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DEVELOPMENT AND RECURRENCE OF VECTOR-BORNE ILLNESSES

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ABSTRACT

India's vast population, diverse environment, and fragmented healthcare system make it particularly susceptible to newly emerging infectious diseases (EIDs), which pose serious threats to global public health. In India, the Aedes mosquito is the vector for a wide range of diseases, but two of the most serious ones, dengue fever and chikungunya, is very prevalent and frequently creates outbreaks. Antibiotic-resistant germs are becoming more common, which puts extra strain on the healthcare system by making treatment more challenging or even deadly. Understanding the virulence factors and host-pathogen interactions of these EIDs is crucial for developing effective management and preventive measures. This article provides an overview of the virulence mechanisms employed by the antibiotic-resistant bacteria that are common in India, the Dengue virus (DENV), and the Chikungunya virus (CHIKV). The chikungunya virus employs a variety of virulence traits to evade the host immune system and spread infection to people. Aedes aegypti and Aedes albopictus mosquitoes are the ones that transmit the virus.

Keyboard: *Host-pathogen Chikungunya, Dengue, antibiotic-resistant ,bacteria*

Introduction

New human illnesses have been reported in this decade, in addition to the recurrence of already known infections, which is a significant cause for concern. At the most fundamental level, emerging infections are diseases whose prevalence has been proved to have increased over the course of the past several decades or that show indicators of additional prospective expansion. In most cases, such emergences are the consequence of the discovery or expansion of a pathogen to regions that had not been studied before, the identification of diseases that have been present in a population for a long time but have not been detected, or the finding of an infectious etiology in disorders that have been present for a long time. There are a number of reasons that contribute to the increase of these diseases. Changes in farming methods, such as mixed farming, as well as unplanned urbanization and deforestation are among these factors. Other factors include a growing human population, poverty, and malnutrition; improved communication both domestically and internationally; societal norms and practices; the prevalence of diseases that depress the immune system; and variations in farming methods. Changes in the genetic makeup of the pathogens have also been a significant contributor to the occurrence of such outbreaks.

On occasion, hosts unwittingly help or hurt their own viruses' chances of survival. The host factors are these facilities. These components play an important role in various processes that involve pathogens, including replication, transcription, integration, growth, propagation, entrance, and interactions between hosts and pathogens. Replication of the influenza virus requires a collection of 295 host cellular cofactors. Out of all the cofactors, 181 play a crucial role in host-pathogen interactions, 219 allow the influenza virus to proliferate efficiently, 23 are involved in entry, and 10 are necessary for reproduction after entry. Influenza virus replication can be inhibited by small molecule inhibitors of several factors, such as vATPase and CAMK2B. The replication of DENV-2 (dengue virus type 2) requires a collection of 116 Dengue Virus Host Factors (DVHF). Human DVHF accounts for 42 of the 82 known homologs of dipteran DVHF. Researchers have identified 311 host variables that contribute to HIV-1 development. The cardinality of the set of intersections is 311 host factors, taking into account HIV dependency factors established previously in. There are six host factors that have recently been identified: AKT1, PRKAA1, CD97, NEIL3, BMP2k, and SERPINB6. In HIV, a set of 250 such variables has been discovered. Virus entry is facilitated by Rab6 and Vps53, viral integration is facilitated by TNPO3, and viral transcription is facilitated by Med28. Viruses are able to adapt and evolve within host cells that carry out essential life cycle processes because HDF genes are more abundant in immune cells. Research has identified a group of 213 host factors and 11 proteins encoded by HIV as being responsible for the replication of HIV-1. Proteins that aid in DNA damage response control, proteolysis, RNA splicing, and ubiquitin conjugation are among those proteins. When it comes to the beginning and/or speed of DNA synthesis, forty additional factors are crucial. It has been discovered that fifteen distinct proteins significantly contribute to nuclear import and viral DNA integration.

Impact of Mass Gatherings and Emerging Viral Infections

According to the World Health Organization (WHO), mass meetings can be planned or spontaneous, but regardless of the nature of the gathering, it always attracts a large number of people, which places a strain on the capacity of the community or nation to respond and organize. A wide range of locations, such as religious houses, sports arenas, cultural centers, and even political rallies, are all potential locations for these types of gatherings. Kumbh Mela is a religious gathering that takes place once every twelve years in the state of Uttar Pradesh in India. It is commonly considered to be one of the largest human mass gatherings that takes place anywhere in the world. Further instances of religious mass gatherings in India include the following: the Maha Pushkaram festival in Andhra Pradesh, which drew 48.1 million people in Andhra Pradesh and 57 million in Telangana in 2015; the annual pilgrimage to the Sabarimala temple in Kerala's Pathanamthitta district, which draws 45-50 million devotees annually; Velankanni, the largest Catholic pilgrimage center in India, which attracts about 3 million visitors between late August and early September; and the Mahamaham in Kumbakonam, Tamil Nadu, which had its last gathering on February 22, 2016, with one million attendees.

