A Social Network Analysis of COVID-19 Transmission Models in Taiwan: Two Epidemic Waves in 2020-2021

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Abstract

The COVID-19 pandemic has made a profound global impact. As it rages on around the globe, social network researchers have been involved in exploring key factors of rapid infection and transmission. For Taiwan, it is thus worthy of exploring the differences between the transmission models of the two epidemic waves in 2020-2021 for any insight that may have been overlooked. In this study, the social network analysis is adopted for revealing any unforeseen threats of infection. In the first wave, 652 confirmed cases were reported from January 21, 2020, to November 30, 2020. In the second wave, 880 confirmed cases were reported from May 03, 2021, to May 17, 2021. The infection source attribute, i.e., local vs. imported, made the transmission models to be structured differently between the first and the second wave. In the first wave, it was found that a community outbreak could easily happen when one node got infected without knowing when and where the transmission occurred. In contrast, in the second wave, it was found that the gender attribute was more effective than the age attribute in quickly identifying the differences in the transmission models among all the confirmed cases.

Keywords: Transmission model, Social network analysis, COVID-19 pandemic, Epidemic wave, Taiwan case study

1 Introduction

Coronavirus 2019 (COVID-19 in short), named by the World Health Organization, is an infectious disease [1]. The virus affects both humans and animals, mainly in the respiratory, enteric, hepatic, and neurological systems [2]. The outbreak has been declared a public health emergency of international concern [3]. It presents a challenge especially to elderly patients as they are more likely to develop severe infections and suffer from the symptoms due to their frailer health conditions [4]. As of March 31, 2022, about 482 million cases have been confirmed worldwide, resulting in 6.15 million deaths (global mortality rate: 1.27%) [5].

On January 21, 2020, Taiwan reported its first confirmed case: A businessman traveler tested positive on a polymerase chain reaction (PCR) test [6]. At that time, there was approximately a 0.3% chance for Taiwanese residents to be tested positive on PCR [5]. A study indicated that this statistic was similar to a population that had been vaccinated or one whose immune systems had naturally produced the antibody against this virus [7]. Between that date and November 30, 2020, a total of 652 confirmed cases were reported. This period has been regarded as Taiwan's first epidemic wave. At first, Taiwanese residents were hesitant to receive the vaccine even when it became available because they were concerned about the serious side effects or death caused by the vaccine [8], and there had been no rapid daily increase of confirmed cases [9] until the second epidemic wave. The containment shows Taiwan's effective control of the deadly virus. For example, people who developed fever, cough, or acute respiratory symptoms were identified by local clinics; those who had a travel history within the past 14 days or close contact with such people were asked to self-quarantine at home. They were required to report to the health authorities and provide a laboratory specimen for further diagnosis. Even with these measures in place, however, a second epidemic spread started on May 18, 2021. The mortality rate reached 4.3% on June 26, 2021 [5].

Taiwan Centers for Disease Control (TCDC) had set up a COVID-19 advisory committee on January 02, 2020, to respond to this pneumonia pandemic. Since then, TCDC has been holding daily press conferences, conducting extensive contact tracing, and implementing airport and border surveillance [5]. At that time, TCDC implemented a national mask ration initiative with the assistance of pharmacies across the country to ensure that the distribution of masks was fair and equal among the entire population. Other preventive measures, such as onboard quarantine of all direct flights from certain places as well as entrance restriction from foreign workers without resident permits started on May 19, 2021, and onward [10-11]. As more and more people received vaccinations, the mortality rates of 7-day rolling averages, as of July 31, 2021, went down to around 0.14 per million confirmed cases [12].

As the Taiwanese government puts great efforts into containing the spreading of the COVID-19 pandemic, a question emerges: What differences between these two epidemic waves will we see if the transmission models based on the confirmed cases in Taiwan are explored? As one of the effective measures is social distancing, which has been widely implemented in Taiwan, this study intends to use the social network analysis (SNA) method to explore the COVID-19 transmission models of all the confirmed cases in the first and the second epidemic wave in Taiwan. The differences between the transmission models of the two waves could also be explored for any insight that may have been overlooked. The

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SNA method is often used to explore an individual's role and its relation with others in a community, both in a face-to-face conversational scenario and on an online platform. The validity of using the SNA method has been established by two recently published studies, which have obtained better interpretations of the social networks analysis results with visualization for the confirmed cases in their countries [13-14].

2 Social Network Analysis, Infections, and Outbreaks

SNA is a process of investigating social structures through the use of networks. SNA software such as Gephi, NodeXL, and UCINET offer various tools that can be used to analyze data similar to those collected in this study. These SNA tools can help us understand the dependencies between the social entities in the data while characterizing their behaviors and their effect on the network as a whole and over time [15]. Every node represents an individual, and every line represents how closely a person is connected with the others in the entire network. The lines with arrows can be regarded as either giving information to or receiving information from others [16].

