Strategy to Control Environmental Factors and Community Behavior Based on a Model of the Endemic Incident of Dengue Fever

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Abstract. Dengue Hemorrhagic Fever (DHF) is an infectious disease caused by the dengue virus, an infectious disease that is endemic in almost 34 provinces in Indonesia. South Kalimantan Province Health Profile Data for 2022: this disease is related to physical environmental conditions and community behaviour. In 2022, Banjar Regency will have the highest number of dengue fever cases, with 228 cases in South Kalimantan, followed by Banjabaru City with 140 instances and Kotabaru Regency with 139 cases. This research aims to find out the dominant factors in community behaviour in preventing dengue fever and factors environment (air temperature, humidity, rainfall, water temperature, water pH, COD (Chemical Oxygen Demand), BOD (Biological Oxygen Demand), and DO) on the number of larvae as a source of dengue fever. So, from these influencing factors, a model of dengue disease can be formed. This model is used to determine the appropriate control strategy. This research was carried out using a sampling technique design method; primary data on community behaviour was obtained by distributing questionnaires while determining environmental factors that influence dengue fever was done by measuring and collecting water sample data. The distribution of questionnaires and sampling of primary data is carried out by the sample size that will be used as the actual data source, taking into account the nature and distribution of the population. Next, the data input process uses multiple regression testing according to the data obtained. The most influential factors were obtained from the regression results, which were then used in the dengue disease model. The results of the dengue disease model can be analyzed so that the results obtained can improve appropriate prevention methods for dengue fever.

Keywords: Dengue hemorrhagic fever, environmental factors, community behaviour.

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1 Introduction

Dengue Hemorrhagic Fever is an infection caused by the Dengue virus. This Dengue virus can threaten and even cause death in the human population [1]. Dengue hemorrhagic fever (DHF) always increases at the start of every rainy season due to the large amount of standing water, which is a place for the Aedes aegypti mosquito to live. This mosquito is the cause of dengue hemorrhagic fever (DHF). Especially after the flood disaster hit the South Kalimantan region in mid-January 2021 with a broad impact. Floods in South Kalimantan were recorded as submerging thousands of houses, according to the Head of the BNPB Disaster Data, Information and Communication Center, Raditya Jati, who noted that reports about flooding incidents in South Kalimantan came from Tapin Regency, Kota. Banjarbaru, Hulu Sungai Tengah Regency, Hulu Sungai Selatan Regency, Banjarmasin City and Banjar Regency. This condition could potentially lead to an extraordinary incident (KLB) of Dengue Hemorrhagic Fever (DHF).

The latest dengue case data submitted by the Head of the South Kalimantan Health Service reported that 764 people in South Kalimantan province were affected by dengue hemorrhagic fever (DBD) from January to the end of 2022. Banjar Regency has the highest number of dengue fever cases in South Kalimantan, with 228 cases, followed by the city of Banjabaru with 140 cases and Kotabaru district with 139 cases. In fact, for data from January 1 to February 7 2023, there have been 43 cases of dengue fever in Banjar Regency.

The government uses many ways through the South Kalimantan Health Service. Specifically, the Banjar Regency government is to be able to overcome this dengue fever problem. However, cooperation from all parties is still needed to deal with this dengue fever problem well. "So research is needed regarding this matter, which is carried out within ULM as one of the leading and competitive universities in wetland environments." Especially about the dengue fever problem [2] and [3].

Many factors cause dengue fever in South Kalimantan, specifically in Banjar Regency; global warming conditions can cause climate change, and this physical factor can be a widespread spread of the Dengue Virus [4]. Climatic factors such as weather, temperature, and humidity also influence the causes of parasites and vectors [5]. Rainfall can cause standing water in places where mosquitoes breed [6], and humidity affects the lifespan of mosquitoes, with low humidity shortening their lifespan. A humidity level of 60% is the lowest limit to allow mosquito life, a supporting factor for the spread of mosquitoes as the cause of dengue fever [7]. Physical and non-physical factors such as density level [8], climate, rainfall and air humidity influence the incidence of dengue fever [9]. Climate influences parasites and vectors such as weather, temperature, and humidity. Temperature or air temperature factors, including environmental factors that influence the life of the Aides Aegypti mosquito, also directly influence dengue fever [10].

This paper involves collecting primary data through questionnaire data and sampling environmental factors in the form of water quality consisting of water temperature, water pH, COD (Chemical oksigen Demand.), BOD (Biological oksigen Demand), and DO. Apart from environmental factors, it also involves people's behaviour regarding knowledge of dengue fever.

