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Identification of Locally Transmitted COVID-19 Spatial Clusters and Hotspots

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ABSTRACT:

Background: The coronavirus disease 2019 (COVID-19) is an emerging and rapidly evolving profound pandemic, which causes severe acute respiratory syndrome and results in significant case fatality around the world. We conducted this study to identify locally transmitted COVID-19 spatial clusters and hotspots in this phrase of the fourth wave in Vietnam.

Data used and Methods: A total of 9,192 locally transmitted cases confirmed in this phrase in the fourth wave were used in study. Global and local Moran's I and Getis-Ord's G_i^* statistics were employed to identify spatial autocorrelation and hotspots of COVID-19 cases.

Results: It was found that global Moran's I statistic indicates a robust spatial autocorrelation of COVID-19 cases. Local Moran's I statistic successfully identified three high-high spatial clusters of COVID-19 cases in Bac Giang (5,083 cases), Bac Ninh (1,407 cases), and Hanoi (464 cases). In addition, hotspots of COVID-19 cases were mainly detected in Bac Giang (5,083 cases), Bac Ninh (1,470 cases), Hanoi (464 cases), Hai Duong (51 cases), and Thai Nguyen (7 cases).

Conclusion: The results of this work offer new perspectives on the geostatistical analysis of COVID-19 clusters and hotspots, which could help policy planners anticipate the dynamics of spatiotemporal transmission and develop critical control measures for SARS-CoV-2 in Vietnam. Future pandemics and epidemics can be avoided and controlled with the help of geospatial analysis techniques.

KEYWORDS: Identification, Spatial Clusters, Hotspots, Locally transmitted COVID-19, Local Moran's I statistic, Local Getis Ord statistic, Vietnam.

INTRODUCTION

Severe Acute Respiratory Syndrome Coronaviruses (SARS-CoV) and Middle East Respiratory Syndrome Coronaviruses (MERS-CoV), which were first discovered in China and later spread throughout the Middle East, particularly in Saudi Arabia, were the products of the alarming morbidity and mortality that the world was facing at the beginning of the twenty-first century (1). To stop further pandemics, numerous researchers have since been working to uncover more coronaviruses. However, by the end of 2019, reports of several pneumonia cases with unclear etiologies led to the outbreak of the current pandemic in Wuhan, China (2,3). The virus was classified as a new coronavirus by the World Health Organization (WHO) in January 2020 (2). As of the end of July, 2020, there were about 20.0 million cases of infection, accounting for 0.75 million deaths globally, or about 5% of all deaths (4). Similar to other Asian nations, Vietnam has been confronted with the COVID-19 pandemic threat since March 2020. The latest data shows that as of 30 November 2023, there have been 772,052,752 confirmed cases of COVID-19, including 6,985,278 deaths, reported to WHO (5). Thus, applications of spatial clustering and hotspots in studies of the spread of COVID-19 play an important roles in the fight against the COVID-19 pandemic.

Movement of people typically contributes significantly to the spread of infectious diseases, and this is especially true for COVID-19 since it is a highly contagious respiratory virus that is disseminated by droplets and aerosols (6). When examining how infectious diseases spread, spatiotemporal analysis is crucial. A modern instrument of a comprehensive computerized system that can efficiently gather, store, manage, compute, display, and analyze spatial-temporal data is the geographic information system (GIS). It is frequently used to analyze the spatial distributions of infectious illnesses and characterize their epidemic features (7,8). The spatiotemporal data are crucial tools for identifying COVID-19 transmission dynamics, which may be used to evaluate ongoing efforts and provide guidance for developing fresh, creative approaches to disease containment (9). The spatial statistics and factors affecting COVID-19 at both, prefecture and county levels were examined in Hubei Province, China (9). The necessity of using GIS science was investigated for COVID-19 mapping (10). Spatial autocorrelation analysis was used to investigate the spatial clustering characteristics of the COVID-19 pandemic in Beijing, China (11). Clarifying the scope and consequences of the pandemic will require an understanding of the spatiotemporal dynamics of COVID-19. Finding the places where health services need to be improved is also helpful. It is a crucial tool for planning, decision-making, and community involvement (12). Spatiotemporal analysis were employed to figure out the epidemic characteristics due to the spatial dependence of COVID-19 (13) in many countries such as China (13), Iran (14), United States (15). In addition, GIS has been also successfully to COVID-19 studies in many countries such the United States (16), England (17), Spain (18), Italy (19), and Iran (20).