The arise of the COVID-19 public health emergency has emphasized the importance of relationships that change in various contexts, and all kinds of structural changes have inspired SNA researchers to explore potential threats or opportunities during the COVID-19 pandemic. A group of 43 university students living in the same hall of residence was found to have experienced significant changes in their relationships when facing the chance of contagion, and four subgroups including one complete subnetwork (also called a "clique") were formed [17]. Starting from 2020 to date, an increasing number of SNA studies have been carried out by collecting posts including hashtags from various social media sites, e.g., Facebook, Instagram, Reddit, Snapchat, TikTok, Twitter, WhatsApp, QQ, Sina Weibo, WeChat, and YouTube. For example, a study has shown that city agencies were able to coordinate with city governments in Atlanta, San Francisco, and Washington, DC by utilizing Twitter posts, mentions, and retweets to quickly distribute public health information and orient the public to achieve policy goals [18]. Another SNA study explores the similarities and differences in the content of the posts that reflect the crisis lifecycle of COVID-19 and the attributes of the opinion leaders of online discourses in China (on Sina Weibo) and the United States (on Twitter) [19]. SNA studies regarding the ongoing COVID-19 pandemic can be expected to generate new findings to make contributions to elaborating theories and enriching literature in different disciplines.

In addition, according to Google Trend, *infection* and *outbreak* are two keywords with relatively high percentiles of English-translated search results in Taiwan during this study's data collection period (mean values of *infection* vs. *outbreak* = 51:20, out of 100; note that the other 29 belong to other related keywords searched by Google users). Also, according to Merriam-Webster, *infection* means "the state produced by the establishment of one or more pathogenic agents (such as bacteria, protozoans, or viruses) in or on the body of a suitable host" [20]; *outbreak* means "a sudden rise in the incidence of a disease" [21]. These two terms are often used by news reports and the media to describe the virus control status or the levels of threat caused by COVID-19 around the world.

Based on the definition of *infection*, network density can be obtained to report the degree of its overall closeness. Network density, including the values of normalized overall out-degree and normalized in-degree centrality, can also be obtained to find the nodes, which are regarded as the informants. If the overall out-degree centrality value in the directed network (i.e., a node giving information to another node, but not the other way around) is higher, the confirmed cases (nodes) can be regarded as more contagious, and their transmissions can be either local-to-local or imported-to-local. A further step is to carry out a cluster analysis to identify if any close groups have formed in the network. Per the definition of *outbreak*, component analysis can further determine if any larger clusters that emerged from the directed network might have formed by more confirmed cases with high virus transmissibility. The number of clusters in the overall network can also be obtained, and by examining how the cluster is composed, the variables critical to causing an infection can be identified quickly.

Overall, for the purpose of this study, the definitions of *infection* and *outbreak* have been interpreted carefully to match the SNA methods to properly analyze the data collected in this study and to present appropriately the COVID-19 transmission model for the two epidemic waves in Taiwan.

3 Two Epidemic Waves' Data Collection and Analysis Methods

The first period of data collection time started when Taiwan was under Epidemic Alert Level 1, and the first dataset was collected between January 21 (when the first case was confirmed) and November 30, 2020. Between November 30, 2020, and May 3, 2021, the nationwide Epidemic Alert was not yet elevated, although an unexpected local-to-local infection case (a Taiwanese resident doctor, case #838) was reported on January 16, 2021, after visiting a hospitalized patient (imported: #812) and became infected, and a group of 21 confirmed local cases were reported. The virus control status was stable for several months. Less than ten confirmed cases were reported daily. The data collection was temporarily suspended until May 2021.

The data collection resumed when several imported cases were identified as being infected with the Alpha variant of the virus, and that resulted in hundreds of new daily local cases reported by TCDC. The nationwide Epidemic Alert was rapidly elevated to Level 3, especially as multiple confirmed cases were reported in northern Taiwan on May 03, 2021, so the second wave's dataset was collected from May 03 to May 17, 2021, the date of the national lockdown. The number of daily confirmed cases (local > imported) increased drastically by mid-May. On May 15, more than a hundred confirmed cases were reported (local: 180, imported: 5), and the number shot up to over 200 on the next day (local: 206, imported: 1). As of May 16, a total of 1,682 confirmed cases had been reported in Taiwan (local: 550, imported: 1,115, including the Dunmu naval fleet and 77 unknown sources), including 1,116 cases of recovery and 12 deaths. The day after, on May 17, more than 300 confirmed cases were reported (local: 333, imported: 2). Then, the nationwide pandemic outbreak started on May 18, 2021.