So, based on the collection of primary data in the form of questionnaire data and aquatic samples, environmental factors in the form of water quality can be involved in the Endemic Event Model of Dengue Hemorrhagic Fever in Banjar Regency, so that it can be an alternative solution and can also be used as an alternative in developing appropriate strategies for the problem of controlling the level of disease spread. DHF, especially in the Banjar Regency area.

2 Methods

The data used in the paper is primary data with a data collection technique using Purposive Sampling, which implicitly selects samples considered representative of a population by taking samples at locations where people are affected by dengue fever. Primary data consists of the influence of the physical environment, air temperature, and humidity. Next, primary data will be obtained from water samples around areas in the Banjar Regency area where residents are affected by dengue fever.

Primary data takes water samples and observes the level of water quality by measuring water quality in the form of water pH, water temperature, Oxygen Demand (DO), Chemical Oxygen Demand (COD) and Biological Oxygen Demand (BOD) using standard measuring instruments and also laboratory services Biochemistry and Biomolecular, as well as the MIPA Basic Laboratory to help observe dengue mosquitoes so that their relationship analysis can be determined. They are starting with preparing several supporting, grand, middle, and applied theories. Followed by preparation for collecting water sample data and then analyzing the data related to the samples obtained. The data analysis method used involves statistics by carrying out the following steps:

a. Collect primary data (COD, DO, BOD, pH, air temperature, water temperature and air humidity) in relation to the number of larvae from the water samples taken. Next, correlation and regression analysis will determine the factors influencing the number of larvae. It also uses secondary data (population numbers and dengue fever data) in connection with the epidemiological mathematical model that is formed.
b. Next, carry out a correlation test to measure the level of closeness of the linear relationship between one variable and another by knowing the correlation coefficient, which is a number that shows the direction and strength of the relationship between 2 variables. This direction is expressed in positive and negative relationships. The positive direction occurs if the value of one variable is increased, causing an increase in another variable. Meanwhile, a negative correlation coefficient means that the value of one variable is increased, causing the value of another variable to decrease and vice versa. Next, there is a regression test to determine the parameters that influence the aquatic model, which is then used in the formed mathematical model.
c. Regression analysis aims to obtain a multiple linear regression model that will be used in regression analysis. The method commonly used to estimate the parameters of multiple linear regression models is the least squares method, carried

out to explain the variables that have a dominant influence, including air temperature, water temperature, air humidity, water pH, COD, BOD and DO about the presence of existing larvae, on water samples.

d. Determine the influencing parameters on water samples related to COD, BOD, DO, water pH, water temperature, air temperature and air humidity on the number of larvae using multiple regression. Next, use the most influential factors in forming the model.

e. Make research conclusions.

3 Observation Results and Presentation Data

The data used in this research is primary data consisting of data on the relationship between the parameters of air temperature, pH, air humidity, water temperature, COD, BOD, and DO about the number of larvae. Questionnaires were also distributed regarding community behaviour, which consisted of Variables X1 (About knowledge of DHF), Variables X2 (About prevention behaviour), and Variables X3 (About knowledge of DHF prevention); the relationship was related to the level of community knowledge about DHF.

Biochemistry and Molecular Department of the Faculty of Medicine measures COD, BOD, and DO data and their relationship with observation data on the number of larvae. This is done to identify factors that significantly influence the mathematical model that will be formed by involving the most influential factors. However, beforehand, data validation and reliability tests were carried out for the questionnaires used and distributed to the public.

Based on the results of the primary data obtained, the initial step of observations carried out in the field is to obtain air temperature, pH, humidity and water temperature data based on direct field measurements. Next, data measurements were conducted in the Laboratory of the Biochemistry and Molecular Department of the Faculty of Medicine. COD, BOD and DO data were obtained, the relationship between each of which and the number of larvae can be presented in graphical form as follows:

