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Modeling of Internal and External Factors affecting a Complex Dengue Network

Abstract

There are different factors that are the cause of abrupt spread of arbovirus. We modelled the factors (internal & external) that can increase the diffusion of dengue virus and observed their effects. These factors have influenced on the *Aedes aegypti* (a dengue virus carrier); factors which increase the dengue transmission. Interestingly, there are some factors that can suppress the *Aedes aegypti*. The species of *Aedes aegypti* formalizes its own network by which dengue virus is spread. Internal & external exposures of the dengue epidemic complex network have been modelled and analyzed. Influence of internal and external diffusion with two scenarios has been discussed. ‘Genetically modified mosquito’ technique has been applied and its associated simulated results are discussed. From the outcomes, the best time duration to contain the spread of dengue virus has been proposed, and our simulation model showed the possibility of suppressing the *Aedes aegypti* network.

Key words: *Complex network; Epidemic network; Arbovirus; Dengue virus; Virus diffusion model; Modeling of I/External Factors;*

1. Introduction

Because of the danger posed by the *Aedes aegypti*, there have been many attempts to control its populations. Unfortunately, in spite of the best endeavors of governments and groups, these endeavors have, up to this point, not been exceptionally fruitful and there are presently no authorized antibodies or particular therapeutics to control this mosquito and its virus [1] [2] [3] [4]. It is important to mention here that *Aedes aegypti* is also the primary vector/carrier of chikungunya, yellow fever and Zika virus (ZIKV). ZIKV has become a serious threat in the

tropical zones in the world. Furthermore, CoViD-19 is very critical for its transmission channels. So, this study is also beneficial for CoViD-19, ZIKV and other diseases that has the spreading transmissions like person-to-person. The topology of biological networks is an important factor to be considered. [5]

Female *Aedes aegypti* is the dengue vector, meaning that only the female mosquito of this species is able to spread the virus [6] [7]. A female *Aedes aegypti* mates with a male mosquito in order to grow its generation through laying eggs (a natural way). It is considered one of the internal factors to increase the dengue network. However, its virus might be transferred by the infected persons (Fig.1), if any other mosquito (not the species of *Aedes aegypti*) bites the infected human and may become a source of dengue virus [8] [9]. It is also another source of external factor to increase the dengue complex network. Therefore, there is a need to break down this chain network by inserting some exogenous factors.

Fig.1. Transmission of Dengue virus

In this study, a dataset of the Dengue Virus (DENV) affected cases from the Ministry of Health (MOH) Malaysia has been used [10] [11]. The dataset of Selangor (a state of Malaysia) has been obtained, in which a weekly number of dengue cases are recorded in all affected localities from the periods of 20 October 2013 to 18 October 2014. Here, weekly number of dengue cases

are edges and affected localities are nodes, that constitute the dengue epidemic network of interest. Furthermore, there are 560 affected nodes with 36,878 dengue cases [10]. Dataset (*Appendix B*) has been modelled into two-mode network and then projected in one-mode network, and after applying different metrics, results have been used in this study [12] [13] [14] [15]. Moreover, in this paper we modelled the internal and external factors and observed their influence on the transmission of dengue virus. It is considered that *Aedes aegypti* has geographically organized itself in Selangor Malaysia to form a network. Here, the ‘network’ is the linkages of *Aedes aegypti* with other factors to transmit its infections. There are a variety of approaches ranging from sterile insect technique (SIT) to Wolbachia which prevents transmission. This ‘genetically modified mosquito’ technique, has been applied in this research. It produced (in simulated results) more efficient outcomes in the scale-free network through targeted attacks in the focal hubs of *Aedes aegypti*. It has been proven that dengue epidemic follows a scale-free network [16] [17]. The outcomes from this study are important for researchers, health officials and decision makers who deal with the arbovirus epidemics, like *Zika* virus, chikungunya, and yellow fever. There are various examples for complex network [18] that gave motivation to model the dengue complex network phenomenon. For CoViD-19 (Corona Virus Disease), transmission is increasing due to person-to-person close contact, so internal and external factors need to be controlled.