To be noted, this study does not include any data after May 18 for three reasons. First, with the increased number of infections, tracing the confirmed cases' infection sources had become too heavy a burden to be accurate in real time, and the government started to backtrack infection data starting May 18 (local: 240, imported: 5) to June 5 (local: 476, imported: 0, backlog: 35). Second, almost all confirmed cases were local after May 18, and three major infection clusters were found, although no specific infection dates and times could be traced back: 1) China Airline Novotel pilots, employees, and their families in Taoyuan City, 2) Lion Club members in New Taipei City, and 3) teahouse customers in Wanhua District in New Taipei City and Luodong Township in Yilan County. Lastly, the TCDC no longer provided the confirmed cases' detailed demographic data to the public starting June 16, 2021 [22].

Three attributes were still retrievable as independent variables, i.e., patients' age and gender (female vs. male), and their infection source (local vs. imported). These three attributes were publicly released during the two periods of data collection; however, some patients' age data retrieved in the second period were only a range rather than the exact number [22]. Fortunately, the total numbers in each age range were still available from news reports. Before carrying out the SNA analyses, the demographical statistics of all confirmed cases in the two waves were calculated. The software NetDraw 2.168 [23], embedded in UCINET 6.698 [24], was used to visualize the social network for the two waves and to identify any differences in the transmission models after entering the gender and the infection source variables. The statistics regarding the transmission models of the two waves were reported by carrying out the network density, including the normalized in- and out-degree of network centrality in UCINET. The cluster analysis was further carried out in UCINET to explore the number of closely connected internal or external groups (i.e., local or imported cases) and to determine which cluster contained more confirmed local/imported cases. Finally, the component analysis was carried out to obtain insights from these analyses to verify the existence of potential threats and changes in the transmission models during the two epidemic waves.

4 Results

The dataset collected in the first wave contained a total of 652 confirmed cases. This number includes 7 cases of death, and most cases have recovered. The Dunmu naval fleet cases were also included in the dataset (n = 36, all imported cases, and mostly between ages 21 and 40). Later on, the number was revised to 651 because two case numbers (#530 and #536) were assigned to the same person in the genetic test, who was an imported case. However, the sequence number of each reported case stays the same in the open-source database. The influence of double-counting the same case compared with the total number is believed to be minimal. Thus, this study claims 652 confirmed cases in the first dataset. Although 47 cases had an unknown origin infection source, only 55 (8.44%) of the cases were locally acquired at that time.

The second dataset contained 880 confirmed cases. Among them, 796 (90.5%) were reported as local cases in the daily news conference, even though the origin of the infection was hard to trace for some cases. So, it is still uncertain where they contracted the disease and whom they infected, and whether they had recovered or were publicly reported as deceased. During the second dataset collection period, the statistics reported and updated daily by the TCDC showed no death count [5]. The first of the three major infection clusters started on May 03, 2021. Thirty-seven people were infected from this cluster with unknown infection sources, including 12 Taiwanese pilots (#1078, #1079, #1091-1092, #1100-1102, #1105, #1122, #1153, #1183, #1187), one Australian pilot (#1090), and two flight attendants (#1154, #1222). The second and the third major infection clusters both started on May 11, 2021. The first two confirmed cases were #1201 (male, age 60) and #1202 (female, age 30). The second infection cluster resulted in 83 people who tested positive on PCR, and the third cluster resulted in 2,686 (by May 11, 2021).

4.1 Demographics of the Confirmed Cases

For the 652 confirmed cases in the first wave, the SNA was carried out based on each demographical attribute as mentioned above, and then the infection source variable was added to each of these analyses. Among all confirmed cases, there were more females (n = 337) than males (n = 315) (Figure 1). By adding the infection source variable (local: 55, 8.44%; imported: 597, 91.56%), the analysis showed a significantly larger number of imported cases (red symbols) in either the male or the female cluster. The transmission paths linking the cases within each gender cluster are similar between the females and the males, with the male cluster having 288 imported cases, and the female cluster having 308 imported cases (Figure 2). This showed that, in the first wave, the gender attribute was irrelevant to the chance of contracting COVID-19 in Taiwan. Notably, most confirmed cases were young to middle-aged adults (age 21-30: 231, age 31-40: 171), and 381 of them were imported cases (female: 173, male: 208).