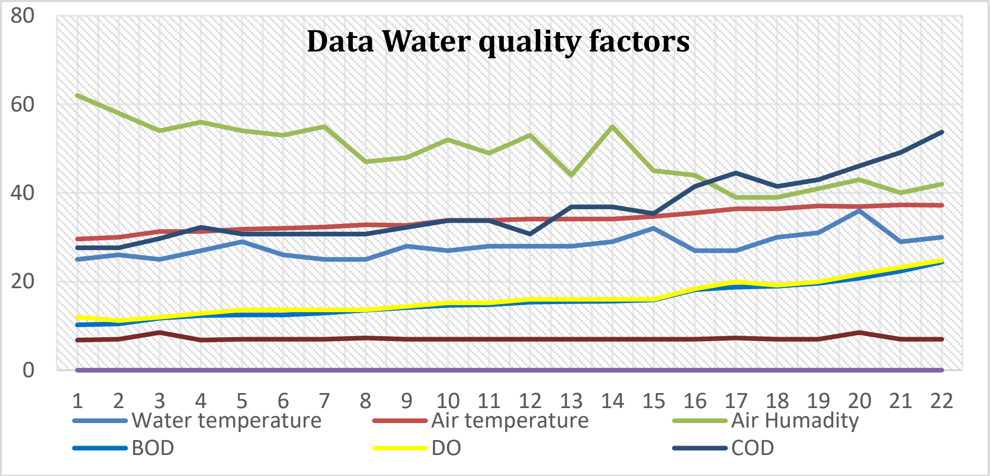

Fig. 1. Relationship between BOD, COD, DO, pH water, temperature water, humidity air and air temperature

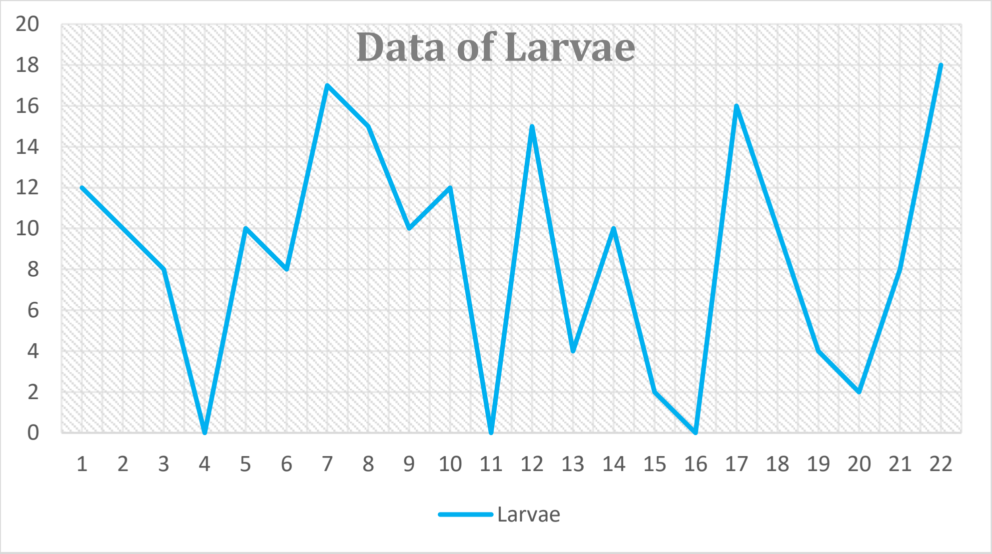

Fig. 2. Data number of Larvae

Apart from this data, the results of a questionnaire were also obtained regarding the relationship between variables X1 (about knowledge of dengue fever), variables X2 (about prevention behaviour), and variables X3 (about knowledge related to dengue prevention), the relationship is associated with the level of public knowledge about dengue fever which is presented in a picture that can be displayed. Via the following graph:

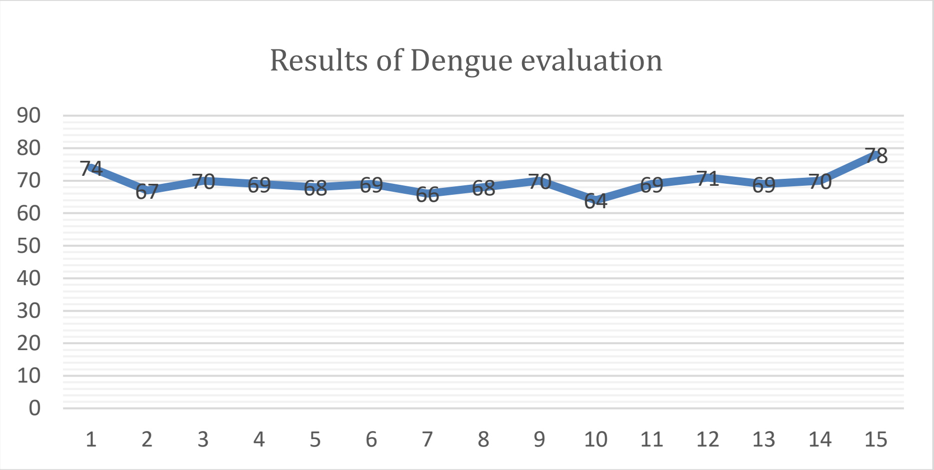

Fig. 3. Results of the DHF evaluation questionnaire

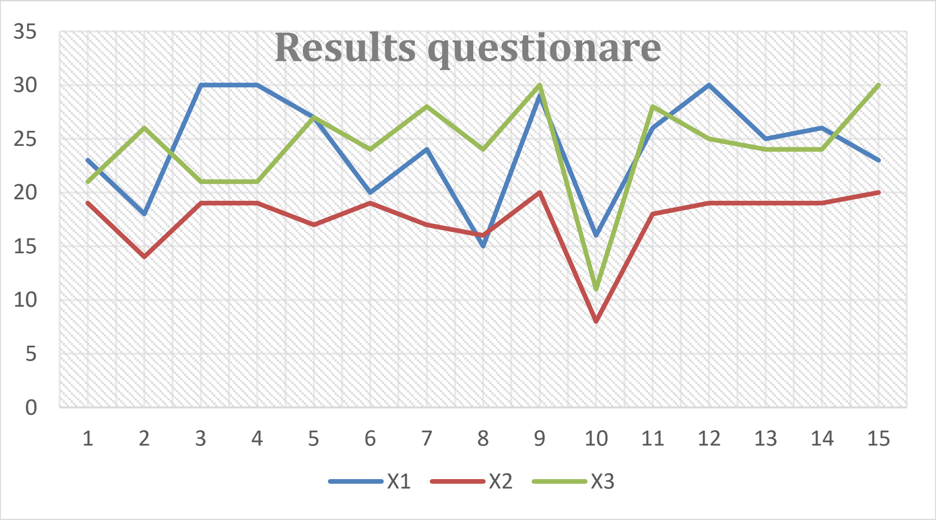

Fig. 4. DHF questionnaire recap results

4 Discussions

After presenting the primary data on air temperature, pH, air humidity, water temperature COD, BOD and DO about the number of larvae. Also, questionnaire data related to community behaviour, which consists of Variables X1 (About knowledge of DHF), Variables X2 (About prevention behaviour), and Variables X3 (About knowledge of DHF prevention), the relationship is related to the level of community knowledge about DHF. Next, tests were carried out on primary data related to water quality and questionnaire data.

4.1 Test the water quality

Water quality factors are also a cause of dengue fever. So, it is necessary to observe the quality of the water. Parameters related to measuring water quality, are water temperature, water pH, and several parameters related to the presence of oxygen in water, namely dissolved oxygen (DO) in the form of dissolved oxygen, Chemical Oxygen Demand (COD), and Biochemical Oxygen Demand (BOD) [11]. A decrease in water quantity and quality will disrupt growth and even cause disease infections to grow and develop in these waters [11].

Water temperature is also directly or indirectly influenced by sunlight. The heat of the water will change slowly between day and night and from season to season. Water temperature significantly affects the amount of dissolved oxygen in the water. If the temperature is high, water will become saturated with oxygen more quickly than if the temperature is low.

COD or chemical oxygen demand is the amount of oxygen needed so that waste materials in water can be oxidized through chemical reactions [11].

The tests carried out were the Bivariate Correlation test and the t-test to determine the parameters that influence the aquatic model, which is then used in the formed mathematical model.

Table 1. Bivariate Correlation Test

Correlations

		Number of larvae	pH	Water Temperature	COD	BOD	DO	Air Temperature	Humidity
Number of larvae	Pearson Correlation	1	-,011	-,237	,747**	,752**	,903**	-,004	,053
	Sig. (2-tailed)		,959	,253	,000	,000	,000	,985	,801
	N	25	25	25	25	25	25	25	25
pH	Pearson Correlation	-,011	1	,040	,000	-,025	-,029	-,277	,419*
	Sig. (2-tailed)	,959		,848	1,000	,906	,892	,180	,037
	N	25	25	25	25	25	25	25	25
Water Temperature	Pearson Correlation	-,237	,040	1	,036	,009	,005	,132	-,049
	Sig. (2-tailed)	,253	,848		,864	,967	,982	,530	,815
	N	25	25	25	25	25	25	25	25
COD	Pearson Correlation	,747**	,000	,036	1	,594**	,692**	,112	,214
	Sig. (2-tailed)	,000	1,000	,864		,002	,000	,594	,304
	N	25	25	25	25	25	25	25	25