2. Research Methodology

We divide the methodology into two aspects; the possible causes of DENV spread and any possible treatments. This is considered as: *Scenario 1* and *Scenario 2*.

Scenario 1: What factors can be a cause of the diffusion of dengue virus? For example; untidy spots, water-holding containers, used tires containing rain water, pots of plants and flower beds. All of these are standard reasons. Within the dengue epidemic network two cases are discussed

in this paper: influence of internal exposure and influence of external exposure. In first case, influence of internal exposure means the source of dengue virus diffusion is present in the same cluster of complex networks. In Fig.2, let's consider Gombak (a district of Selangor, Malaysia) is a cluster (C_i) of i nodes. Where C_i contains some infected nodes (such as: $Li2$, $Li3$, $Li4$, $Li7$) and uninfected nodes (such as: $Li1$, $Li5$, $Li6$, $Li9$). Suppose, an *Aedes aegypti* bites a person in the node $Li3$, and now that person may be a cause of DENV spread to the next-door neighbours within $Li3$ or in the other node such as $Li5$ (see Fig.2). Similarly, $Li7$ is an infected node in the C_i that may infect the $Li6$ which remains to be uninfected. It is referred as internal factor diffusion and called case 1. As well as this, if any *Aedes aegypti* spreads its infections to more than one person within the same cluster, it is also referred to as case 1.

Fig.2. Influence of Internal diffusion (Scenario 1: Case 1), based on the given dataset.

In second case, influence of external exposure in our model of the dengue epidemic network, source of infection transfers from any other cluster (say C_j) onto C_i . For example, travelers originating from the countries that have dengue ailment may be an external factor to the uninfected areas as they are carriers of the disease. Besides the international travelers there may have an impact on locals who travel from one place to another. Especially, dengue infected people travel into the place where the dengue virus is absent. These people might therefore be a cause of the spread of dengue virus. Similarly, any simple mosquito that gets the dengue virus

from a dengue infected person and passes it on to an uninfected person (Fig. 1) also acts as an external source (Fig.3). As described earlier, a dataset of Selangor has been utilized in this study and it is important to note that Kula Lumpur airport is used for international travelers here, and from the result analysis it has been noticed, besides the other places in Gombak, there are many dengue cases especially in the area of Batu Caves (a tourist spot) [13]. In Fig. 3, consider Gombak as cluster C_i that contained various infected and uninfected nodes. On the other side, cluster C_j is the global cluster having some infected (such as: L_{j1} , L_{j2}) and uninfected nodes (such as: L_{i3} , L_{j6}). If any node in C_i gets infected through a node from cluster C_j (other than C_i), it is named as the influence of external factor and called case 2. For this, C_j infects C_i externally; for instance, C_j is Ampang and C_i is Gombak, where Ampang is a neighbouring place of Gombak.

Fig.3. Influence of External diffusion (Scenario 1: Case 2), based on the given dataset.

Scenario 2: What external factors can be inserted in the current dengue epidemic network to control the diffusion of *Aedes aegypti*? Sprays, cleanliness, vaccination and immunization all are the traditional methods and are being used regularly [19] [14] By measuring the prominent features of the scale-free network such as: Power-law, clustering coefficient, short path length, and by applying some centrality measures like, Degree, Betweenness, Closeness, Eigenvector, it is concluded that dataset of the dengue epidemic network has the topology as a scale-free

network [12] [17]. That means there are few areas which work as focal hubs and by using different methods, these hubs are highlighted in the investigation and robustness has been observed [20]. Genetically Modified (GM) mosquito is an advanced technique which is centered on innovative genetic science [21] [22]. In this technique the DNA of the mosquito is changed to stop their generation growth. Here, only male mosquitoes (*Aedes aegypti*) are prepared by changing their DNA which mate with females later. Different countries have tried this new technique [23] [24]. Genetically Modified mosquito technique is preferred to be utilized in focal hubs as external factor to control the wild population of *Aedes aegypti* [25]. (Fig.4). The female *Aedes aegypti* mosquitoes that will have mated with GM male mosquito, lay eggs which later hatch into larvae; the offspring carries the piece of DNA which kills them before they become adults. The life span of the GM mosquito is up to 6 days, after this it dies [24]. The insertion of GM mosquito as an exogenous factor in the dengue epidemic network can produce efficient results especially when the topology of the network is scale-free nature. Furthermore, this way would be cost effective too. In Fig. 4, it has been shown that GM mosquito should be released in most infected nodes. It is referred to scenario 2 as ‘influence of external suppression’.

