The Impact of Host Factors on the Spread of Dengue Hemorrhagic Fever

Ardat[1], Nyi Nyi Naing[2], Basaruddin[3], Wan Arfah[4]

[1]*Ardat, Faculty of Medicine, Universiti Sultan Zainal Abidin, Medical Campus, Jalan Sultan Mahmud, 20400 Kuala Terengganu, Terengganu, Malaysia, Email: si3086@putra.unisza.edu.my/ardat.ahmad@gmail.com*
[2] *Nyi Nyi Naing, Faculty of Medicine, Universiti Sultan Zainal Abidin, Medical Campus, Jalan Sultan Mahmud, 20400 Kuala Terengganu, Terengganu, Malaysia. Email: syedhatim@unisza.edu.my*
[3] *Basyaruddin, Fakultas Pertanian, UISU, Medan, Email:Basyaruddin@fp.uisu.ac.id*
[4] *Nadiah Wan-Arfah, Faculty of Health Sciences, Universiti Sultan Zainal Abidin, Gong Badak Campus, 21300 Kuala Nerus, Terengganu, Malaysia, Email: wanwaj@unisza.edu.my*

KEYWORDS
Dengue Hemorrhagic Fever (DHF), Host, Disease transmission

ABSTRACT

This study uses a survey of the affected human population to evaluate the impact of host variables on the spread of Dengue Hemorrhagic Fever (DHF) in Indonesia. The study investigated observable factors influencing DHF transmission by operationalizing important variables drawn from theoretical frameworks. The findings highlight the significance of host-related factors in understanding the dynamics of DHF, offering useful insights for the development of successful public health initiatives. The study's goal is to lessen the impact of DHF on communities, safeguard vulnerable groups, and reduce the frequency of serious health problems. The study recommends focused interventions to improve community resilience against DHF, emphasizing the importance of health practices and environmental effects. Finally, the study emphasizes the importance of continued public awareness and education measures in Indonesia to tackle this persistent health threat and prevent future epidemics.

1. Introduction

Dengue Hemorrhagic Fever (DHF), also known as Demam Berdarah Dengue (DBD) in Indonesian, is a major infectious disease that requires attention due to its association with serious health problems that can result in hospitalization and, in some cases, death. DHF, which is characterized by a high fever, hemorrhagic symptoms, and plasma leakage, can quickly worsen if not recognized and treated early. Mosquitoes, specifically those of the Aedes genus, such as Aedes aegypti and Aedes albopictus, are the primary vectors of the disease. These vectors thrive in urban contexts, where they spawn in stagnant water, therefore understanding their transmission paths is critical for successful intervention and preventative measures. Public health measures can be created to reduce the risk of DHF outbreaks and protect vulnerable populations by identifying the specific conditions that enable mosquito reproduction and the factors that influence human exposure to bites.

DHF is endemic in many parts of Indonesia, resulting in a major health issue. The tropical climate, with high humidity and moderate temperatures, provides optimal breeding circumstances for Aedes mosquitoes. These environmental variables contribute to the disease's continual spread, making DHF a continuous issue for public health officials. Despite the fact that the dengue virus has been prevalent in Indonesia for over 43 years, efforts to fight DHF have not been entirely successful. The government has launched a number of steps to combat the spread of the disease, including public health campaigns, mosquito control programs, and community involvement efforts. However, these methods have not been universally effective, emphasizing the importance of a more comprehensive understanding of the elements that contribute to DHF outbreaks.

One of the most critical problems to reducing DHF is a lack of public understanding of the necessity of keeping the environment clean and healthy. Poor waste management, stagnant water, and filthy living conditions make perfect breeding grounds for Aedes mosquitos. Communities continue to be vulnerable to dengue because they lack appropriate knowledge about dengue prevention and control strategies. Raising public knowledge is critical in lowering DHF transmission. Educational initiatives aiming at alerting the public about the risks associated with dengue and supporting behaviors like regular cleaning of potential mosquito breeding areas can have a substantial impact on the disease's incidence. Empowering communities with information about dengue symptoms, preventative strategies, and the necessity of obtaining medical care might also help to reduce serious health problems and fatalities, particularly among vulnerable populations such as children. To better understand the dynamics of DHF transmission, the study looked at the health habits of the local community in North Sumatra Province. This location was an important case study for investigating how various health-related activities (host variables) affected the spread of DHF. For example, the study looked at how the level of public knowledge about dengue prevention affects transmission rates.

SEM performed particularly well in this situation because it combined several analytical approaches, including factor analysis, multiple regression analysis, and path analysis. This comprehensive paradigm allowed for a more in-depth analysis of how underlying variables like community awareness and historical context influenced DHF transmission patterns. The study was characterized as a survey, with the focus on the conditions of the DHF-affected human population. Measurements were taken to evaluate tangible elements, which assisted to portray abstract underlying variables. The study intended to build meaningful linkages between selected variables by operationalizing them using observable elements obtained from theoretical frameworks.

The outcomes of this study are crucial for establishing more effective measures to combat DHF in Indonesia. The study revealed useful insights into the function of host-related factors in disease transmission, which can be used to inform public health activities. The ultimate goal was to lessen the impact of DHF on communities, safeguard vulnerable groups, and reduce the number of serious health problems. Understanding the dynamics of Dengue Hemorrhagic Fever in Indonesia is critical for improving public health and avoiding repeat outbreaks. Targeted interventions that focus on local populations' health habits and the environmental elements that contribute to disease transmission can improve community resilience to DHF. Continued efforts to promote awareness and educate the public about dengue prevention are critical in the fight against this recurrent health issue.

Statistical Modeling

Dengue Hemorrhagic Fever (DHF)

Dengue Hemorrhagic Fever (DHF) is a severe infectious disease caused by the dengue virus, which is spread mostly by the Aedes aegypti mosquito. As a member of the Arbovirus family, the dengue virus is unique in that it has four distinct serotypes, each of which can cause sickness. DHF's clinical manifestations vary, however they often include a high temperature, muscular and joint pain, rash, and bleeding tendencies like petechiae. If not treated swiftly and appropriately, the condition can rapidly worsen, resulting in life-threatening consequences such as plasma leakage or shock. The pathophysiology of DHF is complex, involving immunological responses that cause capillary permeability, which is responsible for many of the disease's severe symptoms and consequences.

DHF transmission is dependent on the virus's interaction with the mosquito vector and the human host. The dengue virus is transmitted mostly by the Aedes aegypti mosquito, which is recognized for its anthropophilic character, preferring human blood over animal blood. While Aedes aegypti is the most effective vector, Aedes albopictus also contributes to viral transmission, albeit at a lower rate. Environmental factors, particularly those that influence mosquito breeding sites, such as standing water, play an important role in the transmission of DHF. These circumstances promote mosquito growth, increasing the chance of transmission.