In India, similar rites for other religions are conducted with a great deal of passion, despite the fact that there are not as many pilgrims as in other countries. People are more likely to be in close quarters with one another as a result of these opportunities, which creates challenges for maintaining a clean environment. As a result of these gatherings, a great many of individuals are getting concerned about their health. While these kinds of large-scale meetings are taking place, there is still a significant concern over the transmission of respiratory and gastrointestinal disorders. There have been outbreaks of infectious diseases at some of these meetings. For instance, in 1817, at the Kumbh Mela celebration, cholera broke out. The disease spread throughout Asia during the pandemic that occurred between 1817 and 1824 as affected pilgrims returned home. These have taken on an even greater significance as a result of the constant emergence of novel infectious diseases, notably viral diseases. There is a significant number of Muslim adherents who travel to do the annual Hajj and Umrah pilgrimages. There have been concerns that some of these individuals may contract MERS-CoV diseases while they are in the region, which might then spread to India. Despite the fact that there has not been a single verified case of MERS-CoV infection in the country as of yet, there have been reports that imply that the influenza may have spread through afflicted pilgrims who went home. There is a possibility that these large-scale meetings will create platforms for the exchange of genetic material, which would ultimately lead to the evolution of diseases such as viruses.

Factors Influence Development and Recurrence Of Vector-Borne Illnesses

Diseases that are transmitted by vectors affect millions of people all over the world every year, making them a significant cause for concern in terms of public health security. Among the vectors that are responsible for transmitting diseases like these to humans are insects such as flies, fleas, ticks, and mosquitoes. For example, bacteria, viruses, protozoa, and helminths are all examples of pathogens that are accountable for various disorders. When it comes to the development and continuation of a number of diseases, there is a complicated web of interplay that exists between climatic and environmental factors, human behavior, and therapeutic strategies. In the following section, we will discuss these characteristics, focusing on how they are interconnected and what this means for the prevention and control of diseases.

Vector Population Dynamics: The dynamics of the vector population are the most important factor in the transmission of diseases that are carried by vectors. Some of the elements that influence the behavior, distribution, and number of vectors are temperature, humidity, precipitation, and vegetation. Other influencers include vegetation. On the other hand, mosquitoes, which are responsible for the transmission of diseases such as malaria, dengue fever, and the Zika virus, thrive in pools of water that are stagnant and provide excellent breeding grounds for them. A high relative humidity and a warm temperature are the defining characteristics of these situations. Climate change, which is driven by factors such as global warming, has the potential to increase the transmission zones of illnesses that are transmitted by vectors. This is because climate change can alter the geographic range of vectors as well as their seasonality.

Climate and Weather: climatic conditions and weather patterns have an impact on the dynamics of disease transmission that are transmitted by vectors. There is a correlation between temperature and the rates of pathogen development within vectors as well as the rates of survival of vectors and pathogens outside of the host. The extrinsic incubation period, which is the amount of time it takes for a virus to develop inside of a vector, can be shortened, and the biting rates of vectors can increase when temperatures rise. These factors can all contribute to an increase in disease transmission rates. Vectors are able to replicate infections more quickly when temperatures rise. The spread of diseases can be affected, on the other hand, by decreased vector populations or limited activity as a result of drought or high weather. The distribution of precipitation patterns has an effect on the number of breeding sites that are available for vectors. As an illustration, mosquitoes are able to multiply and spread disease when there is a significant amount of rainfall.

Environmental Changes: Environmental changes that are caused by humans, such as deforestation, urbanization, and modifications to land use, have the potential to have an effect on the ecology of vector populations and the interactions that these species have with humans. As an illustration of this principle, deforestation can create new habitats for vector species, which in turn can increase the amount of contact between humans and vectors and pave the way for diseases that are transmitted by vectors to spread to additional locations that were not previously affected. The ability of urbanization to grow vector populations is influenced by a number of factors, including inadequate waste management, mosquito breeding grounds given by man-made water containers, and inadequate sanitation. In addition, human activities such as mining, construction, and agricultural expansion have the potential to alter natural ecosystems, which can lead to an increase in human exposure to vectors and the diseases that they transmit.