BOD	Pearson Correlation	,752**	-,025	,009	,594**	1	,791**	,060	,031
	Sig. (2-tailed)	,000	,906	,967	,002		,000	,774	,882
	N	25	25	25	25	25	25	25	25
DO	Pearson Correlation	,903**	-,029	,005	,692**	,791**	1	-,063	,111
	Sig. (2-tailed)	,010	,892	,982	,000	,010		,766	,598
	N	25	25	25	25	25	25	25	25
Air Temperature	Pearson Correlation	-,004	-,277	,132	,112	,060	-,063	1	-,514**
	Sig. (2-tailed)	,985	,180	,530	,594	,774	,766		,009
	N	25	25	25	25	25	25	25	25
Humidity	Pearson Correlation	,053	,419*	-,049	,214	,031	,111	-,514**	1
	Sig. (2-tailed)	,801	,037	,815	,304	,882	,598	,009	
	N	25	25	25	25	25	25	25	25

**. Correlation is significant at the 0.01 level (2-tailed).

*. Correlation is significant at the 0.05 level (2-tailed).

In the output above, the correlation number (Pearson Correlation) and the significant value and value of the two-sided test (Sig (2-tailed)) are obtained, which can be interpreted as follows:

a. Relationship between the number of larvae (Y) and DO (X5)

The correlation figure is 0.747. This means that the two variables have a positive relationship (the better the value of the number of larvae, the better the COD value of the water, or vice versa), and the Relationship is weak. At the 95% confidence level, the relationship between these two variables is significant and fragile. (sig value = 0.010 > 0.05).

b. Relationship between the number of larvae (Y) and COD (X3)

The correlation figure is 0.752. This means that the two variables have a positive relationship (the better the value of the number of larvae, the better the COD value of the water, or vice versa), and the Relationship is solid. At the 95% confidence level, the relationship relationship between these two variables is significant or has a strong relationship. (sig value = 0.000 < 0.05).

Table 2. T test the water quality

Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients		
		B	Std. Error	Beta	t	Sig.
bv1	(Constant)	-33.348	45.050		-.740	.471
	PH Water	-.935	1.805	-.096	-.518	.613
	Water Temperature	-1.215	.422	-.732	-2.877	.012
	Air Temperature	1.779	.998	.957	1.783	.096
	Humidity Air	.568	.290	.873	1.962	.070
	BOD	.208	1.446	.181	.144	.888
	DO	2.411	1.762	2.066	1.368	.193
	COD	-1.301	.597	-2.171	-2.181	.047

Dependent Variable: Number of Flag

Results: Water temperature factor (0.012) and COD (0.047) < 0.05. SIGNIFICANT impact

Based on the t-test output, the correlation value between the COD variables and water temperature is 0.525. This means that the two variables have a positive relationship (the better the DO value, the better the water temperature value and vice versa). However, the relationship between DO and water temperature can be classified as very strong. At the 95% confidence level, the relationship between these variables is very significant, based on the table of sig value = 0.012 (Sig value = 0.012 < 0.05).

Based on the t-test results, the parameters that most influence the aquatic factors involved in the model are the water temperature and COD factors that will be used in the model in the following discussion.

4.2 Test data questionnaires

The results of distributing questionnaires related to community behaviour, which consists of Variables X1 (About knowledge of DHF), Variables X2 (About prevention behaviour), and Variables X3 (About knowledge of DHF prevention), the relationship is related to the level of community knowledge about DHF.

The tests carried out on the questionnaire were validity, reliability, and regression tests, including the F test, t-test and determination. Questionnaire data validity and reliability tests are carried out to ensure the validity and consistency of the questionnaire used.

The next step in carrying out a regression test includes the F, T-test and determination tests.

Table 3. F test data questionnaires

ANOVA[a]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	80.598	3	26.866	4.275	.031[b]
	Residual	69.135	11	6.285		
	Total	149.733	14			

a. Dependent Variable: value

b. Predictors: (Constant), TOTAL X3, TOTAL X1, TOTAL X2

SIGNIFICANT of results (0,031 < 0,05).

Table 4. T-test data questionnaires

Coefficients[a]

Model		Unstandardized Coefficients		Standardized Coefficients	t	Sig.
		B	Std. Error	Beta		
1	(Constant)	55.053	4.650		11.840	.000
	TOTAL of X1	-.087	.101	-.204	-.863	.407
	TOTAL of X2	.786	.262	.815	3.004	.012
	TOTALof X3	-.001	.143	-.002	-.007	.995

a. Dependent Variable: value

Results:

Factor X2 (0,012) < 0,05, SIGNIFICANT impact.

