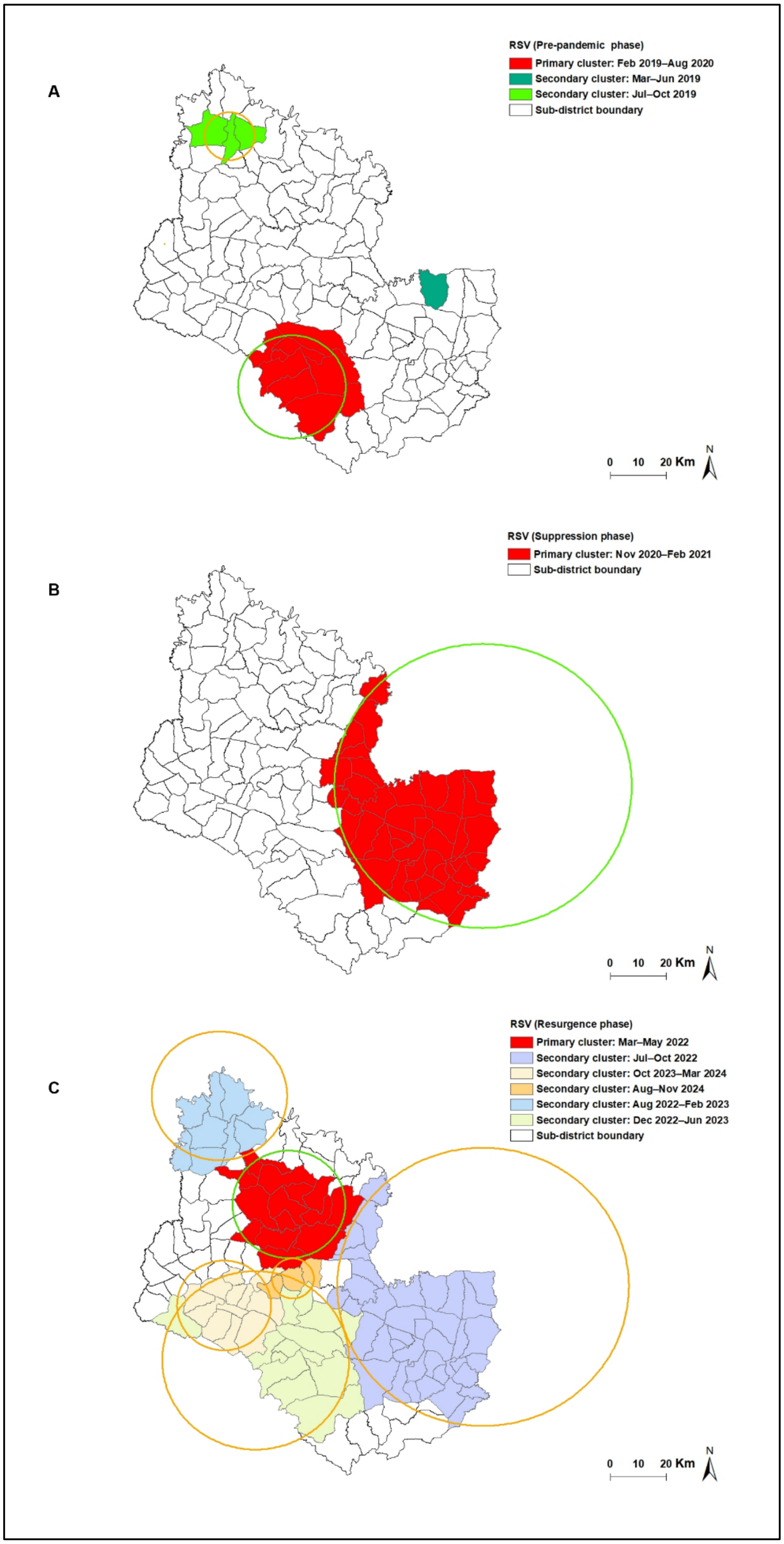

Fig. 4 SaTScan-detected space–time clusters of RSV during the three epidemiological phases in Sakon Nakhon Province, 2019–2024.