DHF transmission and severity are heavily influenced by host variables. Host variables include a variety of biological and physiological parameters that influence an individual's susceptibility to the virus and the severity of the disease after infection. Genetic predispositions, immunological condition, overall health, and mosquito vector exposure are all considerations to consider. While DHF can afflict people of all genders, female children die at a higher rate than male children, implying that the host response to the virus may be hereditary or hormonal in nature. The human immune response to the dengue virus is complex and can have serious consequences, particularly in cases of secondary infection with a different serotype of the virus, when the process known as antibody-dependent enhancement (ADE) worsens illness severity.

DHF pathogenesis is dependent on the virus's interaction with the host's immune system. Upon infection, the dengue virus targets specific cells in the human body, such as macrophages, generating an immune response that, while intended to eliminate the virus, can instead cause excessive inflammation and increased vascular permeability. This heightened immune response is a double-edged sword, since it not only adds to illness symptoms but also increases the risk of serious consequences such as pleural effusion and gallbladder wall thickening. These consequences indicate extensive plasma leakage, which might result in hypovolemic shock, the major cause of death in severe DHF cases.

Environmental factors increase the prevalence of DHF, especially in tropical regions with significant rainfall, which provide excellent breeding conditions for Aedes mosquitos. The interaction of the environment, mosquito vector, and host results in a dynamic and complicated epidemiological landscape for DHF. Seasonal fluctuations, particularly during the rainy season, have a substantial impact on the frequency of DHF, with transmission rates being higher during periods of increasing rainfall. This seasonality is an important issue in epidemiological surveillance and management attempts to reduce the incidence of DHF.

The landscape of Dengue Hemorrhagic Fever is shaped by the interaction of numerous elements, a disease known for its complexity and serious health consequences. Host variables, in particular, play an important role in illness outcome by regulating both infection susceptibility and disease severity. Understanding these characteristics is critical for creating targeted therapies and improving DHF management and control, particularly in areas where the illness is prevalent. As research into the complexity of DHF transmission and pathogenesis continues, a better knowledge of host variables will be critical in minimizing the disease's potential fatality.

The Transmission of Dengue Fever

The transmission of Dengue Hemorrhagic Fever (DHF) refers to how the disease spreads among communities, moving from one place to another and affecting public health on a larger scale. Understanding this mechanism is critical for developing successful disease treatment and prevention methods. In this context, we will look at the disease transmission model based on John Gordon's theory, notably the epidemiological triangle, which offers a framework for understanding the dynamics of infectious illnesses.

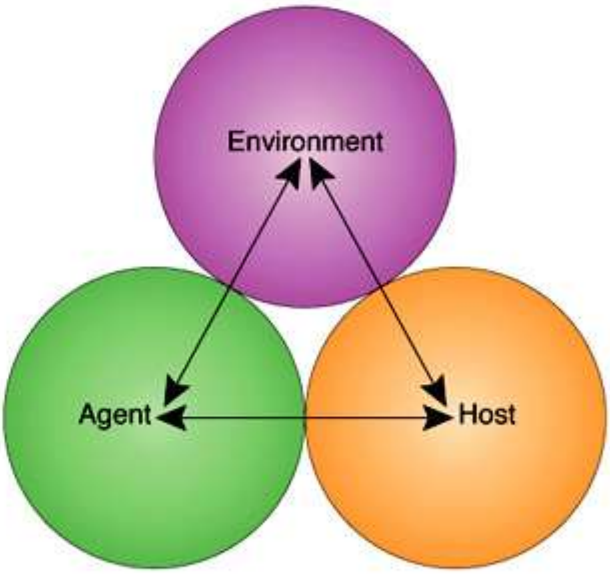

Figure I. The Connection Between Host, Agent, and Environment in DHF

Disease occurrence in humans is determined by three main factors: the host, the agent, and the environment. The formation of DHF is caused by an imbalance between the agent and the host, and this equilibrium is highly influenced by each component's distinct qualities and traits. The host, usually a person, plays an important part in the disease's course because individual susceptibility, immunological response, and demographic factors can all influence the severity and spread of the illness. The dengue virus is transmitted largely by the bites of infected Aedes mosquitos, including Aedes aegypti and Aedes albopictus.

These vectors flourish in specific environments, which can help or hinder their reproduction and transmission. The interaction between the agent and the host is intimately related to environmental factors, which include social, physical, economic, and biological aspects that determine the occurrence of DHF. For example, urbanization and population density might provide optimal breeding circumstances for mosquitos, whereas socioeconomic variables may influence access to healthcare and understanding of preventive measures.

The epidemiological triangle stresses the interdependence of the host, agent, and environment in the spread of DHF. By addressing each of these elements, public health professionals can develop effective prevention and control tactics, lowering the likelihood of outbreaks and protecting vulnerable people from the disease's severe health effects (Rajab, 2009).

The Gordon Model

The Gordon model, often known as the Epidemiological Triad, emphasizes three key ecological elements: the agent (the causal cause), the host (the human), and the environment. When these three components work together in harmony, a healthy state emerges, whereas sickness occurs when this balance is disrupted. For example, decline in environmental quality might generate conditions that allow disease organisms to easily enter the human body. Understanding the dynamic interplay is critical for effectively managing health concerns. (Chandra 2009)

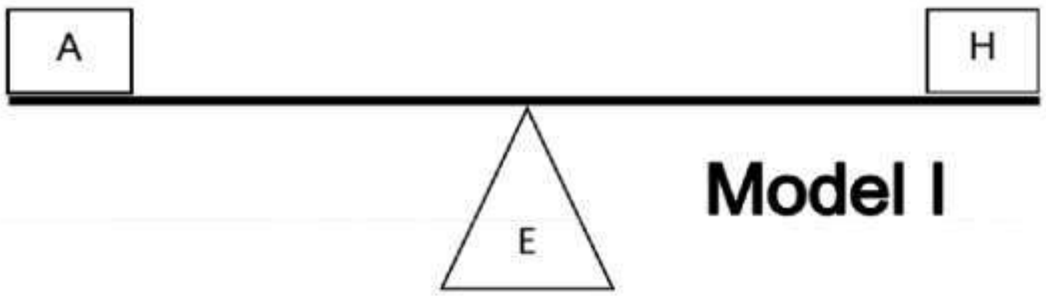

Figure 2. Model I Gordon

The host remains healthy as a result of a balanced condition created by interactions between the pathogen, the host, and the surrounding environment. This equilibrium is critical because it guarantees that the elements that contribute to health and disease are in balance, avoiding illness and allowing the host to flourish.