Table 5. Coefficient of determination

Model Summary[b]

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate

1	.734^a	.538	.412	2.507

a. Predictors: (Constant), TOTAL X3, TOTAL X1, TOTAL X2

b. Dependent Variable: value

The magnitude of the influence of R2 53.8%

4.3 Early phases of mosquito life and model formation

Mathematical models for dengue fever, either SIR [12], [13] , [11] or SEIR [10], [14], and their modifications [15], [16], [17] have been widely used to help solve disease problems. Aquatic factors are also part of the model that is considered.

The aquatic phase (Av) is the phase that shows the mosquito is still in the water; this aquatic phase will be included in the model discussion. This aquatic phase consists of the part that influences the growth of mosquitoes before they form into adult mosquitoes.

Several assumptions are stated before explaining the SEITR-ASI mathematical model (susceptible, exposed, infected, treated, recovered, aquatic, susceptible and infected).

The assumptions used in this model are as follows:

a. The birth rate of the human (host) and mosquito (vector) populations is constant.
b. Humans are the only food source for mosquitoes. This means that mosquitoes get a food source (blood) by biting humans'.
c. The population of the class is people who are registered and given treatment because they have been identified as dengue fever patients.
d. Any infected human population can recover without having to go to class.
e. All human populations that are given treatment and confirmed as dengue fever patients do not produce infections in mosquitoes and do not spread the disease.
f. Individuals who are given treatment may die from the disease.
g. Human infection only occurs if an infected mosquito bites a healthy but susceptible human. Likewise, mosquito infection only occurs if a healthy but susceptible mosquito bites an infected human.
h. Each human subpopulation has the same natural death rate. Likewise with mosquitoes, each subpopulation of mosquitoes has the same natural mortality rate of .
i. Every individual exposed mosquito that passes the incubation period becomes an individual infected with the dengue virus and thus enters the Infected subpopulation. Likewise, with humans, every exposed human individual who passes the incubation period becomes an infected human individual and thus enters the Infected subpopulation.
j. Closed population.

From the assumptions above, an epidemiological model for dengue fever is derived by taking into account the aquatic phase of the Aedes aegypti mosquito as follows:

For example, Nh is the total human population, divided into three subpopulations: the susceptible human subpopulation Sh, the infected human subpopulation Ih and the recovered human subpopulation Rh. Meanwhile, the Nm mosquito population is divided into three subpopulations, namely: the aquatic phase subpopulation (Am), the susceptible mosquito subpopulation (Sm) and the infected mosquito subpopulation (Im). Schematically, the pattern of the spread of dengue fever between the host (human) and vector (mosquito) can be depicted in a compartment diagram.

The parameters used in this discussion are as Table 6. follows:

Table 6. Table of parameters

PARAMETER	DESCRIPTION
$\boldsymbol{\Lambda_v}$	Mosquito birth rate
$\boldsymbol{\beta}$	Average bite rate per mosquito per person
$\boldsymbol{\alpha_v}$	Possible transmission from infected humans to susceptible mosquitoes
$\boldsymbol{\mu_v}$	Natural death rate of mosquitoes
$\boldsymbol{\gamma_v}$	Extrinsic incubation of mosquitoes
$\boldsymbol{\Lambda_h}$	Human birth rate
$\boldsymbol{\alpha_h}$	Possible transmission from infected mosquitoes to susceptible humans
$\boldsymbol{\gamma_h}$	Human extrinsic incubation
$\boldsymbol{\eta}$	Treatment Rate in infected humans
$\boldsymbol{q_1}$	Natural recovery rate of infected humans
$\boldsymbol{q_2}$	The level of recovery of people who are given treatment
$\boldsymbol{\delta}$	Disease-related human death rates
$\boldsymbol{\mu_h}$	Natural human mortality rate
$\mathbf{a_{1v}}$	The level of influence of air temperature on aquatics
$\mathbf{a_{2v}}$	The level of influence of COD on aquatics
$\mathbf{b_v}$	The growth rate of mosquitoes from the aquatic phase to Susceptible

The process of forming the SEITR-ASI mathematical model for dengue fever can be explained as follows.