Fig.4. Influence of external Suppression (*Scenario 2*)

2.1 Modelling the infection influence

To model the emergence of dengue epidemic network in Selangor, there is a need to ponder on the movement of the undetectable exogenous source of this network that transforms the dengue virus to the nodes of the dengue network (via infected person or mosquito). The probabilistic generative model of virus occurrence is utilized in the dengue epidemic network, in which a dengue virus can approach a node through the links (infected person or mosquito) of this network or via the influence of the external source. Exposure and infections have different meanings in the model used in this study [26]. When any node gets exposed to dengue virus (DENV) that means an exposure event has occurred, and an infection event occurs when any patient appears in a node with DENV. Exposure to the virus leads to an infection. Through two ways, a node can get exposed to virus. Firstly, $Li1$ a node might be exposed to or becomes aware of DENV if any of its neighbours in the dengue epidemic network of cluster i (Ci), pass on a DENV. Hence, any uninfected node of Ci which is exposed by any other infected node within the Ci , it is referred as an “internal exposure” (Fig.2), where Ci contains the localities $Li1, Li2 \dots Li_N$. Secondly, $Li1$ might be exposed to DENV through any other cluster j (Cj) which may be the neighbour of Ci . This activity of the external source is named as “external exposure”. Hence, here any node of cluster Ci is exposed to the node of locality of any other cluster Cj , where Cj contains the localities $Lj1, Lj2 \dots Lj_N$. It is alluded to the quantity of exogenous exposures after a period as the ‘event profile’. So, to build up the association between exposures and infections, the concept of the exposure curve is characterized that maps time that node Li_N has been exposed to DENV, into the possibility of Li_N receiving infections.

By applying the virus diffusion model, we are able to consolidate the extent of virus from node to node along edges in the dengue epidemic network [17]. Event profile is proportional to the probability of any node (Li_N) getting an exogenous exposure at a specific period [17] ‘contagion’ is used to mention a specific carrier evolving in the dengue epidemic network and when a DENV appears in an uninfected node it is referred as an infection of node by a

contagion. These contagions are utilized jointly meaning these are considered together. The current model is delineated in a node-centric framework and it is assumed that after a time period, contagion becomes the reason to spread the intensity of exogenous exposure which a node gets and directed by the event profile $\lambda_{ext}(t)$. Moreover, by that contagion, the neighbours in the dengue epidemic network can also get infected which further become the cause of internal exposure. Every exposure has the probability to spread the infections to the uninfected node and the infection probability varies with the exposure curve $\eta(x)$. Ultimately, it might generate any of the two possibilities that either exposure stops, or node gets infection and exposed to its next neighbour. It is also required to gather the amount of exposure which is produced by the exogenous means by time (t) also, in order to form the exposure curve $\eta(x)$ which sees the probability of infection of node. Furthermore, we have given the modelling of internal and external exposures in *Appendix A*.

2.2 Data Analysis

For the modelling of internal and external exposure, we have utilized the data set given in *Appendix B*. That dataset has been divided into six clusters namely, Gombak, Klang, Hulu Langat, Petaling, Sepang and Hulu Selangor. The diffusion concept has already been explained in Fig.2 and Fig.3. Particularly, it can be observed that Hulu Selangor is in the neighbourhood of Gombak and Petaling. Therefore, cases appeared in Hulu Selangor (HS) are considered as internal exposure whereas with regard to HS, cases in Gombak are considered as external exposure and vice versa.