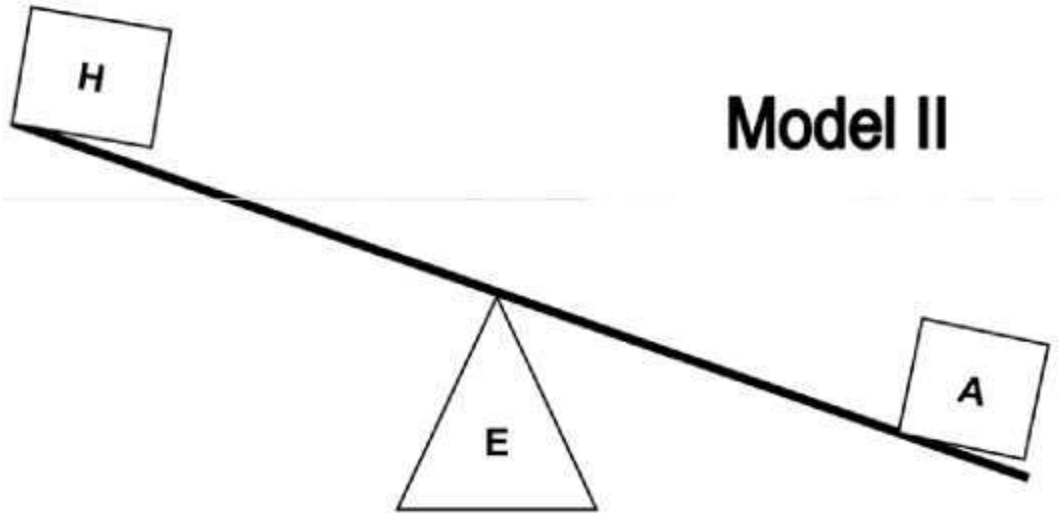

Figure 3. Model II Gordon

This depicts a scenario in which an imbalance has occurred, allowing the pathogen to grow more numerous and facilitate its potential to cause disease in the host. As a result, the host becomes unwell due to the increased pathogenicity. A notable example of this phenomena is pathogen mutation, which can boost virulence or allow it to elude the host's immunological response. Such alterations can complicate treatment efforts and increase the overall health situation, emphasizing the importance of continuous surveillance and adaptive public health interventions to reduce the consequences of new infections.

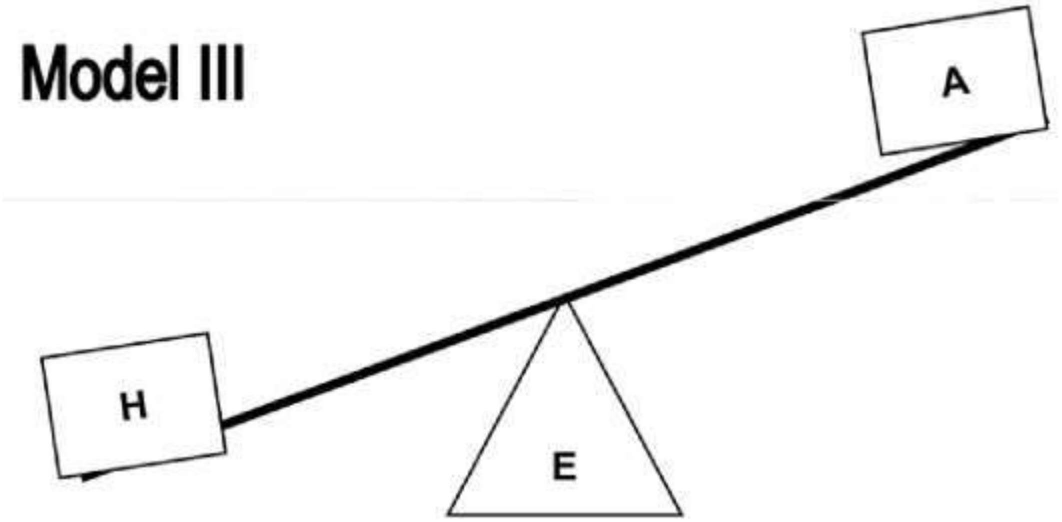

Figure 4. Model III Gordon

An imbalance has created, increasing the host's vulnerability to disease and, ultimately, resulting in illness. A significant example of this scenario is the large population of young children, who are particularly sensitive to illnesses due to their developing immune systems. This age group has a higher risk of being ill, rendering them especially vulnerable to pathogenic illnesses. Their vulnerability highlights the need for targeted public health actions to safeguard this vulnerable population from potential health risks.

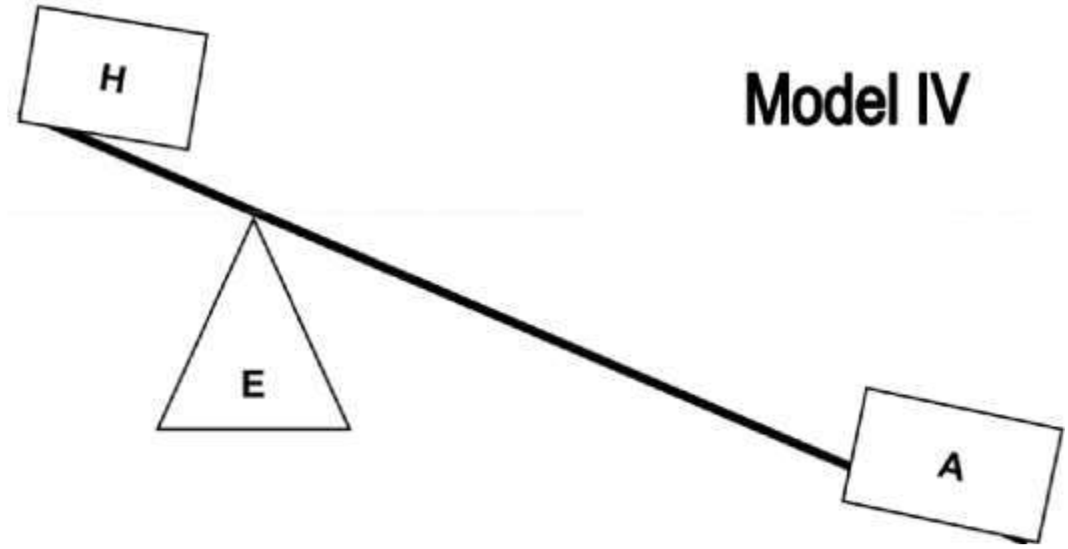

Figure 5. Model IV Gordon

Environmental alterations have emerged, allowing viruses to enter hosts and cause sickness. For example, urbanization can alter natural ecosystems, generating conditions that promote the spread of disease-carrying vectors like mosquitos. This raises the risk of diseases like malaria and dengue fever among urban residents. Furthermore, extreme weather events, such as hurricanes, can contaminate water and accelerate the spread of waterborne infections, exposing communities' increased sensitivity to new health hazards in these changing environments.