4.4 Establishment of models for human subpopulations

4.4.1 Healthy Human and ***Susceptible*** $(\boldsymbol{S_h})$ Subpopulations

Changes in the number of healthy and susceptible human subpopulations over time will increase due to new individuals, namely in the form of births with a birth rate of, by assumption 1. Then, based on assumption 7, changes in the number of susceptible human subpopulations will decrease due to deaths with a natural death rate of. Furthermore, based on assumption 6, the susceptible human subpopulation will fall by the amount due to transmission of the virus through mosquito bites infected with the virus to humans (humans in the incubation period) so that these individuals will move to the Exposed subpopulation. Based on this, the change in the number of human subpopulations that are healthy and classified as susceptible over time t is:

$$\frac{dS_h}{dt} = \Lambda_h - \beta\alpha_h I_v \frac{S_h}{N_h} - \mu_h S_h \tag{4.1}$$

4.4.2 Healthy Human *Exposed* $(\boldsymbol{E_h})$ subpopulations

Exposed humans are infected with the virus but cannot infect healthy and susceptible mosquitoes. The subpopulation of liable humans increases due to the transmission of the virus from mosquitoes to humans, which occurs due to infected mosquito bites on healthy and susceptible humans, so these humans are categorized as humans who are exposed within an incubation period of $\beta\alpha_h I_v \frac{S_h}{N_h}$. Assumption 7 states that changes in the number of human subpopulations exposed over time will decrease due to death with a natural human death rate of $\mu_h E_h$. Then, according to assumption 8, the number of exposed human subpopulations will also decrease due to exposed human individuals going through the incubation period or, in other words, these individuals have become infected individuals, namely by $\gamma_h E_h$. Based on this, changes in the number of human subpopulations exposed over time are:

$$\frac{dE_h}{dt} = \beta\alpha_h I_v \frac{S_h}{N_h} - (\gamma_h + \mu_h)E_h \tag{4.2}$$

4.4.3 Healthy Human ***Exposed*** $(\boldsymbol{E_h})$ **subpopulations**

The number of infected human subpopulations that can be infected over time will increase due to the presence of exposed human individuals who turn into infected human individuals as a result of passing the incubation period by assumption 8, which is equal to $\gamma_h E_h$. In addition, according to the assumption that seven infected human subpopulations will decrease due to natural death with a crude death rate of $\mu_h I_h$. The Infected subpopulation will also decrease due to infected human individuals moving and being given DHF Treatment (T_h) in the form of providing healthy food, regular drinks and lowering body temperature or in other words these individuals move into the Treatment (T_h) class at a rate of ηI_h. In assumption 4, the Infected subpopulation will also decrease due to the natural recovery rate of infected humans of $q_1 I_h$. Based on this, changes in the number of human subpopulations infected and able to infect over time are:

$$\frac{dI_h}{dt} = \gamma_h E_h - (\eta + q_1 + \mu_h)I_h \tag{4.3}$$

4.4.4 *Treatment* $(\boldsymbol{T_h})$

Changes in the number of Treatment(T_h) subpopulations over time will increase because infected individuals are given DHF Treatment or in other words these individuals move into the Treatment class at a rate of ηI_h . In accordance with assumption 8, the human subpopulation treated will decrease due to individual deaths due to the disease byδT_h . Furthermore, the reduction in the number of treatment subpopulations is also due to the recovery rate of infected humans of $q_2 T_h$. In addition, based on the assumption that 6 treatment subpopulations will decrease due to natural deaths with a natural death rate of $\mu_h T_h$. Based on this, the change in the number of Treatment subpopulations over time is:

$$\frac{dT_h}{dt} = \eta I_h - (\delta + q_2 + \mu_h) T_h \tag{4.4}$$

4.4.5 Recovered $(\boldsymbol{R_h})$

Changes in the number of recovered human subpopulations over time will increase because there are individuals from the Infected class who can recover without having to go to the Treatment class, with a natural recovery rate of infected individuals of $q_1 I_h$, this is by assumption 4. The number of recovered subpopulations also increases due to the recovery of individuals in the Treatment class of $q_2 T_h$. Apart from experiencing an increase in the Recovered subpopulation, it also experienced a reduction due to individuals dying naturally; this refers to assumption 8. Thus, the change in the number of the Recovered subpopulation over time is:

$$\frac{dR_h}{dt} = q_1 I_h + q_2 T_h - \mu_h R_h \tag{4.5}$$

4.5 Establishment of a model for mosquito populations

4.5.1 Aquatic (A_v) phase mosquito subpopulation

Changes in mosquito subpopulations in the aquatic phase can be seen in how mosquitoes interact in spreading dengue fever. Changes in the number of mosquito subpopulations in the aquatic phase increase with the influence of natural birth factors and decrease with the influence of the mosquito growth rate of 0, which is influenced by growth which is directly proportional to COD (a_{1v}) and air temperature (a_{1v}) and will decrease due to death with the natural death rate According to assumption A7, it can be defined as followsthat μ_v. Aquatic Mosquito Subpopulation equation:

$$\frac{dA_v}{dt} = \Lambda_v + a_{1v} + a_{2v} - \mu_v A_v - b_v S_v \tag{4.6}$$