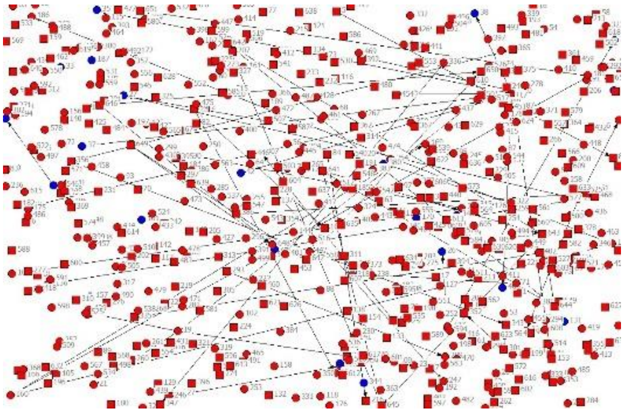

Figure 1. A snapshot of random-visual representation of the transmission model by gender and infection source in the first wave (red = imported, blue = local, square = male, circle = female) (55 local case numbers: 8, 9, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 38, 41, 42, 43, 45, 46, 50, 92, 100, 103, 124, 130, 134, 156, 168, 169, 186, 216, 246, 247, 268, 269, 289, 299, 307, 322, 335, 336, 343, 347, 352, 365, 379, 380, 386)

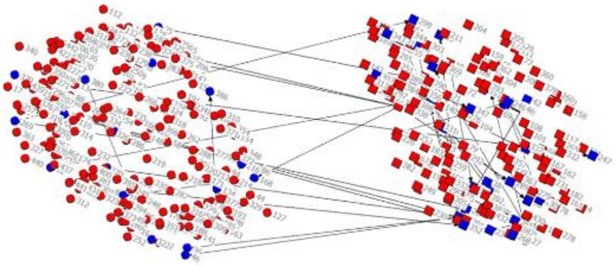

Figure 2. A snapshot of gender and infection source attribute-based visual representation of the transmission model in the first wave (red = imported, blue = local, square = male, circle = female)

In the second wave, among the 880 confirmed cases, the number of females (n = 485) was still greater than males (n = 395), and the difference between the two genders was quite noticeable (Figure 3). Since the original infection source was hard to trace, only 25 ties linked from one node to one or more nodes could be added to the transmission model. Then, by adding the infection source variable (local: 796, 90.5%; imported: 84, 9.5%), an obvious difference was found between the two waves' transmission models, in that there were many more local (blue symbols) than imported cases in the second wave. The male and the female clusters also had a multitude of local cases as illustrated in Figure 4. In the female cluster, there were 459 local cases, while in the male cluster, there were 337. Specifically, node #1203 in the transmission model had 19 direct links connected to other nodes (#1218, #1219, #1223-#1230, #1245, #1246, #1248, #1250, #1251, #1253, #1255-#1257). Node #1257 linked directly to #1275 and #1276. Other nodes are linked directly to only one node, or first one node and then another (#1210→#1232→#1278, #1211→#1231, #1229→#1289). These nodes formed other transmission paths in their communities, especially family-related transmission paths. In addition, the male cluster had 58 imported cases, twice the imported cases in the female cluster (n = 26). Even though the age data were only given in a range (e.g., age 10-40) in the public space for the second wave, most confirmed cases (n = 784) were young children and older people. The youngest case was at the age of 5, and the oldest case was at the age of 90 (age 5-90: 333, age 5-80: 386, age 10-70: 29, age 30-80: 26, age 50-70: 10; note that the cases in each age range are mutually exclusive from the cases in the other age ranges), and most were local cases (n = 776). There were 96 youths and middle-aged adults confirmed cases aged 10 to 49 (age 10-29: 49, age 30-49: 41, age 10-49: 6), and most of them were imported cases (n = 76).

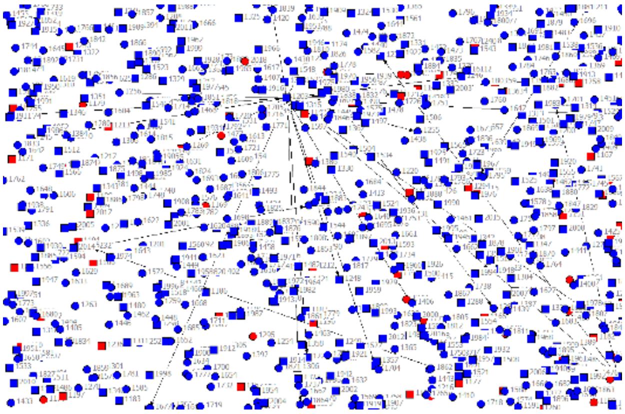

Figure 3. A snapshot of random-visual representation of the transmission model by gender and infection source in the second wave (red = imported, blue = local, square = male, circle = female) (84 imported case numbers: 1139 - 1144, 1147 - 1152, 1155 - 1173, 1175 - 1182, 1185, 1188 - 1198, 1204 - 1207, 1212 - 1215, 1233 - 1244, 1258 - 1262, 1292 - 1296, 1477, 2017, 2018)

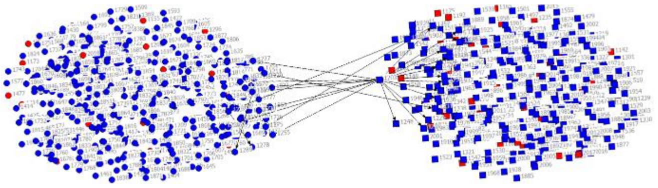

Figure 4. A snapshot of gender and infection source attribute-based visual representation of the transmission model in the second wave (red = imported, blue = local, square = male, circle = female)