Many researchers from all over the world, including those from Vietnam, have discussed the pandemic's potential epidemiology; nevertheless, little information about the spatial diversity of COVID-19 in Vietnam has been published. As a result, the goal of the current study is to examine the features and the spatiotemporal distribution of the COVID-19 pandemic throughout Vietnam's provinces. We aimed to identify locally transmitted COVID-19 spatial clusters and hotspots in this phrase of the fourth wave in Vietnam A total of 9,192 locally transmitted cases confirmed in this phrase in the fourth wave were used in study. Global and local Moran's I and Getis-Ord's G_i^* statistics were finally employed to identify spatial autocorrelation and hotspots of COVID-19 cases.

DATA USED

Vietnam was a remarkable COVID-19 success story, logging zero cases for months on end and keeping life close to normal for much of the population (21). As of June 24, 2021, the COVID-19 pandemic in Vietnam can be classified into four waves. A total of 89,992 confirmed cases (87,847 locally transmitted cases and 2,145 internationally imported cases) and 63 deaths were reported to the Ministry of Health of Vietnam (22). Vietnam's fourth wave began on April 27 (21). The first phrase of the COVID-19 pandemic in Vietnam's fourth wave will be the main topic of this investigation. Thus, to determine the COVID-19 pandemic's spatial clustering and hotspot, a total of 9,192 locally transmitted cases confirmed in this phrase in the fourth wave were used in study.

METHODS

Global Moran's I statistic

The global Moran's I indicates whether spatial autocorrelation is present overall or not. In order to determine the global spatial clustering of COVID-19 cases, this study used the global Moran's I statistic (23,24). Equation represents the definition of the global Moran's I statistic:

$$I = \frac{n}{S_0}\frac{\sum_{i=1}^{n}\sum_{j=1}^{n} W_{ij}(x_i-\bar{x})(x_j-\bar{x})}{\sum_{i=1}^{n}\sum_{j=i}^{n} W_{ij}\sum_{i=1}^{n}(x_i-\bar{x})^2} \tag{1}$$

where x_i and x_j are the COVID-19 cases for district i and district j; $\bar{x}$ is the mean of COVID-19 cases and be given by $\bar{x} = \sum_{i=1}^{n}\frac{x_i}{n}$; n is the total number of districts in the whole study area; and W_{ij} is a $(n \times n)$ spatial weight matrix (25).

The global Moran's I coefficient values are in the interval [-1, +1] (25). When there is positive geographic autocorrelation in the data, global Moran's I values are positive; conversely, when there is negative spatial autocorrelation, global Moran's I values are negative (26). The COVID-19 distribution shows no signs of randomness or regional autocorrelation when global Moran's I coefficient values are near zero.

Local Moran's I statistic

Since the local Moran's I statistic is one of the LISA statistics that is most frequently employed in research, this study used it to measure the spatial clustering of low and high COVID-19 cases in each district (25). The following formula provides the local Moran's I statistic (I_i) of COVID-19 cases at district i (27):

$$I_i = \frac{(x_i-\bar{x})}{\sigma^2}\sum_{j\#i, j\in J_i}^{N} W_{ij}(x_j-\bar{x}) \tag{2}$$

where x_i, x_j, $\bar{x}$, and W_{ij} are defined in equation (1); N is the total number of neighborhood districts (25); J_i denotes the neighborhood set of COVID-19 cases at district i; j#i implies that the sum of all $(x_j-\bar{x})$ of nearby neighbourhood districts of district i but not including x_j; and σ^2 is the variance of x, given in equation (3). W_{ij} defines neighbor connectivity and can be constructed using the order of contiguity.