4.5.2 S*usceptible* (S_v) phase mosquito subpopulation

Changes in the number of mosquito subpopulations that are healthy and classified as susceptible to being attacked by viruses will increase due to the rate of increase in the aquatic phase, according to assumption 1. Then, based on assumption 7, changes in the number of susceptible mosquito subpopulations will decrease due to deaths with a natural death rate of $\boldsymbol{\mu_v S_v}$. Furthermore, based on assumption 6, the subpopulation of susceptible mosquitoes will decrease by $\boldsymbol{\beta\alpha_v S_v \frac{I_h}{N_h}}$ due to interaction with infected humans (mosquitoes bite infected humans), individual mosquitoes will move to the Infected subpopulation. Based on this, the change in the number of mosquito subpopulations that are healthy and classified as susceptible over time t is:

$$\boldsymbol{\frac{dS_v}{dt} = b_v\, S_v - \beta\alpha_v S_v \frac{I_h}{N_h} - \mu_v S_v} \tag{4.7}$$

4.5.3 *Infectious* $(\boldsymbol{I_v})$ phase mosquito subpopulation

The number of mosquito subpopulations that are infected and can transmit it to healthy humans and are classified as susceptible will increase over time due to interactions between healthy mosquitoes that bite humans infected with the virus so that these mosquitoes are categorized as mosquitoes that are exposed within an incubation period of $\beta\alpha_v S_v \frac{I_h}{N_h}$. In addition, according to the assumption that seven subpopulations of infected mosquitoes will decrease due to natural death with a crude death rate of $\mu_v I_v$. Based on this, changes in the number of infected mosquito subpopulations that can infect healthy and susceptible humans over time are:

$$\frac{dI_v}{dt} = \beta\alpha_v S_v \frac{I_h}{N_h} - \mu_v I_v \tag{4.8}$$

Based on Equations (4.1), (4.2), (4.3), (4.4), (4.5), (4.6), (4.7) and (4.8), the SEITR-ASI model for the spread of Dengue Hemorrhagic Fever is obtained, namely:

$$\frac{dS_h}{dt} = \Lambda_h - \beta\alpha_h I_v \frac{S_h}{N_h} - \mu_h S_h \tag{4.9}$$

$$\frac{dE_h}{dt} = \beta\alpha_h I_v \frac{S_h}{N_h} - (\gamma_h + \mu_h)E_h \tag{4.10}$$

$$\frac{dI_h}{dt} = \gamma_h E_h - (\eta + q_1 + \mu_h)I_h \tag{4.11}$$

$$\frac{dT_h}{dt} = \eta I_h - (\delta + q_2 + \mu_h)T_h \tag{4.12}$$

$$\frac{dR_h}{dt} = q_1 I_h + q_2 T_h - \mu_h R_h \tag{4.13}$$

$$\frac{dA_v}{dt} = \Lambda_v + a_{1v} + a_{2v} - \mu_v A_v - b_v S_v \tag{4.14}$$

$$\frac{dS_v}{dt} = b_v S_v - \beta \alpha_v S_v \frac{I_h}{N_h} - \mu_v S_v \tag{4.15}$$

$$\frac{dI_v}{dt} = \beta \alpha_v S_v \frac{I_h}{N_h} - \mu_v I_v \tag{4.16}$$

The system of equations (4.9), (4.10), (4.11), (4.12), (4.13), (4.14), (4.15) and (4.16) is referred to as the SEITR-ASI model of Dengue Hemorrhagic Fever.

5. Conclusion

Based on the discussion of this paper, the following conclusions are obtained:

a. Primary water quality data consists of parameter data on air temperature, pH, air humidity, water temperature, COD, BOD and DO about the number of larvae. From the tests carried out, it was found that the most influential factors were water temperature and COD.

b. Likewise, the results of tests on questionnaires or questionnaires related to community behaviour consist of Variable dengue fever. From the tests carried out, it was found that the most influential factor was Variable X2 (Regarding preventive behaviour).

c. The dominant factors are water temperature, COD, and preventive behaviour, which are then used to establish a dengue disease model in the form of SEITR-ASI.

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