4.2 Network Density, Normalized In- and Out-Degree of Centrality, and Cluster Analysis Results

The overall density of the transmission network in the first wave was 0.0001 (Std Dev = 0.0117; cut-off value = 0.5 or 50%), with a total of 58 ties, indicating that the transmission structure was very weak, with only 0.01% of transmissions occurring within the confirmed cases' social networks. However, it was found that local transmissions had a higher density of 0.7% (with 22 ties) than imported transmissions (with 15 ties, density value close to zero). The density of the local cases was considered very weak, for its value was much lower than the cut-off value.

Table 1. Degree of centrality – the first and the second waves

	The first wave		The second wave	
	Nrm out deg	Nrm in deg	Nrm out deg	Nrm in deg
Mean	0.014	0.014	0.003	0.003
Std Dev	0.076	0.050	0.074	0.019
Sum	8.909	8.909	2.844	2.844
Variance	0.006	0.002	0.005	0.000
Minimum	0.000	0.000	0.000	0.000
Maximum	1.227	0.461	2.162	0.114

Table 1 shows the same mean value for the normalized in- and out-degree network centrality in the first wave, but the out-degree centrality had a higher standard deviation and variance than the in-degree centrality did, indicating that the entire network structure could easily change over time and one person infected by any source (local or imported) can easily infect others to develop transmission paths in the local community. The maximum values of the normalized in- and out-degree centrality were respectively 0.461 and 1.227. Upon a close examination of the in- and out-degree centrality of each case or node, ten groups were found. The first and largest group was composed of 41 nodes without out-degree centrality, but the in-degree centrality was 0.082 (8.2%). In contrast, the second-largest group was composed of 16 nodes without in-degree centrality and had a total out-degree centrality of 0.032 (3.2%). The rest of the groups were small and had a total out-degree ranging from 0.008 (0.8%) to 0.015 (0.15%) and in-degree centrality ranging from 0.005 (0.5%) to 0.009 (0.9%).

These statistics showed that there was an 8.2% chance or more to have a local-to-local outbreak in a community if preventive measures were dismissed or unavailable to effectively protect other non-infectious members in the same community with the confirmed cases. This indicated a higher chance to be infected locally if a local case was confirmed. There was another 3.2% chance of infection by an imported-to-local outbreak if any onboard quarantine measures were dismissed.

A formal cluster analysis was carried out to verify the above findings regarding the differences between local and imported cases in terms of normalized in- and out-degree of centrality. As a result, four major clusters were found, and each accounted for a different proportion of the total population (Cluster 1: 223 nodes, 34.2%; Cluster 2: 217 nodes, 33.3%; Cluster 3: 209 nodes, 32.1%, and Cluster 4: 3 nodes, 0.5%). These clusters were similar in the ways their nodes were linked. Furthermore, these clusters had common imported sources of infection (e.g., case #34) in the network. It was also found that a cluster with more imported cases, e.g., Cluster 1, was more infectious than other clusters (e.g., Cluster 4); the virus in such a cluster might mutate more easily and then transmit to others. Overall, the statistics showed that the imported cases had a higher but still very low chance of infecting the local cases since most of them were isolated immediately upon entry. In the first wave, the virus was not able to easily penetrate the country's border.

In the second wave, even though most confirmed cases were local, their transmission paths were uncertain because age data were not given in exact numbers. According to the density analysis, it was certain that there were 25 known links among 30 nodes (all local cases), and the density value of the entire network was zero to the fifth decimal place. The overall network degree of centrality was computed as zero since having 30 nodes with 25 links indicates having many very small local-local networks within the entire network. However, the overall out-degree centrality was 0.0216 (2.16%), higher than the overall in-degree centrality (0.001 or 0.1%), indicating that several clusters had common sources of infection in the network (e.g., case #1203). The overall normalized out- and in-degree centrality were expected to be much higher than the numbers reported here if the transmission paths for all the nodes could be completely retrieved from publicly available datasets. No further analysis was worth conducting to obtain the statistics of the out-degree and in-degree centrality of each case/node, since the data on how one or more nodes linked to others were incomplete.