$$\sigma^2 = \frac{1}{N}\sum_{j=1}^{N}(x_i-\bar{x}) \tag{3}$$

If I_i follows a normal distribution, the statistical significance of Moran's I statistic can be examined, and the Z-scores can be ascertained as follows:

$$Z_{I_i} = -\frac{I_i - E(I_i)}{\sqrt{Var(I_i)}} \tag{4}$$

where $E(I_i)$ and $Var(I_i)$ are the arithmetic expectation and variance of the Moran statistic at district i, respectively.

Similar to the global Moran's I statistic, the local Moran's I value at district i (I_i) also ranges between -1 and +1 (25). A high positive I_i shows the district i has a similarly high or low number of COVID-19 cases as its neighbors and called the ''spatial cluster''(26)

Identification of Locally Transmitted COVID-19 Spatial Clusters and Hotspots

Getis Ord G_i^* statistic

Hotspot analysis is based on the Getis-Ord's G_i^* statistic. Hotspot analysis characterizes the presence of hotspots (high clustered values) and coldspots (low clustered values) over an entire area by looking at each feature within the context of its neighboring features (28). Hotspot can separate clusters of high values from cluster of low values. It is, therefore, Getis-Ord's G_i^* statistic was used to identify the counties of high and low numbers of COVID-19 cases (25,29). The form of Getis-Ord's G_i^* statistic is defined as follows (23):

$$G_i^* = \frac{\sum_{j=1}^{N} W_{ij} x_j - \bar{x} \sum_{j=1}^{N} W_{ij}}{S\sqrt{\frac{N\sum_{j=1}^{N}[W_{ij}^2 - (W_{ij})^2]}{N-1}}} \quad (5)$$

with:

$$\bar{x} = \frac{1}{N}\sum_{j=1}^{N} x_j \quad (6)$$

and:

$$S = \sqrt{\frac{\sum_{j=1}^{N} x_j^2}{N} - (\bar{x})^2} \quad (7)$$

Expectation:

$$E(G_i^*) = \frac{W_i^*}{n-1} \quad (8)$$

with:

$$W_i^* = \sum_{j=1}^{n} w_{ij}(d) \quad (9)$$

and variance:

$$Var(G_i^*) = \frac{W_i^*(n - W_i^*)Y_{i2}^*}{n^2(n-1)(Y_{i1}^*)^2} \quad (10)$$

with:

$$Y_{i1}^* = \frac{\sum_{j=1}^{n} x_j}{n}; \quad (11)$$

and:

$$Y_{i2}^* = \frac{\sum_{i=1}^{n}\sum_{j=1}^{n}(x_i x_j)^2}{n} - (Y_{i1}^*)^2; \quad (12)$$

where: the Getis-Ord's G_i^* statistic is computed for the number of COVID-19 cases at county i; x_i, x_j, $\bar{x}$, and W_{ij} are spatial weight matrix; and N is the total number of neighborhood counties as defined in equation (2). W_{ij} can be constructed using the methods of the first order and second of contiguity.

RESULTS AND DISCUSSION

Spatial distribution of COVID-19

On January 23, 2020, the first case of COVID-19 in Vietnam was reported. The patient, a 65-year-old Chinese male, had a fever on January 17, four days after arriving in Hanoi by plane with his spouse from Wuhan's Wuchang District (22). As of 4 April 2020, Vietnam was rated 94th out of 206 nations and territories afflicted by COVID-19, with 240 confirmed cases and no deaths reported. A 3-month-old girl was the youngest person affected, and an 88-year-old woman was the oldest (30). Vietnam's fourth wave began on April 27 (21). Data from Figure 1 depicted the spatial distribution of these locally transmitted cases reported in the first phrase of the fourth COVID-19 wave in Vietnam. Figure 1 shows that the number of COVID-19 cases was divided into 5 different levels: very low (0-36 cases), low (37-463 cases), medium (463-1345 cases), high (1346-3000 cases) and very high (3001-5083 cases). The number of high and very high COVID-19 cases was mainly concentrated in the northeast region and some provinces in the south of Vietnam. Meanwhile, the low number of COVID-19 infections was mainly concentrated in rural and mountainous areas.