3. Results and discussion

Fig.5 presents the simulated results of above discussed scenario 1 (case 1 and case 2) which is related to the sections ‘modelling the internal exposure’ and ‘modelling the external exposure’. In this figure the dotted line shows the infections due to internal factors and the continuous line

represents infections due to external factors, where x-axis shows the time in days. Here, the dengue infections are observed for 30 days, considering a month. On the y-axis the probability of infection is shown, which depends on the number of dengue cases that might appear in the C_i . Firstly, it is considered as case 1 (dotted line), the graph showed the maximum infections during 8 to 13 days. Possible DENV symptoms appear in 4 to 14 days. Here, it has been observed that the probability of infection approaching to maximize the value on the 11th and 12th day that is 0.8, meaning this time period is most crucial for the spread of DENV. This simulation has few conditions: 1- Time span is fixed up to 30 days. 2- It is supposed that there would be no external factors influence in case 1 network (like Fig.2). 3- It is assumed that *Aedes aegypti* bites only from day 1 to 5 (to see its maximum effects).

Fig.5. Comparison between case 1 and case 2 (*Scenario 1*)

Secondly, in case 2 (continuous line), the graph (Fig.5) clearly showed the increasing trend of the dengue epidemic network in the C_i as some external factors from the global cluster C_j influenced the network (see Fig.3). Here, the infection rate is high, and duration has been expanded due to the impact of external elements. In this case Infection range is high which is from day 4 to 14 and the peak of infection has been found during 5th to 12th day. Further, the probability of infection has reached between 0.9 to 1.0. This demonstrates how external factors have influenced the dengue epidemic network in Gombak Selangor.

Simplifying both cases (1 and 2) it can be observed that the peak of $P(\text{infection}) = 0.8$ in the first case whereas in the second case, due to the addition of some external factors peak of $P(\text{infection})$ has raised and ranged between 0.9 to 1. More specifically, $P(\text{infection})$ in the case of internal exposure is at the peak only, on two days: the 11th and 12th day. While in the external exposure case it is at its peak from 5th to 12th day and this indicates that infection time span has increased. In case 2, peak in the graph has been increased and shifted on the left side as well, that means external factors have expended the infection duration and maximized the probability of infections as well.

Fig. 6 is the simulated representation of the scenario 2 (shown in Fig. 4), where it was described how DENV might be suppressed by any external factors and how the chain network (Fig. 1) of dengue virus infection can be broken down. In the graph (Fig. 6), x-axis shows the time in number of days up to 34, as the average life span of *Aedes aegypti* is 34 days. While y-axis shows the probability of destruction of the dengue epidemic network. Here, the simulated results are shown by considering 1000 *Aedes aegypti* mosquitoes in the epidemic network. Five hundred Genetically Modified (GM) mosquitoes are inserted/ released on the network of *Aedes aegypti* (it has been discussed that only female *Aedes aegypti* can spread the DENV and GM mosquito are only male mosquitoes with changed DNA. The life span of GM mosquito is up to 6 days). The result showed that as 500 GM mosquitoes were released in the *Aedes aegypti* network, they mated with *Aedes aegypti* females (say 600 females) that means these 600 females were now unable to produce a new generation. These 600 females *Aedes aegypti* laid eggs, and larvae died before they grow up, because of the changed DNA characteristic of GM mosquitoes. The graph showed almost 60% network is destroyed in 5 to 6 days. Moreover, female *Aedes aegypti* mates with any male mosquito only once in her life [27]. Furthermore, after 6 days GM mosquito dies [27]. As a result of this, 60% of female mosquitoes cannot reproduce its new generation and 40% remaining female *Aedes aegypti* could live their average

life up to 34 days before being finally wiped out from the network. Ultimately, infections remain very low and finally may be removed from the network and threshold value is achieved. There are some simulation conditions in this network: the numbers of days are fixed up to 34, number of *Aedes aegypti* females are 1000 in the fix time interval and the released 500 GM mosquitoes work properly.