Objectives of the study

1. To study on Factors Influence Development and Recurrence Of Vector-Borne Illnesses
2. To study on Impact of Mass Gatherings and Emerging Viral Infections

Research method

Study Area

An outbreak of chikungunya fever occurred in the Andaman Islands during the months of June and December of 2006. This phenomenon occurred in the year 2006. The findings of the investigation that was carried out by the Regional Medical Research Centre (ICMR) showed that over the course of this epidemic, there was an attack rate that was consistently higher than sixty percent. Acute flaccid paralysis was reported by more than 10 of the subjects who had clinical features that were consistent with chikungunya fever.

Recent Pandemic of Chikungunya

For example, the recent pandemic of Chikungunya fever that occurred in neighboring states like as Kerala, Andhra Pradesh, and Tamil Nadu in 2008 raised the possibility that the Chikungunya virus may spread to the Dakshina Kannada area. This pandemic happened in 2008. One of the causes that contributed to the outbreak of Chikungunya was this condition, which was also one of the elements that triggered the pandemic.

Chikungunya Virus Isolation and Molecular Characterization

During the pandemic that occurred in Port Blair in 2006, an attempt was made to isolate CHIKV from the acute serum of patients who had clinical signs of CHIKF. This was done in an effort to determine whether or not CHIKV was present in the serum. At the same time, attempts were made to isolate CHIKV at both the National Institute of Virology (NIV) and the Regional Medical Research Center (RMRC) in Port Blair. Both of these institutions collaborated on the project. Research in the medical field is the primary focus of both of these establishments.

Witnessing the cytopathic effect (also known as CPE)

Using culture supernatant, an inoculum was applied to a monolayer of the Vero cell line that had reached confluence. In order to inoculate the sample, a dilution of Minimum Essential Medium (MEM) with 2% FBS was carried out. This dilution consisted of 100 µl of the sample and 900 µl of maintenance medium. One milliliter of a dilution of one to ten was used to prepare the sample. The diluted sample was then injected into the Vero cell monolayer that was contained inside the T-25 cm2 flask after the growth media that was already present was removed. The flask was then shaken in between the two hours of incubation, which took place in a horizontal position at 37 degrees Celsius. The flask then incubated for two hours.

In order to determine the pairwise (P) distances between Andaman isolates and the reference that was discovered in the current investigation, the K2P distance and pairwise approach that is included in the MEGA 4.1 program was used. For the purpose of determining the distances that separate the two groups of isolates, this was carried out. Using a K2P distance converter, we were able to determine the proportion of homologies that were associated with each pair. Also, we were able to determine the distance between each pair. In addition, the K2P distance was computed for the whole genome of CHIKV, which was collected from a wide range of sites at different times and places all over the globe.

Table 1: This is a list of CHIKV isolates that were recovered during the outbreak that occurred in Port Blair in 2006, along with their NCBI Genbank Accession number.

S.No	CHIKV isolate	Genotype	Genbank Accession ntunber	
			nsP- I	El
I	CHIKV JG-05	ECSA	JN578240	JN578249
2	CHIKV JG-03	ECSA	JN578241	JN578250
3	CHIKV JG-07	ECSA	11\1578242	JN578251
4	CHIKV DF02	ECSA	1N578243	JN578252
5	CHIKV H-8	ECSA	11\1578244	JN578253
6	CHIKV DEL-7	ECSA	11\1578245	JN578254
7	CHIKV DEL-2	ECSA	1N578246	JN578255
8	CHIKV DEL-03	ECSA	1N578247	JN578256
9	CHIKV H6	ECSA	11\1578248	JN578257

* ECSA: East Central and South India n genotype

Data analysis

Table 2: When individuals with CHIKF were in their first month of sickness, the prevalence of symptoms varied among age groups of patients with the condition.

Symptom (no.)	Prevalence' in age groups (can)					
	10-13	14-19	20-29	30-44	>45	Overall (n = 203) (95%
Joint pain (198)	95 (21/22)	93 (12/13)	97 (38/39)	97 (60'62)	103 (67/67)	98 (94.3–
Fever 1172)	100(22/22)	100(13/13)	87 (34/39)	81 (50'62)	79(53/67)	85 (79.0–