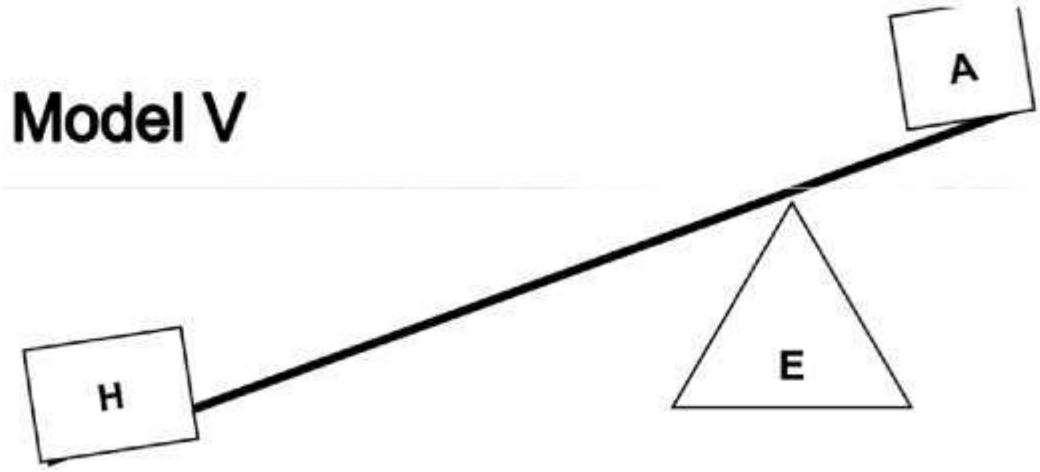

Figure 6. Model V Gordon

Recent modifications have made hosts more susceptible to infections, resulting in disease. One relevant example is the effect of inadequate nutrition, which can weaken the immune system and make people more susceptible to infection. When the body lacks vital nutrients, it becomes less effective in combating germs, increasing the risk of sickness. Furthermore, people with weakened immune systems, such as those suffering from malnutrition, are more likely to acquire serious consequences from common infections, underscoring the importance of appropriate nutrition in maintaining overall health and resilience to disease.

John Gordon used two disease transmission models, the Epidemiologic Triangle and the Gordon Model (Epidemiologic Triad), to describe how illness occurrence is impacted by three major factors: host, agent, and environment. Disease spread can occur when these three elements are out of balance. Gordon also described various interactions between these components, such as the agent promoting illness start, the host becoming more vulnerable to the agent, and environmental changes that promote disease transmission. Understanding the interactions that influence whether a person remains healthy or becomes ill is essential for effective disease prevention.

Host as a Factor Influencing Dengue Fever Transmission

Many factors contribute to the spread of dengue fever, including environmental conditions and mosquito activity, but the host's characteristics, such as age, gender, ethnicity, and genetic makeup, are equally important. These human factors have a profound impact on individual susceptibility and the disease's transmission patterns. A better knowledge of these components is required for developing focused public health interventions to effectively combat dengue fever.

Dengue fever transmission and severity are heavily influenced by host factors, particularly human features. Age, gender, race, ethnicity, anatomy, and nutritional state are all important factors influencing an individual's vulnerability to the disease. According to historical data from 1968 to 1984, children under the age of 15 were especially vulnerable, accounting for 90% of dengue cases, with a minor male-female ratio (1.34:1). However, this pattern has shifted with time, with statistics from 1999 to 2009 revealing a rise in cases among the elderly, particularly those of working age.

Gender, while marginally favoring males in previous data, does not appear to have a substantial impact on susceptibility in the present context. By 2008, the gender distribution was about equal, with men accounting for 53.78% of cases and women for 46.23%. This near parity shows that biological sex has little effect on the likelihood of developing dengue fever, making it a relatively neutral determinant in vulnerability.

Race and ethnicity are more complex variables. While there is no convincing evidence of racial vulnerability to dengue in Indonesia, cultural practices and community development levels may influence exposure and response to the virus. In some worldwide contexts, specific racial groups are more prone to various illnesses due to genetic predispositions or traditional practices, albeit such linkages to dengue fever in Indonesia are hypothetical.

Genetic factors also influence illness vulnerability. Although not directly related to dengue, genetic predispositions, such as those found in sickle cell anemia, which is more common in persons of African descent, can have an impact on an individual's overall health and immune response to viral infections. This genetic feature, while not fully understood in the context of dengue, demonstrates the broade consequences of hereditary variables on illness outcomes.

The significance of host variables in dengue transmission is critical for developing effective public health treatments. By understanding how age, gender, race, and genetics influence the spread and effect of dengue, health officials may develop ways to better protect vulnerable people, thereby lowering the frequency and severity of this prevalent disease.

Larval Surveys as a Measure of Vector Density

Increased vector density increases the risk of dengue fever transmission (WHO, Prevention and Control of Dengue Hemorrhagic Fever). Translated from WHO Regional Publication SEARO No. 29: Prevention Control of Dengue and Dengue Hemorrhagic Fever (Jakarta: Depkes RI, 2000). When observing vectors for dengue, one crucial factor to consider is vector density. Surveys are required to collect this information, and many survey methods are available, including egg surveys, larvae surveys, and mosquito surveys (Kemenkes RI, 2014). To determine vector density in a certain location, numerous randomly selected surveys, such as mosquito surveys, larval surveys, and egg trap surveys, can be conducted. This study will concentrate on larval surveys. Larval surveys involve evaluating all water sources inside and outside of one hundred residences in a certain area for the presence of larvae. Two methodologies are used in the survey.

Single Larva Method

The Single Larva Method is a targeted approach used in larval surveys to measure mosquito vector density for diseases like dengue fever. This method begins by identifying various water accumulation sites where mosquito larvae may be present. Surveyors then collect one larva from each site using a net or pipette, which minimizes disturbance to the ecosystem. The collected larva is subsequently identified in a laboratory to determine the mosquito species, a crucial step for assessing the risk of disease transmission. Each collection is documented, including the location, date, and habitat type, which contributes to a broader understanding of vector density and distribution. The data from multiple sites is analyzed to estimate overall vector density and identify hotspots for potential intervention.

Visual Method

The Visual Method is a straightforward approach used in larval surveys to assess mosquito vector density, particularly for diseases like dengue fever. This method involves inspecting water accumulation sites, such as puddles, containers, and stagnant water, to observe the presence or absence of mosquito larvae. Surveyors conduct a careful visual inspection of each site without collecting any samples, allowing them to determine whether larvae are present.