Fig.6. Destruction of network due to external factor (*Scenario 2*)

4. Conclusion

Despite of many regular methods such as aerosol, cleanliness and immunization *Aedes aegypti* is still uncontrolled, and is increasing exponentially, particularly in tropical zone in the world. Here, the complex network of dengue epidemic phenomenon has been analyzed through two aspects. Firstly, different factors that could be the reason of dengue virus diffusion are discussed. The spread can be due to internal factors or/and external factors (Fig.2 and Fig.3). Secondly, various elements are described which can control or suppress the wild population of *Aedes aegypti* (Fig.4). Here, the internal and external exposure of dengue epidemic network is modelled (*Appendix A*) and simulated results are presented for both factors. An increase in the dengue infections has been seen, as some external factors act in the *Aedes aegypti* network. External factors influence not only increased the probability of infection but have also

expanded the infection intervals. Further, the results of the insertion of GM (genetically modified) mosquito into the *Aedes aegypti* network showed the destruction of the network (Fig.6). Hence, it is recommended that this technique will work more efficiently in the scale-free network through targeted attacks in the focal hubs of *Aedes aegypti*. Additionally, by considering the spatio-temporal technique, from the results of internal and external exposure modelling the best time period has been observed that could be utilized to suppress the dengue epidemic network. If a specific ratio of GM mosquitoes could be release at the particular time in specific nodes then that could produce better outcomes as compared to random procedure. *Aedes aegypti* is also the cause of Zika virus (ZIKV) which has become a serious threat for the whole world. Furthermore, this can be applied on ZIKV and other arboviruses to control these. Moreover, we have aim to apply this methodology on the CoViD-19 to see its network propagation and to observe the internal and external factors for its growing transmission.

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Appendix A and **Appendix B** are given below:

Appendix A: Modelling of internal exposures and external exposures

Modelling the internal exposures

There is some important information regarding DENV that has been used in the model of the dengue epidemic network. Scientists found four serotypes of dengue virus namely, DENV-1, DENV-2, DENV-3 and DENV-4 [1] [16]. All these dengue serotypes can be detected from the

infected person's blood samples. Any person who is infected by any one of these serotypes will never be infected again by the same [8]. The average life of the *Aedes aegypti* is 34 days and when *Aedes aegypti* bites any person the symptoms appear in 4 to 14 days [8] [12].

In this model, internal exposure is considered only when virus is exposed within the same cluster (say C_i) and then DENV infections appear. Exposure transmission has no fixed time limit, as nodes are exposed after random time interval t . Let's observe an example from the real dengue epidemic network. Gombak is a cluster C_i of the said network that contained the various infected and uninfected nodes, where different contagions act to spread the DENV (Fig.2). These contagions can diffuse the virus only in the closed system (local network). They can only affect their neighbours so then, and only then, there is internal diffusion propagated along the edge. Moreover, an infected entity that exposes the DENV to its neighbours can spread infections only once, as stated above DENV infected person cannot be infected again by the same serotype.

Let λ_{int} be the internal hazard function, for any neighbouring nodes i and j .

$$\lambda_{int}(t)dt \equiv P(i \text{ exposes } j \in [t, t + dt) | i \text{ has not exposed } j \text{ yet})$$

where t is the quantity of time that has gone since node i was infected. In our setting, λ_{int} efficiently models to what extent it takes a node to notice one of its neighbours getting infections [17] [21]. It is a component of the recurrence with which nodes observe each other. To Gombak dengue epidemic network, if any person is infected with dengue virus, the neighbour of that person is exposed by this virus. Means Li_N which is a neighbour of locality 2 (Li_2) within the cluster C_i might be exposed. The probable amount of internal exposures, which any node i has received during time t , is defined as $\Lambda_{int}^{(i)}(t)$, the total number of the cumulative distribution function of exposures propagating alongside with every node's inbound edges and can be resultant as equation (1).

$$\begin{aligned}\Lambda_{int}^{(i)}(t) &= \sum_{j; j \text{ is } i\text{'s infected neighbour}} P(j \text{ exposed } i \text{ before } t) \\ &= \sum_{j; j \text{ is } i\text{'s infected neighbour}} \left[1 - \exp\left(-\int_{\tau_j}^t \lambda_{int}(s - \tau_j) ds\right) \right]\end{aligned}\quad (1)$$

where τ_j is the time when node j gets infections.