Identification of Locally Transmitted COVID-19 Spatial Clusters and Hotspots

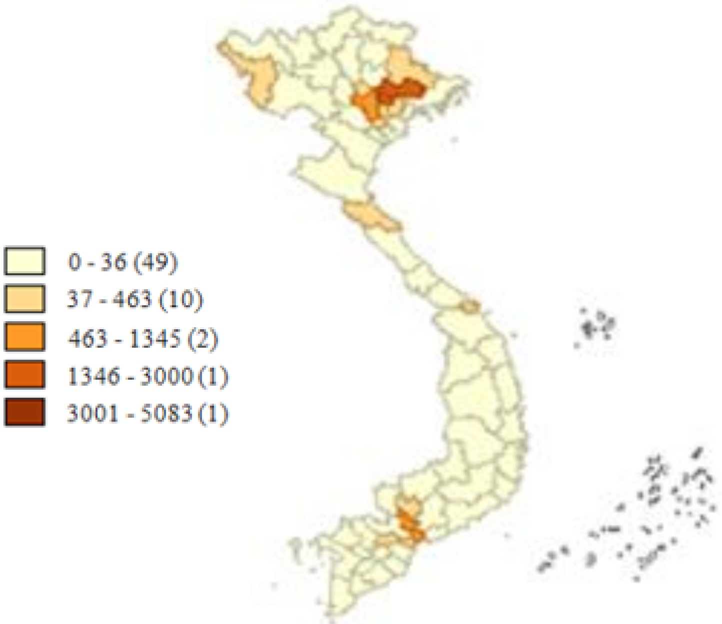

Figure 1. Map of locally transmitted COVID-19 cases in the first phase of the fourth wave in Vietnam.

Spatial clustering of the COVID-19 pandemic

The initial phase of the fourth COVID-19 wave had global Moran's I coefficients of 0.01 ($p<0.001$) as shown in Figure 2. Overall, the value of global Moran's I coefficient was around zero, suggesting that there were no spatial auto-correlation or random distribution of the COVID-19 pandemic in this phrase in the fourth wave.

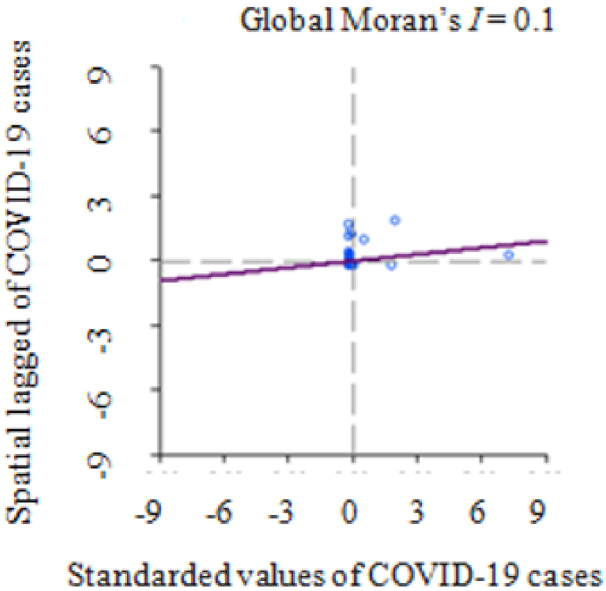

Figure 2. Moran scatterplot of COVID-19 cases in the first phase of the fourth wave in Vietnam.