The measures used to determine larval density are as follows:

a. Free Larva Index (ABJ)

$$ABJ = \frac{\text{Number of houses/buildings without larvae}}{\text{Total number of houses/buildings inspected}} \text{ x } 100\%$$

> The Free Larva Index is one of the indicators of the success of vector control programs for dengue fever (Hairani LK. Epidemiological Description of Dengue Fever [Thesis]. Jakarta: Faculty of Public Health, University of Indonesia; 2009).

b. House Index (H.I)
HI = (Number of houses/buildings with larvae) / (Total number of houses inspected) × 100%

$$HI = \frac{\text{Number of houses/buildings with larvae}}{\text{Total number of houses inspected}} \text{ x } 100\%$$

c. Container Index (C.I)
CI = (Number of containers with larvae) / (Total number of containers inspected) × 100%

$$CI = \frac{\text{Number of containers with larvae}}{\text{Total number of containers inspected}} \text{ x } 100\%$$

d. Breteau Index (B.I)
BI = (Number of containers with positive larvae) / (100 houses inspected) × 100%

$$BI = \frac{\text{Number of containers with positive larvae}}{\text{100 houses inspected}} \text{ x } 100\%$$

The Free Larva Index and House Index better reflect the extent of mosquito distribution in an area. There is no definitive theory regarding the standard values for the Free Larva Index and House Index; they are based on consensus. It is agreed that a House Index of less than 5% is acceptable, meaning that the percentage of inspected houses with positive larvae should not exceed 5%, or conversely, 95% of the inspected houses should be negative for larvae. The House Index is a better indicator of mosquito distribution in an area.

Interaction Factors in Dengue Fever Transmission

The interaction in dengue fever (DBD) transmission refers to a scenario in which the disease agent, humans, and the environment mutually influence and amplify one another, facilitating the entry of the pathogen into the human body, both directly and indirectly (Chandra, 2007). In the Chain of Infection model, disease transmission occurs when a pathogen or agent leaves its reservoir through a portal of exit and is spread via a transmission route. The pathogen enters the body through a portal of entry and infects the host if the host is in a vulnerable condition.

The chain of etiological agents includes bacteria, viruses, worms, chemicals, or substances from animals or plants that can cause disease. The source or reservoir is the medium or habitat where pathogens or infectious agents thrive, multiply, and reproduce rapidly. Reservoirs can include humans, animals, and environmental conditions. Once the agent or pathogen leaves the reservoir, it employs a means of transmission to move to a susceptible host, either directly or indirectly. The final link in this chain is the susceptible host, typically humans or animals. If the pathogen successfully enters the host's body, illness may ensue, particularly if the host lacks immunity (Timmreck, 2005).

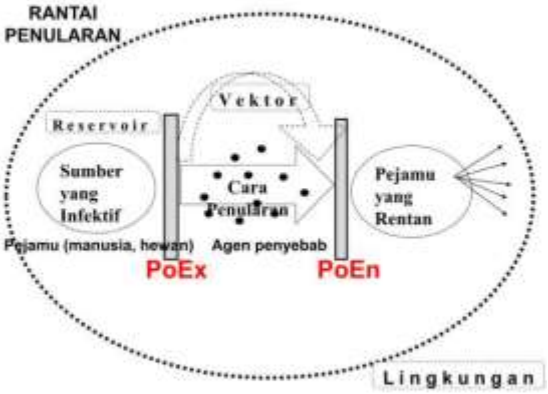

Figure 7. The Chain of DHF Transmission

Simulation Studies

Simulation Design

This study adopts a quantitative approach that combines cross-sectional studies and retrospective record reviews to investigate dengue fever (DHF) among the human population. As an epidemiological study, it is inherently multidimensional, aiming to explain practical phenomena through various dimensions and intricate causal relationships. To effectively analyze this complexity, the research employs Structural Equation Modeling (SEM) and multinomial Poisson regression. SEM serves as a comprehensive analytical tool, integrating factor analysis, multiple regression analysis, path analysis, and both exploratory and confirmatory factor analyses alongside multinomial Poisson regression (Biricik Gulseren & Kelloway, 2019; Kelloway, 2015; Skrondal, 2004).

The focus of the research is on measuring tangible factors related to the population affected by DBD to gain insights into abstract concepts, particularly latent variables that can be observed through measurable (observable) variables. Conducted between January and June 2021, the study's timeframe allows for the observation of the effects of the rainy season, typically occurring at the end of the year, on the incidence of DHF. This duration was essential for accurately identifying epidemic factors, considering the extensive area covered by the research. Set in North Sumatra, Indonesia, a region with a high endemic rate of DHF, the study highlights fluctuations in incidence rates over the years, with the province reporting significant case numbers and demonstrating a widespread presence of the disease across all districts.

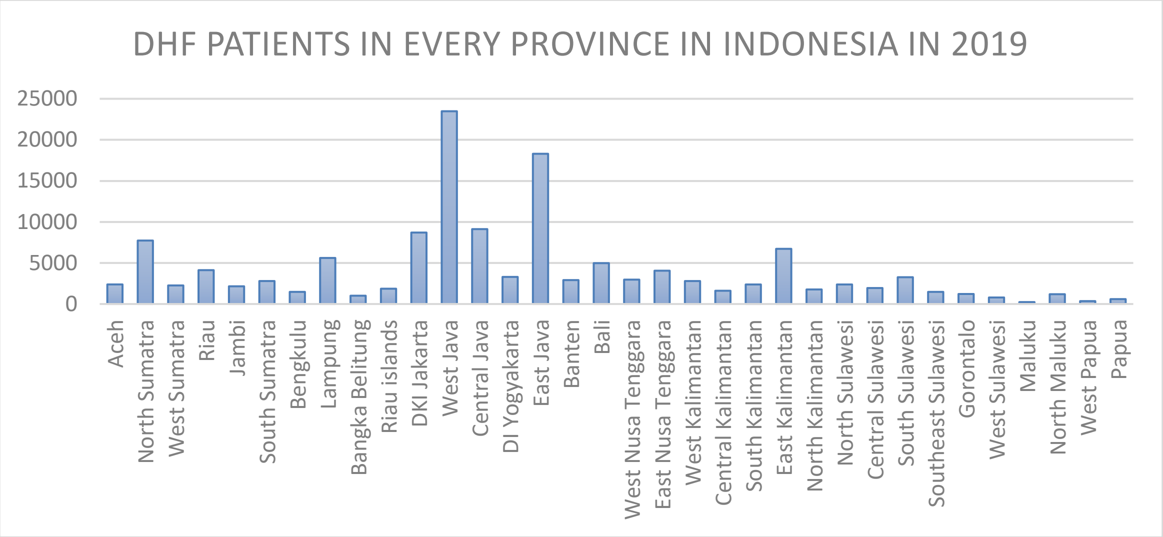

Figure 8. Diagram of the Number of Dengue Fever Cases by Province in Indonesia for the Year 2019

The source population for this research consists of all dengue fever (DBD) patients recorded in North Sumatra province in 2019, totaling 7,731 individuals. This study focuses specifically on participants from two key areas within the province: Medan city and Batubara regency, both of which experienced significant DBD outbreaks during that year. Among the affected population, 1,682 individuals were identified as participants, with 192 cases reported in Batubara and a notably higher number of 1,490 cases in Medan city. This selection of participants allows for a comprehensive analysis of the DBD incidence within these regions, providing valuable insights into the epidemiological patterns and factors influencing the spread of the disease in a densely populated area of North Sumatra.