Modelling the external exposures

There may be many external factors that affect the whole dengue epidemic network. Here, some possible contagions are discussed that might be a cause of exposure in C_i . It has been a core issue that exogenous elements cannot be measured. External source does not have the same intensity. It changes from time to time; this function is referred to the ‘event profile’ which is defined as $\lambda_{ext}(t)$. Specifically, for any node i ,

$$\lambda_{ext}(t)dt \equiv P(i \text{ receives exposure } \in [t, t + dt))$$

where t represents the quantity of time when the contagion appears for the first time in the dengue epidemic network [17]. A few points are to be noted. There is an equal probability for all nodes that they can get any external exposure at any time t . Secondly, there is a chance that any of the infected nodes may get the external exposure again. Simplifying this, any node may be infected more than once. As in the real dengue infection scenario, any infected person who gets DENV-1 serotype may be infected by DENV-2, DENV-3 or DENV-4. It is said λ_{ext} the event profile as it defines the real world event which caused the virus to reach the localities network and start diffusion. As the event grows over time t , its efficiency in the network varies.

Suppose that λ_{ext} is fixed for all time and that time is discretized into limited interims of length Δt . At that point probability that n exogenous exposures have been occurred after T time interims is precisely a binomial distribution [17], such as equation (2).

$$P_{exp}(n; T \cdot \Delta t) = \binom{T}{n} (\lambda_{ext} \cdot \Delta t)^n \cdot (1 - \lambda_{ext} \cdot \Delta t)^{T-n} \quad (2)$$

Set $t = T \cdot \Delta t$. if the limit is considered as $\Delta t \rightarrow 0$ and $T \rightarrow \infty$ such that t does not change. Then this probability approaches such as equation (3).

$$P_{exp}(n;t) = \binom{t/dt}{n} (\lambda_{ext} \cdot dt)^n \cdot (1 - \lambda_{ext} \cdot dt)^{t/dt-n} \quad (3)$$

To relax the constraint that λ_{ext} is constant, average of $\lambda_{ext}(t)$ over t is used as equation (4).

$$P_{exp}^{(i)}(n;t) \approx \binom{t/dt}{n} \left(\frac{\Lambda_{ext}(t)}{t} \cdot dt \right)^n \cdot \left(1 - \frac{\Lambda_{ext}(t)}{t} \cdot dt \right)^{t/dt-n} \quad (4)$$

where $\Lambda_{ext}(t) \equiv \int_0^t \lambda_{ext}(s) ds$. Eventually, nodes in the dengue epidemic network get both external and internal exposures at the same time, so both practices need to be taken into account. This would indicate receiving the convolution of the two probabilities that would not be feasible computationally. Instead, the mean value of $\lambda_{ext}(t) + \lambda_{ext}^{(i)}(t)$ is used as equation (5).

$$P_{exp}^{(i)}(n;t) \approx \binom{t/dt}{n} \left(\frac{\Lambda_{int}^{(i)} + \Lambda_{ext}(t)}{t} \cdot dt \right)^n \cdot \left(1 - \frac{\Lambda_{int}^{(i)} + \Lambda_{ext}(t)}{t} \cdot dt \right)^{t/dt-n} \quad (5)$$

Productively, the unsteadiness of exposures is assessed as consistent in time such that every interim of time has an equivalent likelihood of an exposure arriving, so the entirety of the event is a standard binomial arbitrary variable.

Appendix B: Dataset (20 October 2013 to 18 October 2014) of dengue patients in Selangor, Malaysia. Dataset protects patients' privacy.