Surging around joint **(107)**	41 19/221	23 (3/13)	46 (18/39	61 (38/62)	58 (39/67)	53 (45.6–
Rash 1102)	55 (12/22)	23 (3/131	54 (21/39)	61 (39'62)	40(27/67)	53 (45.6–
Fatigue (103)	0	23 (3/13)	54 (21/39)	60 (37/62)	58 (39'67)	49 (42.2–
Headache (78)	27(6/22)	23 (3/13)	56122/39)	40 (25/62)	33 (22/67)	49 (42.2–
Facial sueling (58)	32 (7/221	0	21 (8/39)	45 (2(62)	22 (15/67)	29 (22.5–
Body sehe[b](50)	0	15 (2/13)	36 (14/39)	27 (17/62)	5 (17/67)	25 (18.9–
Neuritis' (49)	0	0	21 (8/39)	26 (16/62)	37 (25/67)	24 (18.4–
Conjunctival redness (38)	0	0	21 18391	31 (19'62)	16(11/67)	19 (13.6–
Giddiness (30)	0	0	IS (939)	16 (10/62)	21 (14(67)	15 (10.2–
Vomiting 1M)	**14** (3/22)	**8(1/13)**	IS (6'39)	13 (81621	6(4/67)	11 (6.9–
Running nose(21)	0	0	13 (539)	18 (11/62)	7 (5/67)	11 (6.9–
lint sueling (19)	0	0	8(3/39)	16 (10'62)	9(6/67)	9 (5.7–14.2
Diarrhoea (9)	**0**	**0**	**8** (3/39)	5 (3/62)	**413/67)**	4 (2.0–8.2)
Oral uket (10)	0	8(1/13)	5(2/39)	8 (5162)	3(2/67)	5 (2.4–8.9)

The results are presented in the form of prevalence (expressed as a percentage) and absolute numbers for each age group.

b. Pain that is experienced all over the body, in addition to headaches and joint pain-related discomfort It is possible that a sensation of tingling and numbness will accompany the sensation throughout the body.

As an example, 82% (18/22), 92% (12/13), 13% (5/39), 11% (7/62) and 6% (4/67) of individuals had a remission of their symptoms. The results of the study demonstrated that there was a statistically significant difference in the rate of cure across different age groups ($\alpha = 97.29$, 2 degrees of freedom = 4, $P < 0.001$).

Among the 198 patients who were affected by joint involvement, the large joints of the upper limbs, the small joints of the upper limbs, the big joints of the lower limbs, and the small joints of the lower limbs were found to be involved in 93% (185/198), 93% (185/198), 96% (191/198), and 92% (183/198) of the cases, respectively. Based on the statistical analysis, it was determined that the difference between these proportions did not satisfy the threshold for significance ($\alpha = 3.42$, d.f. = 3, $P = 0.3315$). When it came to the joints, the knee joint was one of the ones that was afflicted so often. Within the population that was being studied, two and three persons, respectively, said that they had experienced soreness in their hip and shoulder joints. There were five people in the same group who reported experiencing pain in the sacroiliac joint (SI), five people who reported experiencing pain in the lumbo-sacral joint (LS), and four people who reported experiencing pain in the cervical vertebral joint.

There was a symmetrical pattern seen in each and every one of the patients who were suffering pain in their joints (198). There were a total of 188 people who were diagnosed with polyarthritis, whereas there were 10 patients who were identified with oligoarthritis. The total number of people was 203, and nine of them had pre-existing headaches that came and went, and fourteen of them had pre-existing problems with their joints. These symptoms, which had been prevalent before to the attack by CHIKF, were far more severe than they had been previously. Every single one of the fourteen people who had previously had joint pain exhibited the symptom, which was a clear indication that they were suffering from degenerative joint disease.

There were around 91% of persons who were gone from work or school for a mean of ten days (the range was from one to thirty days), and there were 185 out of 203 people who were missing. Forty-five patients were unable to go back to work at the end of the month due to the persistent pain they were experiencing in their joints as well as the weariness they were experiencing. When the fever persisted for more than six days for the patient, it was of an intermittent nature in those instances (18 out of 172) where it was present.

The reaction of cytokines and chemokines in chronic children with CHIKV arthritis

Additionally, the distribution of cytokines that were different between patients with chronic arthropathy and controls following CHIKV infection was another component that was explored. This was done in order to determine whether or not there was a difference. As can be shown in Figure , the levels of six cytokines, namely IL1-RA, IL-6, IL-8, MIP-1α, MIP-1ε, and MCP-1, were discovered to be higher in patients who had chronic arthropathy as a consequence of CHIKV infection. This was in contrast to the levels that were discovered in the control group. While the levels of IL1-RA and IL-6 were high in patients with chronic patients, they were also raised in patients with acute patients. This was the case at the same time. While on the other hand, neither recovered nor chronic patients exhibited any indications of an increase in the levels of IL-10 that they were now experiencing. In patients who had been diagnosed with chronic arthritis, the levels of IL-8 and MCP-1 were much greater than those of controls, acute patients, and patients who had completely recovered from their disease. This was the case when compared to patients who had fully recovered from their ailment. During the course of the present inquiry, it was discovered that the levels of MIP-1α and MIP-1α were significantly elevated in patients who were suffering from chronic arthritis. This was in comparison to patients who were participating in other groups and patients who were serving as controls.