The Anselin local Moran's I statistic, as a local statistic of spatial correlation, represents the spatial correlation between a research area and its neighboring areas for the research variables, including low-low, low-high, high-low, and high-high, and not significant. The low-low and high-high types indicate spatial aggregation, that is, cold spots and hot spots, respectively. The spatial distribution of the local Moran's I statistic is shown in Figure 3.

Identification of Locally Transmitted COVID-19 Spatial Clusters and Hotspots

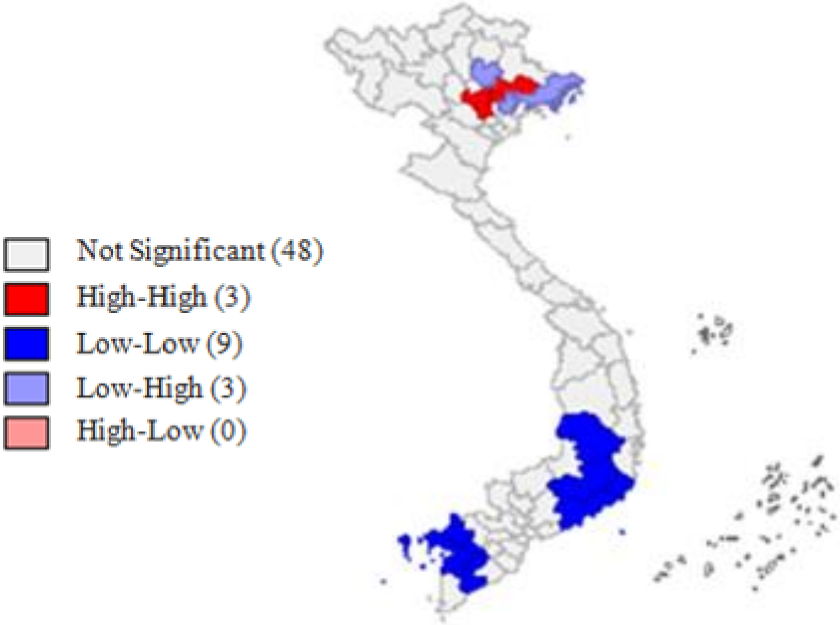

Figure 3. Hotspots of COVID-19 cases in the first phase of the fourth wave in Vietnam.

A total of 9,192 locally transmitted COVID-19 cases was confirmed in Vietnam during the first phase of the pandemic's fourth wave. Three high-high spatial clusters were found in Bac Giang (5,083 cases), Bac Ninh (1,407 cases), and Hanoi (464 cases), wheareas nine low-low spatial clusters were identified in the south-central region, including Ninh Thuan (12 cases), Binh Thuan (11 cases), and Dak Lak (6 cases). Very few COVID-19 cases were reported in southern provinces of Vietnam, including Lam Dong, An Giang, Kien Giang, Can Tho, Hau Giang, and Bac Lieu as shown Figure 3. In the initial stage of the fourth COVID-19 wave, as shown in Figure 3, the north-eastern provinces of Vietnam were the primary locations for the spatial clustering of the COVID-19 pandemic, which included high-high spatial clusters and low-high spatial outliers. More than 6,500 infected workers in industrial parks in Bac Giang and Bac Ninh provinces were the primary cause of these spatial clusters and outliers after a series of COVID-19 confirmed cases were detected due to viral virus strains from the UK and India on April 27, 2021 .

Hotspots of the COVID-19 pandemic

The specific spatial clustering positions of high and low values can be observed, and the specific distribution of cold spots and hot spots can be identified using G_i^* analysis. When the Getis-Ord G_i^* value is higher than the expected value and the Z score is positive, it indicates that the high value is clustered, that is, there is a hot spot; and when the Getis-Ord G_i^* value is lower than the expected value and the Z score is negative, it indicates that the low values have a tendency to gather, that is, there is a cold spot. The spatial distribution of hotspots and coldspots associated with the COVID-19 pandemic in Vietnam during its fourth wave is depicted in a map shown in Figure 4.