GL: Gombak Location

KL: Klang Location

HLL: Hulu Langat Location

PL: Petaling Location

SP: Sepang Location

HSL: Hulu Selangor Location

Ref. code	Cases	Ref. code	Cases	Ref. code	Cases	Ref. code	Cases	Ref. code	Cases
GL18	128	GL27	8	HLL13	76	HLL36	28	HLL168	14
GL5	111	GL57	7	HLL63	74	HLL88	28	HLL52	13
GL1	105	GL28	7	HLL89	73	HLL18	27	HLL103	13

GL15	85	GL23	7	HLL129	71	HLL73	27	HLL148	13
GL39	80	GL21	7	HLL82	70	HLL141	27	HLL16	12
GL49	79	GL11	7	HLL139	70	HLL43	26	HLL28	12
GL34	55	GL19	6	HLL174	66	HLL142	25	HLL116	12
GL56	53	GL16	6	HLL34	60	HLL91	24	HLL132	12
GL40	43	GL52	5	HLL12	59	HLL97	24	HLL149	12
GL43	41	GL37	5	HLL75	54	HLL101	23	HLL167	12
GL24	41	GL10	5	HLL77	54	HLL45	22	HLL35	11
GL50	40	GL9	4	HLL152	53	HLL134	22	HLL110	11
GL13	38	GL53	4	HLL164	52	HLL138	21	HLL156	11
GL17	35	GL29	4	HLL166	52	HLL108	20	HLL172	11
GL12	32	GL2	4	HLL24	51	HLL115	20	HLL56	10
Ref. code	Cases	Ref. code	Cases	Ref. code	Cases	Ref. code	Cases	Ref. code	Cases
GL25	31	HLL130	729	HLL165	51	HLL21	19	HLL61	10
GL14	29	HLL64	435	HLL182	51	HLL31	19	HLL69	10
GL38	27	HLL84	317	HLL185	50	HLL68	19	HLL79	10
GL47	26	HLL117	251	HLL143	48	HLL74	19	HLL157	10
GL8	23	HLL161	250	HLL146	46	HLL114	19	HLL40	9
GL51	23	HLL46	237	HLL9	45	HLL136	19	HLL54	9
GL36	23	HLL60	231	HLL170	45	HLL17	18	HLL83	9
GL42	21	HLL87	228	HLL11	44	HLL29	18	HLL171	9
GL54	16	HLL44	217	HLL2	43	HLL41	18	HLL178	9
GL26	15	HLL184	194	HLL86	43	HLL55	18	HLL8	8
GL6	14	HLL15	183	HLL90	42	HLL153	18	HLL20	8
GL4	14	HLL85	179	HLL50	41	HLL98	17	HLL48	8
GL22	14	HLL158	159	HLL123	41	HLL1	16	HLL53	8
GL48	13	HLL65	149	HLL137	40	HLL113	16	HLL80	8

GL41	13	HLL120	141	HLL39	39	HLL121	16	HLL94	8
GL45	12	HLL72	122	HLL70	39	HLL133	16	HLL106	8
GL44	12	HLL151	116	HLL67	38	HLL147	16	HLL118	8
GL30	12	HLL183	113	HLL26	36	HLL154	16	HLL131	8
GL3	12	HLL127	110	HLL38	36	HLL181	16	HLL4	7
GL7	11	HLL59	103	HLL135	35	HLL105	15	HLL47	7
GL58	11	HLL145	96	HLL180	34	HLL144	15	HLL58	7
GL20	11	HLL150	96	HLL19	31	HLL7	14	HLL92	7
GL35	10	HLL14	95	HLL42	31	HLL30	14	HLL93	7
GL32	9	HLL175	95	HLL96	31	HLL51	14	HLL99	7
GL31	9	HLL76	90	HLL112	31	HLL57	14	HLL162	7
GL55	8	HLL25	83	HLL104	30	HLL78	14	HLL169	7
GL46	8	HLL10	81	HLL37	29	HLL126	14	HLL179	7
GL33	8	HLL49	79	HLL163	29	HLL159	14	HLL3	6
HLL5	6	PL158	237	PL208	65	PL10	27	PL49	13
HLL22	6	PL59	227	PL224	65	PL226	27	PL93	13
HLL23	6	PL26	223	PL68	63	PL40	26	PL129	13
HLL27	6	PL171	206	PL111	63	PL166	26	PL144	13
HLL66	6	PL174	192	PL95	61	PL75	24	PL113	12
HLL102	6	PL131	181	PL206	59	PL105	24	PL157	12
HLL107	6	PL79	170	PL3	55	PL27	23	PL183	12
HLL111	6	PL175	166	PL169	55	PL48	23	PL191	12
HLL119	6	PL179	153	PL53	49	PL112	23	PL214	12
HLL173	6	PL69	150	PL57	47	PL156	23	PL227	12
HLL33	5	PL18	145	PL145	46	PL73	22	PL12	11
HLL81	5	PL65	136	PL228	45	PL223	22	PL58	11
HLL100	5	PL87	136	PL118	44	PL6	21	PL155	11