Simulation Frame

This research was carried out in two districts/cities of North Sumatra province, specifically in Medan city and Batubara regency. For the exploratory factor analysis (EFA), a sample of 136 individuals was randomly selected from a larger research sample of 748 participants. In contrast, the confirmatory factor analysis (CFA) and structural equation modeling (SEM) utilized the full sample of 748 individuals. The detailed breakdown of the samples for this study is as follows:

No.	District/City	Number of Patients	Sample Size
1	Batubara Regency	192	192
2	Medan	1,490	556
Total		**1,560**	**748**

Simulation Sampling

The sampling method in this study is as follows: First, purposive cluster sampling was used to determine the study locations, resulting in Medan City and Batubara Regency. Second, total sampling was employed in Batubara Regency, with a sample size of 70 participants. Third, proportional random sampling was used to select participants in Medan City, yielding a sample size of 678 individuals. The sampling process involved calculating the proportion of dengue fever cases for each subdistrict in Medan using the following formula:

$$Proportion\ of\ each\ subdistrict = \frac{Number\ of\ Cases\ in\ Subdistrict}{Total\ Number\ of\ Cases\ in\ Medan\ City}$$

To calculate the number of samples for each subdistrict, the researcher used the formula:

Number of Samples for Each Subdistrict = Proportion of Each Subdistrict × 556.

Simulation of Data Analysis

The analysis of starting with descriptive statistics followed by inferential statistics. Inferential statistical analysis commenced with path analysis, leading to the development of a factor analysis model and ultimately a structural equation model (SEM) that adjusted for latent variables. Descriptive statistics provided an overview of each measurable variable, allowing for concise descriptions of the data to understand respondent characteristics. Inferential statistics focused on hypothesis testing, which included both analysis of measurement models and structural models to establish causal relationships. The SEM approach encompassed all necessary analyses and required assumptions such as adequate sample size, normality, linearity, and the absence of outliers or multicollinearity. After meeting these prerequisites, the study explored the effects and contributions of various factors on latent variables, utilizing parameters such as Lambda, Beta, and Gamma to assess direct and indirect influences. The findings were analyzed using AMOS software, with key outputs including parameter estimates, total effects, and the largest eigenvalue of the covariance matrix, all aimed at elucidating the relationships between environmental, vector, and host factors in the spread of dengue fever.

The Contribution of Host Factors to Dengue Hemorrhagic Fever Spread

In examining the spread of Dengue Hemorrhagic Fever (DHF), this study identifies four primary latent variables: Environment, Host, Vector, and DHF itself. Each variable comprises specific factors that collectively influence the dynamics of DHF transmission. The Host variable in this study encompasses several key factors that influence the spread of Dengue Hemorrhagic Fever (DHF). These factors include knowledge, which reflects the understanding of DHF symptoms and transmission methods; attitude, which pertains to how individuals perceive the disease and its risks; and behavior, which relates to the actions taken to prevent infection. Additionally, perception and motivation play crucial roles in determining how individuals respond to DHF risks. Education level, age, and profession further contribute to the host's susceptibility and response to DHF. Moreover, personal and family histories of DHF are significant, as they can shape individuals' experiences and awareness of the disease. By examining these host factors, the study aims to highlight their impact on the overall dynamics of DHF transmission and control.

Host, which is one of the factors analyzed from an economic perspective, demonstrates that income levels have a significant influence on the spread and control of Dengue Hemorrhagic Fever (DHF). The statistical distribution analysis of income data can be illustrated through the following frequency distribution table.

Table 4.1

Income Distribution Frequency

		Frequency	Percent
Valid	Low	262	35.0
	Medium	262	35.0
	High	224	29.9
	Total	748	100.0

It is known that respondents with low income account for 262 individuals or 35%, those with medium income also account for 262 individuals or 35%, while those with high income make up 224 individuals or 29.9%. From this data, it can be concluded that the majority of respondents fall into the medium and low income categories.

Table 4.2

Distribution of Frequency of Number of Dependents

		Frequency	Percent
Valid	Low	230	30.7
	Medium	425	56.8
	High	93	12.4
	Total	748	100.0

The number of respondents with a low number of dependents is 230 people, or 30.7%. Respondents with a medium number of dependents total 425 people, or 56.8%, while those with a high number of dependents amount to 93 people, or 12.4%. From this data, it is evident that the majority of respondents have a medium number of dependents, typically ranging from 4 to 6 people per family.

Host Factor

In analyzing the host factors that contribute to the spread of Dengue Hemorrhagic Fever (DHF), knowledge emerges as a critical component. Understanding the symptoms of DHF is essential not only for individual awareness but also for community health outcomes. When individuals are informed about the signs and symptoms of DHF, they are better equipped to recognize the illness early, seek medical help promptly, and take necessary precautions to prevent further transmission.

The study explores respondents' knowledge levels regarding DHF symptoms, which directly correlates with their ability to respond effectively to potential infections. Knowledge influences behaviors related to health-seeking practices, such as visiting healthcare facilities and adhering to preventive measures, including eliminating mosquito breeding sites and using protective measures like insect repellent.

To illustrate the distribution of knowledge among respondents, Table 4.3 provides a detailed breakdown of their understanding of DHF symptoms.

Tabel 4.3

Distribution of Knowledge about DHF Symptoms

		Frequency	Percent
Valid	Rendah	206	27.5
	Sedang	326	43.6
	Tinggi	216	28.9
	Total	748	100.0

It is evident that the number of respondents with low knowledge about DHF symptoms is 206, accounting for 27.5%. Those with medium knowledge comprise 326 respondents, or 43.6%, while 216 respondents, or 28.9%, have high knowledge. This data indicates that the majority of respondents possess a moderate level of understanding regarding DHF symptoms. Such knowledge is vital, as it directly influences their ability to recognize symptoms early and seek appropriate medical attention, ultimately impacting the dynamics of DHF transmission within the community.

Vector

The data analysis for mosquito population density shows a distribution with most samples falling into the medium to high categories. Specifically, 10% of the samples have a low mosquito population density, while a significant 44.8% are categorized as medium, and 45.2% fall into the high density range.

Table 4.4

Frequency Distribution of DHF Cases

		Frequency	Percent
Valid	Low	75	10.0
	Medium	335	44.8
	High	338	45.2
	Total	748	100.0

When looking at larva density, the majority of samples, about 70.2%, have a high larva density, whereas 29.8% are classified as having a medium density. This indicates a predominance of high larva density in the studied samples.

Tabel 4.5

Frequency Distribution of DHF

		Frequency	Percent
Valid	Medium	223	29.8
	High	525	70.2
	Total	748	100.0

For dengue hemorrhagic fever (DHF) cases, more than half of the samples (51.7%) are in the low severity category, 34.1% are medium, and 14.2% are high. This distribution suggests that most cases are less severe, with fewer cases being highly severe. Regarding the serotypes of the DHF virus, Den 2 is the most common, accounting for 55.1% of the cases. Den 3 is next with 29.9%, followed by Den 1 with 9.6%, and Den 4, which is the least common, with 5.3%. This distribution provides insight into the prevalence of different virus strains.