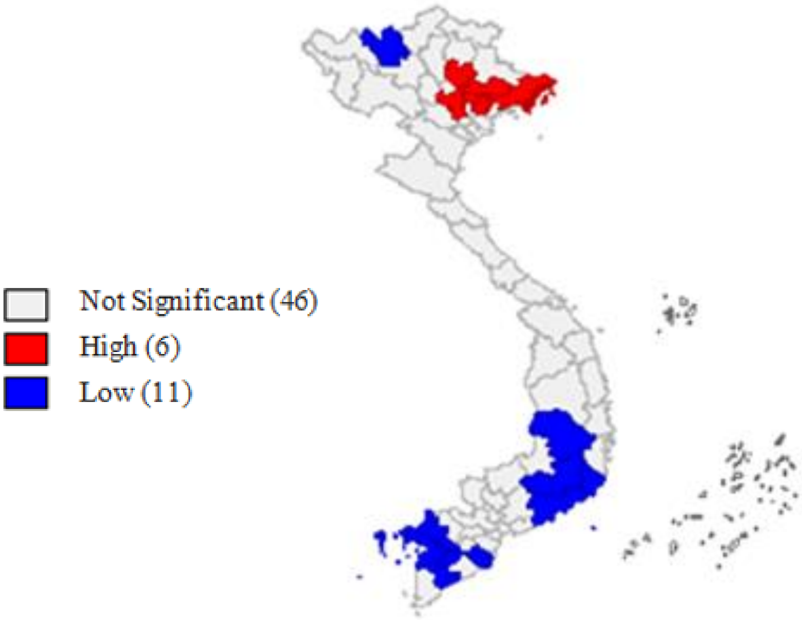

Figure 4. Spatial clustering of COVID-19 cases in the first phase of the fourth wave in Vietnam.

Identification of Locally Transmitted COVID-19 Spatial Clusters and Hotspots

Data from Figure 4 demonstrate that a total of six COVID-19 hotspots was successfully identified in the first phase of the fourth COVID-19 wave in the northeastern region of Vietnam by the local Getis-Ord's G_i^* statistic. These hotspots were detected in Bac Giang (5,083 cases), Bac Ninh (1,470 cases), Hanoi (464 cases), Hai Duong (51 cases), Thai Nguyen (7 cases), and Quang Ninh (1 case). Furthermore, a total of 11 coldspots with extremely low COVID-19 case counts in provinces and cities were effectively identified in the center and southern regions in this phrase.

CONCLUSION

This study was conducted to identify locally transmitted COVID-19 spatial clusters and hotspots in the first phrase of the fourth wave in Vietnam. A total of 9,192 locally transmitted cases confirmed in the first phrase in the fourth wave were used in study. Global and local Moran's I and Getis-Ord's G_i^* statistics were then employed to identify spatial autocorrelation and hotspots of COVID-19 cases. It was found that global Moran's statistic indicates a robust spatial autocorrelation of COVID-19 cases. Local Moran's I statistic successfully identified three high-high spatial clusters of COVID-19 cases in Bac Giang (5,083 cases), Bac Ninh (1,407 cases), and Hanoi (464 cases). In addition, hotspots of COVID-19 cases were mainly detected in Bac Giang (5,083 cases), Bac Ninh (1,470 cases), Hanoi (464 cases), Hai Duong (51 cases), and Thai Nguyen (7 cases). It can be concluded that the results of this work offer new perspectives on the geostatistical analysis of COVID-19 clusters and hotspots, which could help policy planners anticipate the dynamics of spatiotemporal transmission and develop critical control measures for SARS-CoV-2 in Vietnam. Future pandemics and epidemics can be avoided and controlled with the help of geospatial analysis techniques.

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CONFLICT OF INTEREST: None

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