HLL124	5	PL178	135	PL89	43	PL25	21	PL187	11
HLL125	5	PL44	130	PL130	43	PL72	21	PL15	10
Ref. code	Cases	Ref. code	Cases	Ref. code	Cases	Ref. code	Cases	Ref. code	Cases
HLL128	5	PL82	90	PL115	20	PL20	8	PL241	5
HLL160	5	PL172	89	PL201	20	PL78	8	PL39	4
HLL176	5	PL193	85	PL203	20	PL81	8		
HLL6	4	PL124	83	PL94	19	PL84	8		
HLL32	4	PL1	82	PL121	19	PL108	8		
HLL62	4	PL80	82	PL125	19	PL149	8		
HLL71	4	PL139	80	PL135	19	PL163	8		
HLL95	4	PL182	79	PL148	19	PL219	8		
HLL109	4	PL66	73	PL216	19	PL220	8		
HLL122	4	PL98	72	PL217	19	PL230	8		
HLL140	4	PL46	70	PL212	18	PL9	7		
HLL155	4	PL238	70	PL64	17	PL119	7		
HLL177	4	PL51	65	PL211	17	PL143	7		
PL126	3107	PL186	43	PL2	16	PL159	7		
PL31	2826	PL52	42	PL104	16	PL160	7		
PL134	1174	PL184	42	PL215	16	PL177	7		
PL127	1022	PL204	42	PL234	16	PL188	7		
PL137	720	PL63	41	PL237	16	PL198	7		
PL54	548	PL106	41	PL43	15	PL213	7		
PL128	488	PL222	40	PL47	15	PL218	7		
PL200	434	PL50	39	PL55	15	PL239	7		
PL114	393	PL185	39	PL221	15	PL242	7		
PL138	345	PL102	37	PL232	15	PL29	6		
PL33	327	PL152	37	PL233	15	PL30	6		

PL17	298	PL100	35	PL122	14	PL35	6		
PL173	287	PL99	34	PL146	14	PL56	6		
PL132	282	PL14	33	PL77	10	PL62	6		
PL133	275	PL32	33	PL110	10	PL71	6		
PL147	114	PL91	33	PL153	10	PL86	6		
PL141	113	PL97	33	PL194	10	PL90	6		
PL189	113	PL5	32	PL235	10	PL116	6		
PL196	110	PL67	32	PL21	9	PL117	6		
PL22	109	PL120	32	PL38	9	PL142	6		
PL23	109	PL229	32	PL70	9	PL168	6		
PL136	109	PL167	31	PL83	9	PL205	6		
PL92	107	PL37	30	PL103	9	PL231	6		
PL4	104	PL74	30	PL151	9	PL24	5		
PL164	103	PL192	30	PL154	9	PL42	5		
PL225	102	PL34	29	PL162	9	PL150	5		
PL123	100	PL7	28	PL197	9	PL161	5		
PL236	100	PL61	28	PL202	9	PL190	5		
PL41	98	PL85	21	PL209	9	PL195	5		
PL19	95	PL207	21	PL8	8	PL210	5		