Table 3: There was a significant difference in the median concentrations of cytokines and chemokines (pg/ml) between healthy controls and patients with recovered, acute, and chronic CHIKF.

SI No	Cytokine	Controls	Recovered	Acute	Chronic
1	IL1-8	0.0	0.0	0.0	15.9
2	IL1-RA	379.9	312.7	5349	594A
3	*R2.8*	213.7	2049	3491	2619
3	IL-5	0.90	110	0.97	0.87
4	IL-6	0.06	0.01	11.8	63.5
5	IL-8	573.7	1911.6	754.1	12,543.6
6	IL-10	2.9	3.1	5.6	2.4
7	Gar	88.5	50.4	66.8	79.4
8	IP-10	135	149	4578	19.2
9	tAIG	19.3	15.9	42.4	22.5
10	PAIP-1.	60A	41.1	63.6	145.0
11	tAIP-1h{	783	96.8	66.6	354.9
12	***MCP-1***	190.0	2388	*3549*	*2.5398*

13	FLAMES	519.697	4.20,697	436653	33,990

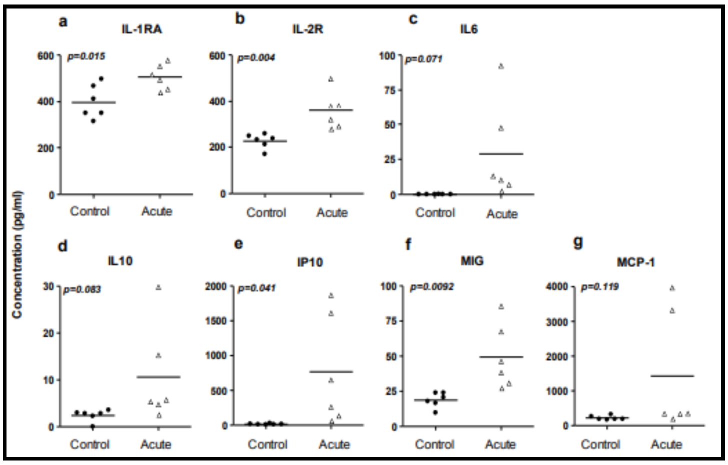

Figure 1: Cytokine levels in acutely infected patients and controls. (a) IL-1RA, (b) IL-2R, (c) IL-6, (d) IL-10, (e) IP10, (f) MIG, and(g) MCP-1.

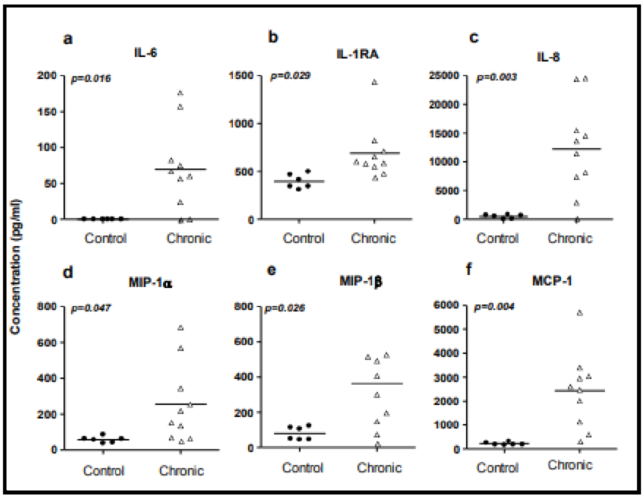

Figure 2: Contrast between the levels of cytokines found in patients with chronic joint involvement and those found in controls who were chronically infected. There are four different types of interleukin (IL): (a) IL-6, (b) IL-1RA, (c) and (f) MCP-1.

CONCLUSION

A conceptual framework for a federated cloud environment has been developed to facilitate the effective management of cloud workloads. To extract the key characteristics from the raw data, a unique feature extraction approach was proposed. An innovative prediction technique that makes use of artificial neural networks has been put into practice to forecast future workloads. A new optimization strategy to optimize the QoS parameters has been presented using the Meta-heuristics technique. The first contribution is made in the region where all of the modules are dependent on one another in some fashion that is not explicitly stated. The framework, which can be found in the chapter that was explained, is comprised of a complete collection of conceptual components that have been assembled into it. As the main lens through which the framework was created, the cloud broker perspective was taken into consideration. The entities that are important and the ways in which they are reliant on one another are stated throughout all of the modules. The architectural design and the abstract design of each module are also shown here for your perusal.

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