In the second wave, Table 1 again showed the same mean value for the normalized in- and out-degree network centrality. The maximum normalized in- and out-degree centrality were 2.162 and 0.114, respectively. The standard deviation and variance values in the in-degree centrality were also higher than the out-degree centrality, indicating a potential change in the network's structure. That is, if a person gets infected, his/her family and friends will be easily infected. Since the data were incomplete for the age attribute, and most confirmed cases were local but had unknown original infection sources, the true numbers would be higher than what the table reports. After closely examining the in- and out-degree centrality of each case or node in the second wave, four groups were found. The largest group was composed of 44 nodes without out-degree centrality, but the total in-degree centrality was 0.022 (2.2%). The other three groups were very small and were composed of two to six nodes with the total out-degree centrality ranging from 0.002 (0.2%) to 0.022 (2.2%) and with the total in-degree centrality ranging from 0 to 0.003 (0.3%). Although the statistics reported here did not reflect reality, it was clear that the actual chance of local-local and import-local outbreaks may be much higher than this percentage (about 2.2%).

The formal cluster analysis was carried out to verify the above findings for the second wave. However, as the links among most of the nodes were unknown, there were only two major clusters: Cluster 1 had 407 nodes (46.3% of the network's nodes), and Cluster 2 had 473 (53.8%). Cluster 1 had more imported cases, and Cluster 2 had more local cases. Each cluster had an equal chance of transmitting the virus to others in their local communities.

4.3 Component Analysis Results

The component measure for the first wave, in which two vertices are members of the same component if there is a path connecting them, showed that there were a total of 600 components, including the Dunmu naval fleet's 36 cases. The component ratio reached 92.31% (600 out of 652), indicating that the overall network in the transmission model of COVID-19 in Taiwan was highly decentralized with multiple fragmented sub-networks. Table 2 displays the detailed component analysis results. Most components contained only one or two nodes. Since there were too many fragments with weak links, high normalized heterogeneity (99.94%) was reported in UCINET, and this again echoed the low value of the overall network density found in the previous analysis results.

A comparison between the local and imported cases via the component analysis for the first wave showed that the former was composed of 33 components (ratio: 59.26%) and had a lower diversity in the linked nodes than the latter, which was composed of 589 components (ratio: 98.49%). The normalized heterogeneity value of the local cases was also lower than that of the imported cases (0.9549 vs. 0.9999), even though it was still considered a high value. In other words, the way or the direction in which the local cases spread the virus to others inside or outside their communities was expected to be highly diverse.

Table 2. Component analysis results – the first wave

Component index	Number of components	Size	Proportion
1	1	9	0.014
2	1	6	0.009
3 - 6	4	5	0.008
7 - 10	4	3	0.005
11 - 25	15	2	0.003
26 - 600	585	1	0.002

In the second wave, the component measure showed that there was a total of 855 components, including the three major infection clusters. Table 3 displays the detailed component analysis results. The component ratio reached 97.16% (with high normalized heterogeneity, i.e., 99.82% as reported in UCINET). Note that the statistics reported here should be taken as reference numbers. The network might be highly centralized with several fragmented sub-networks, and each sub-network had strong and probably short links among its nodes.

Table 3. Component analysis results – the second wave

Component index	Number of components	Size	Proportion
1	1	23	0.026
2	1	3	0.003
3	1	2	0.002
4 - 855	852	1	0.001

5 Discussion

5.1 Different Transmission Models for the Two Waves

This study adopted the SNA to explore two COVID-19 transmission models for two epidemic waves in Taiwan. According to the analysis results, the transmission model in the first wave was formed by mostly imported cases transmitting the virus to the local community, causing a large outbreak of domestic infections. The high percentage of imported cases could be a result of extensive travels taken by Taiwanese citizens for leisure, work, or study abroad. The demographic analysis showed that there were more females than males among the confirmed cases. Most of the confirmed cases were young and middle-aged adults. Therefore, most of the imported cases were also young and middle-aged adults, showing that statistically, the majority of Taiwan's imported cases were relatively young. This is contrary to a previous report indicating that the virus hit older patients the hardest and those vulnerable seniors scramble to adjust and minimize potential damage [4]. The Ministry of Transportation and Communications of Taiwan has reported similar results: 14.8% of the people who travel abroad are aged 20 to 29, 21.9% are aged 30 to 39, 19.7% are aged 40 to 49, and 18.8% are aged 50 and above [25].

In addition, the network density was low, and the normalized out-degree network centrality was larger than the in-degree in the first wave. These numbers indicated that the threat of being infected locally was low, but a single confirmed case, especially the imported ones, may easily infect others to make an import-to-local community outbreak. Detailed network centrality analysis results for each case/node in the first wave also showed a higher chance of local-to-local infection than imported-to-local infection. Additional cluster analysis results showed that the transmission model in the first wave can be partitioned into four clusters that shared some similarities in terms of age, gender, and infection source. Finally, the component analysis showed that the transmission model in the first wave had several small groups, and these groups reflected a high normalized heterogeneity and were decentralized in the entire network.