The shifting spatial landscape of RSV transmission across the three phases highlights the need for strengthened RSV surveillance, particularly at sub-district levels where transmission hotspots may persist or reappear. Early detection of RSV transmission is crucial for pediatric care planning, hospital surge preparedness, and timely deployment of preventive interventions such as maternal RSV vaccines and monoclonal antibodies, which have recently become available in several regions [38, 39]. The large and geographically diffuse clusters observed in the resurgence period underscore the importance of flexible, adaptive surveillance systems capable of detecting atypical seasonal patterns.

A major strength of this study is the use of high-resolution spatial data over six years, enabling detailed characterization of RSV clustering across phases of major epidemiological disruption. The use of the space–time permutation model avoids the need for population-at-risk denominators and is well-suited for analyzing case-based surveillance data. Limitations include potential under-diagnosis or variability in healthcare-seeking behavior, particularly during the COVID-19 pandemic, which may have influenced case detection. Additionally, the absence of viral sequencing limits interpretation of whether different RSV genotypes contributed to resurgence dynamics.

4. Conclusion

RSV transmission in Sakon Nakhon Province underwent marked spatial reconfiguration across the COVID-19 pandemic, transitioning from localized seasonal clustering to more diffuse community-wide circulation during the resurgence period. Several limitations should be acknowledged. First, RSV case detection relied on routine surveillance data, which may be influenced by variability in healthcare-seeking behavior, diagnostic capacity, and reporting practices—particularly during the COVID-19 pandemic when healthcare systems were strained. Such changes may have affected the apparent spatial intensity of detected clusters. Future studies could integrate healthcare utilization metrics, testing rates, or syndromic surveillance data to better adjust for detection bias.

Second, although the space–time permutation model is well suited for case-based surveillance, it does not incorporate population denominators; thus, detected clusters reflect relative case aggregation rather than population-based incidence risk. Complementary analyses using discrete Poisson or Bayesian spatial models incorporating population data could provide additional insight into true risk differentials across sub-districts. Third, the absence of viral genomic data limits the ability to assess whether spatial shifts were influenced by genotype replacement or strain-specific transmission dynamics. Integration of molecular surveillance and phylogenetic analysis in future work would enable more comprehensive interpretation of transmission pathways. Fourth, climate and environmental drivers were inferred but not directly modeled. Incorporating meteorological variables, land-use indicators, or mobility data into spatio-temporal regression or Bayesian hierarchical frameworks could clarify the relative contributions of climatic forcing and contact structure to observed cluster evolution.

Despite these limitations, the study demonstrates how high-resolution spatial analysis can reveal dynamic restructuring of respiratory virus transmission during periods of epidemiological disruption. Future research integrating demographic, climatic, genomic, and mobility data will be essential to anticipate RSV transmission patterns in the context of evolving immunity and emerging preventive interventions.

5. Suggestions

As RSV epidemiology continues to evolve in the post-pandemic era, fine-scale spatio-temporal analyses will be essential for anticipating and responding to future atypical outbreaks.

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7. Declaration of Generative AI in Scientific Writing

We used a generative AI tool solely to assist with checking grammar and linguistic clarity.

8. CRediT Author Statement

Kulwadee Suwannatrai: Conceptualization; Methodology; Software, Formal analysis, Visualization; Investigation, Writing - Original Draft, Supervision, Funding acquisition.

Kavin Thinkhamrop: Methodology; Software, Formal analysis, Visualization; Writing - Reviewing and Editing.

Komsan Raksaseng: Resources, Writing - Review & Editing.

Apiporn Suwannatrai: Conceptualization; Methodology; Software, Formal analysis, Visualization; Investigation, Writing - Original Draft.

9. Research Involving Human and Animals Rights

The study complied with ICH-GCP and institutional guidelines for the ethical conduct of human research. All procedures minimize risk and preserve confidentiality. No animal subjects were involved.

10. Ethics Approval and Consent to Participate

The study protocol was reviewed and approved by the Sakon Nakhon Rajabhat University Human Research Ethics Committee (Approval No. HE 68-067).

11. Declaration of Competing Interest

The authors declare no competing financial interests or personal relationships that could have influenced the work reported in this paper.

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