Data Analysis

This study investigates the impact of host factors on the spread of dengue hemorrhagic fever (DHF) using Structural Equation Modeling (SEM) analysis with IBM SPSS AMOS 26. The analysis process includes several stages, starting with the Measurement Model Test, which examines the relationship between indicators (host factors) and latent variables related to DHF. This integrated approach allows for the assessment of measurement error alongside hypothesis testing (Ghazali, 2014).

Validity is Assessed through Confirmatory Factor Analysis (CFA), which tests the unidimensionality, validity, and reliability of constructs that cannot be directly measured. In the context of host factors, CFA aims to identify unidimensional indicators that significantly influence the spread of DHF and to determine which host-related characteristics are most dominant in forming the underlying constructs. The correlation of each variable—both exogenous (host-related factors) and endogenous (DHF outcomes)—is analyzed through the loading factor values of each indicator. Validity in the CFA model is measured by examining the standard factor loadings for observed host factors against latent variables for first-order models and the standard structural coefficients for higher-level models.

Reliability refers to the consistency of measurements of host factors, indicating that high reliability suggests these indicators consistently measure their latent constructs related to DHF. Reliability is assessed using composite reliability and variance extracted measures. A construct is considered reliable if its Construct Reliability (CR) is ≥0.70 and its Variance Extracted (VE) is ≥0.50 (Hair et al., in Wijanto, 2008).

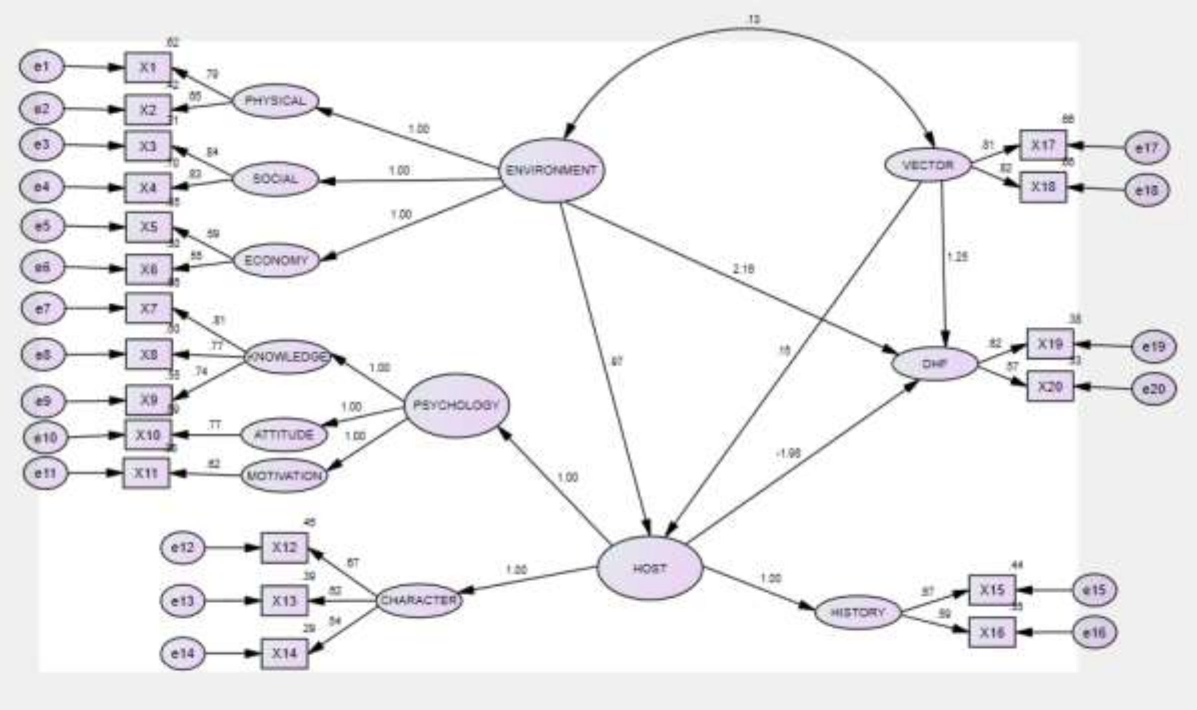

Figure 9. Measurement Model of VariablesUsing IBM SPSS Amos

The results of the measurement model estimation in Figure 4.1 were obtained using the Maximum Likelihood estimation method.

Table 4.6 Results of Construct Validity Test

Regression Weights: (Group number 1 - Default model)							
			Estimate	S.E.	C.R.	P	Label
DHF	<---	ENVIRONMENT	2.924	0.693	4.221	***	
SOCIAL	<---	ENVIRONMENT	1.221	0.076	16.048	***	

ECONOMY	<---	ENVIRONMENT	1				
PHYSICAL	<---	ENVIRONMENT	0.946	0.068	13.823	***	
DHF	<---	HOST	-2.799	0.721	-3.882	***	
PSYCHOLOGY	<---	HOST	0.917	0.058	15.699	***	
CHARACTER	<---	HOST	1.138	0.082	13.809	***	
HISTORY	<---	HOST	1				
HOST	<---	VECTOR	0.088	0.012	7.497	***	
DHF	<---	VECTOR	1				
MOTIVATION	<---	PSYCHOLOGY	1				
ATTITUDE	<---	PSYCHOLOGY	1.271	0.072	17.541	***	
KNOWLEDGE	<---	PSYCHOLOGY	1.691	0.099	17.076	***	
X1	<---	PHYSICAL	1.223	0.065	18.696	***	
X2	<---	PHYSICAL	1				
X3	<---	SOCIAL	1.013	0.035	28.638	***	
X4	<---	SOCIAL	1				
X5	<---	ECONOMY	0.963	0.074	13.011	***	
X6	<---	ECONOMY	1				
X7	<---	KNOWLEDGE	1.188	0.052	23.001	***	
X8	<---	KNOWLEDGE	1.082	0.05	21.737	***	
X9	<---	KNOWLEDGE	1				
X10	<---	ATTITUDE	1				
X11	<---	MOTIVATION	1				
X12	<---	CHARACTER	1.324	0.095	13.879	***	
X13	<---	CHARACTER	1.219	0.092	13.234	***	
X14	<---	CHARACTER	1				
X15	<---	HISTORY	1				
X16	<---	HISTORY	0.877	0.058	15.048	***	
X17	<---	VECTOR	1				
X18	<---	VECTOR	0.905	0.046	19.596	***	
X19	<---	DHF	1				
X20	<---	DHF	0.955	0.074	12.952	***	

The construct validity test is conducted to ensure that the dimensions of the constructs of the latent variables under study are valid. From Table 4.6 above, it is indicated that all dimensions within the exogenous variables, specifically indicators X1-X20, have a CR value greater than +2.58. Therefore, all indicators within the exogenous variables meet the validity assumption.