In the second wave, many local confirmed cases were infected without knowing how and from whom they originally contracted the virus or to whom they might have passed it on. When the Alpha variant was found amid a local-to-local outbreak, a few imported cases carried the more serious Delta variant and posed a huge threat to different local communities in Taiwan [26-27]. The demographic analysis results for the second wave also found that there were more females than males. However, as indicated in a prior study [28], more children and older people were infected than the other age groups. Due to the privacy concerns raised in the second wave, the complete dataset could not be obtained from a public source. The statistics obtained in the second wave should be taken as reference numbers to help make sense of the transmission model for the first wave. For example, if the network density was higher, more local confirmed cases will be reported in a community, and its network density will increase along with a high out-degree centrality. This means that a cluster composed of confirmed cases having a high transmission speed will become a threat to quickly spread the virus and infect others.

Overall, the transmission models in the two waves had obvious different social network structures and their compositions were quite different in terms of the infection source. The infection source can easily change the network structure of a transmission model. In the first wave, no virus variants, at least not the detrimental ones, were found in the imported cases. However, when analyzing the data for the second wave, this study confirmed that passively maintaining the same prevention measures became a critical factor influencing the network structure which had many imported cases and fragmented groups. In addition to the infection source, the gender attribute became more influential than the age attribute to the differences between the transmission models. Fortunately, Taiwanese residents became more active in getting vaccinated in the second wave, and almost everyone followed the TCDC mandatory policies such as wearing masks while outside of their homes and implementing entrance control in traditional markets as part of Epidemic Alert Level 3 measures. Thus, this transmission model with mostly local cases was not affected by the highly infectious Delta virus variant.

5.2 Remaining Concerns and Some Suggestions

The transmission models have been clearly presented by conducting the SNA for the two epidemic waves when different Epidemic Alert Levels were implemented in Taiwan. The differences in the two transmission models have also been found by utilizing the SNA method. However, several concerns remain after carrying out this study. First, there will be more virus variants [26]. It is critical to have more people getting vaccinated. One vaccine dose is expected to be effective against the virus variants, but more and more countries are requiring foreign travelers to receive at least two doses (or a booster shot after the first dose) with specified vaccines before entry [29]. WHO has even released an interim statement to recommend an additional booster for optimizing the vaccine's effectiveness and for public health [30]. Different types of vaccines have been developed under the United States emergency use authorization (EUA), such as BNT, Moderna, and Janssen [31], and more are available to use (e.g., AstraZeneca, Novavax, Sputnik V, Covishield, Covaxin, and Taiwan's Medigen) [32]. Second, Taiwanese residents may expect to get their choice of EUA-approved vaccines two to three times annually, but researchers have not concluded on the benefits of mixing vaccines [30, 33-34]. Third, the new normal has not yet formed in different aspects of society that can fit the lifestyles of Taiwanese residents. For example, students and teachers in K-12 are not used to online learning; higher education teachers are also finding it inconvenient to work from home with their family members around [33-37].

This study suggests advancing the techniques of contact tracing by mobile devices and investing in medical treatment breakthroughs [38-39]. We also suggest that the government should make complete datasets openly available to researchers by using de-identification techniques [40]. An example of how such a database may be used can be found in an SNA study on the relational dynamics (i.e., fragmented, polycentric, and complex) of three types of international actors before and after WHO's announcement regarding the COVID-19 outbreak by using a big dataset (i.e., the Global Database of Events, Language, and Tone) to extract media-reported interactions of the actors out of trillions of data points [41].

Holding online meetings with international institutes also helps broaden our knowledge about how to build a future lifestyle based on the current new normal in the different dimensions of society. In other words, international collaboration is suggested to help the development of vaccines, effectively control new types of virus variants, and trace the transmission paths for confirmed cases around the world at the borders. For example, if more travelers are coming from abroad, a stricter test (e.g., 24 hours before arrival) and border quarantine (note: effective on January 11, 2022) or a longer self-quarantine period (e.g., 21 instead of 14 days) might help prevent local community outbreaks.

Some reflections on utilizing SNA to identify unforeseen threats of infection in Taiwan can be made here. First, based on a study that suggests protecting the frontline workers during the COVID-19 pandemic [42], the network density of the medical communities can be examined closely, so that the transmission model can be presented differently. Instead of only examining the patient nodes and their links to each other, different kinds of hospital service providers including doctors, nurses, and administrators, should be considered in the network. For example, an SNA study carried out with 92 medical workers in Wuhan, China indicated the super factor causing COVID-19 infection was whether they wore their medical protective equipment or surgical masks correctly [43]. That study also found that touching the cheek, nose, and mouth while working had the strongest influence on the infection for the infected group. Second, COVID-19 variants are now confirmed around the globe [44]; thus, the transmission models of the imported cases will be different after carrying out the component analysis because they were infected in different countries before arriving at Taiwan's airports. Different virus mutations from different places will change the component analysis results as well. In other words, the component analysis results will change when comparing different clusters of imported cases by traveling route/stop, by country, or by virus variant. Different countries have different vaccination rates, so different transmission models can be expected after a while. Notably, using different tools (e.g., betweenness, connectivity, external-internal index, reachability, reciprocity, transitivity) offered by UCINET can help with finding different network structures for different algorithms in statistics, but the same results can be reached when examining the same dataset.

More and more Taiwanese residents have realized the crucial need for vaccination. The first batch of vaccines (AstraZeneca, AZ) donated by Japan was delivered to all cities on June 4, 2021, followed by the Moderna vaccines donated by the United States that were delivered on June 6. Additional donations were received from the United States (Pfizer-BioNTech, BNT) on June 20 and then from Japan (AZ) on July 6. Lithuania and Slovakia will also donate vaccines (AZ) to Taiwan. With the prevention measures prescribed under Epidemic Alert Level 3 coupled with the increasing vaccination rate, the daily new cases began to drop by mid-June. The number dropped to 75 (imported: 0) by June 21, and below 50 by July 3. The social distancing policy is still implemented in Taiwan.

Fortunately, the Epidemic Alert Level was lowered from 3 to 2 starting on July 27, 2021. To be noted, starting from July 13, less than 30 new cases were reported per day and deregulation had started. Also, during the same week, all citizens aged 18 or above became eligible for free vaccines (AZ or Moderna) by making a reservation on the TCDC's Covid-19 Publicly Funded Vaccine Platform (https://1922.gov.tw/vas/) even though the citizens had limited options to choose their preferred type of vaccine. At the time of this writing, Epidemic Alert Level 2 was still in effect nationwide. The relaxed pandemic prevention regulations under the same alert level are being enforced starting from March 1 to 31, 2022. For example, travelers flying from abroad are allowed to have a 10-day self-quarantine period starting from March 7. As of March 28, 2022, a total of 49,481,298 doses have been administered in Taiwan, with a coverage rate of 83.40% (first dose) or 78.28 (second dose); however, the third booster dose has only reached 50.50% [9]. As of March 31, 2022, a total of 23,393 confirmed cases and 853 death had been reported, not including the deaths after receiving the vaccines [5]. As the second epidemic wave ended, it was found that the daily reported imported cases were always more than the local ones. The daily infection counts reported on March 31 were 152 imported and 87 local cases, compared with 124 imported and 15 local cases just one week before. There was also a surge on March 27 when 83 local cases (plus 120 imported cases on the same day) [5]. This increase is probably because the efficacy of the first two doses has been declining, and the low vaccination rate of the third dose causes the risk of rapid local transmission to children (children under 18 are not yet eligible to receive COVID-19 vaccines in Taiwan) and elders having weaker immunity. Taiwanese citizens are certainly expected to remain on guard against COVID-19 since no one wishes to face another epidemic wave [45].

6 Conclusion

In this study, the transmission models have been clearly presented by conducting the SNA for the two epidemic waves when different Epidemic Alert Levels were implemented in Taiwan. The differences in the two transmission models have been found by utilizing the SNA method. The SNA outcomes revealed that instead of gender or age, the infection source variable made the largest differences in Taiwan's transmission models between the two waves of COVID outbreaks. Most of the imported cases were young and middle-aged adults aged 21-40 in the first wave, whereas most were local cases including children and older people (aged 5-90) in the second wave. However, in the second wave, the gender attribute was more effective to identify the difference in its transmission model than the age attribute when compared with the transmission model of the first wave. Importantly, the transmission model in both the local-to-local and imported-to-local cases should be considered volatile as shown by the wide range of the normalized out-degree centrality.

Overall, it is evident that early and strong containment measures, contact tracing, rapid control of all passengers arriving at the border, and effective treatment methods have been the most significant factors in dealing with the pandemic in Taiwan. These measures have kept the transmissions mostly within one-generation spread within the patients' communities and have prevented large-scale transmissions to external communities. In addition, TCDC's daily press conference at 2 pm not only has raised the public's awareness but has also taught the citizens how to protect themselves against COVID-19. To combat virus variants, a high vaccination rate is critical to prevent potential, larger outbreaks in any nation.

The limitations of this study include the constraints of obtaining some patients' exact age data in the second wave, and the constraints of obtaining other demographic statistics, such as employment status and religion to find other influential factors in the COVID-19 transmission models. As virus variants are different in transmission speed and transmissibility, the transmission model might change rapidly during data collection in different study contexts. Thus, international research collaboration is suggested to obtain an updated and complete dataset in different countries to explore different transmission models in future research. Large-scale global research can be carried out using the same SNA software to achieve different network analysis purposes, such as exploring infection sources by country, by virus variant, and by traveling route. A comparative study of transmission models before vaccine implementation and one year after might be enlightening. Finally, new SNA techniques or alternative applications of artificial intelligence techniques are suggested for future research in computer science.

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