Based on the analysis, the latent variables, including Host, have met the requirements for validity and reliability testing.

Structural Model Fit Test and Model Assessment

Table 4.7 Results of Normality Assessment (Normality Test)

Assessment of normality (Group number 1)			
Variable	min	max	skew
Knowledge	1	3	0.069
Attitude	1	2	-0.314
Motivation	1	2	0.513
Physical	1	2	-0.154
Social	1	2	0.171
Economy	1	3	0.291
X20	1	4	-0.062
X19	1	3	0.182
X18	1	3	-0.914
X17	1	3	-0.293
Character	1	3	0.295
History	1	3	0.135

Based on the calculations in Table 4.7, all indicator skewness values are below ± 2.58. The data from these indicators are normally distributed and suitable for use.

Table 4.8. Resuts of the Good Fit Model

GOF Index	***Cut-Off Value***	**Output**	**Keterangan**
Probability	p > 0,05	0.476	**Fit**
RMSEA	RMSEA ≤ 0,08	0.001	**Fit**
RMR	RMR < 0,08	0.007	**Fit**
GFI	GFI ≥ 0,9	0.994	**Fit**
AGFI	AGFI ≥ 0,8	0.983	**Fit**
CMIN/DF	CMIN/DF ≤ 2	0.992	**Fit**
TLI	TLI ≥ 0,95	1.000	**Fit**
CFI	CFI ≥ 0.95	1.000	**Fit**
IFI	IFI ≥ 0.90	1.000	**Fit**

The interpretation of Table 4.8 reveals that the model exhibits a good fit based on several criteria. The Probability value of 0.476 indicates model fit since it exceeds the threshold of 0.05. Additionally, the RMSEA value of 0.001 suggests a good fit, as it is less than the acceptable limit of 0.08. The GFI value is 0.994, which signifies a strong model fit, given that it is well above the 0.9 benchmark. Furthermore, the CMIN/DF ratio is 0.992, indicating a good fit as it is below the 2.00 threshold.

The Tucker Lewis Index (TLI) shows a value of 1.0, which meets the recommended acceptance level of 0.95, affirming the model's fit. The Comparative Fit Index (CFI) also achieves a perfect score of 1.0, indicating an excellent fit that is not affected by sample size. Lastly, the Incremental Fit Index (IFI) of 0.997 further supports the model's good fit since it exceeds the minimum acceptable value of 0.9. Overall, with all nine criteria indicating a model fit, it can be concluded that the structural model in this study is a good fit.

The Influence of Latent Variables on the Vector

The analysis from Table 4.13 indicates several significant effects. First, there is a notable positive influence of the Environment (X) on the Vector, with a p-value of 0.044, suggesting that Environment increases the Vector by 9.8%, thus accepting hypothesis H1. Similarly, Environment positively affects the Host, with a p-value of 0.001 and an estimate of 74.7%, leading to the acceptance of hypothesis H3. Additionally, the Environment has a positive influence on Dengue Hemorrhagic Fever (DHF), shown by a p-value of 0.023 and an increase of 38.5%, validating hypothesis H5.

The Host also significantly influences Psychology, as indicated by a p-value of 0.001 and an estimate of 1.075, which accepts hypothesis H2. However, the Host's influence on DHF is significant and negative, with a p-value of 0.033 indicating a reduction of 42.7%, accepting hypothesis H4. Furthermore, the Vector positively influences the Host with a p-value of 0.032, resulting in a 2.9% increase, thus validating hypothesis H4. Finally, the Vector has a significant positive effect on DHF, with a p-value of 0.001 and an increase of 88.9%, accepting hypothesis H7.

Moreover, the SEM method highlights its capability to identify indirect effects between exogenous and endogenous constructs not directly connected, illustrating the complexity of relationships in this research model.

The Influence of Hosts on the Spread of Dengue Fever in North Sumatra

Analysis indicates that hosts significantly impact the spread of dengue fever in North Sumatra, demonstrating that the condition of the host can have a tangible and strong effect on the disease's dissemination. In this context, a host refers to organisms, typically humans or animals, that serve as carriers of the disease. The study specifically focuses on human respondents, assessing their psychological conditions, including knowledge of dengue, attitudes towards prevention, and motivation for seeking information about the disease. It also considers respondent characteristics such as education, age, occupation, and personal or family history related to dengue.

The findings reveal that respondents possess a moderate understanding of dengue transmission, with 18.4% categorized as having low knowledge, 50.4% as moderate, and 28.9% as high. This knowledge varies among individuals, shaped by their learning experiences, which can influence their ability to evaluate and apply prevention strategies effectively. A lack of awareness regarding dengue significantly impacts health management within families, hindering their capacity to recognize and mitigate health threats.

Higher levels of knowledge correlate with better acceptance of preventive measures, such as the 3M Plus strategy (draining, covering, and burying), essential for controlling dengue cases. In contrast, individuals with low awareness are less likely to take preventative actions, potentially allowing the disease to spread more widely.

Educational background also plays a crucial role, with most respondents having completed secondary education. A higher educational level facilitates the absorption of health-related information, improving preventive decision-making. Educated individuals are more likely to engage in proactive measures, have better health status, and respond effectively to health issues. This suggests that increasing public knowledge can positively affect health outcomes.

Dengue fever can affect anyone, regardless of status, as evidenced by the study showing that most respondents previously infected with dengue had good knowledge about the disease. However, possessing knowledge does not guarantee immediate and appropriate actions; there can be a disconnect between understanding and behavior. A strong sense of awareness, combined with knowledge, is essential for effective prevention.

The behaviors observed among respondents included regular cleaning of bathrooms, not leaving clothes hanging indoors, using mosquito repellents, and taking precautions with water storage. Additionally, respondents were proactive in seeking medical care for family members showing dengue symptoms and reporting cases to community health workers.

Awareness and early intervention are vital to prevent the widespread outbreak of dengue. Government attention is necessary to manage the endemic nature of the disease across various regions, aiming to minimize occurrences. Community participation and governmental support are essential for the eradication and prevention of dengue, reinforcing that knowledge should be accompanied by a high level of awareness to optimize public health efforts.

The actions taken by individuals can greatly influence their environment, necessitating consistent and sustainable community efforts to combat the spread of Aedes aegypti mosquitoes and dengue fever. Overall, a community-driven approach to regular preventive measures can significantly reduce dengue transmission risks.

The Influence of Hosts on the Spread of Dengue Fever in North Sumatra

The study on the factors influencing the spread of dengue fever (DBD) in North Sumatra identifies three main components: environment, host, and vector. The findings reveal that these factors significantly affect the transmission of DBD. The model of interaction indicates that the host conditions in North Sumatra are moderate, with the community exhibiting average levels of education and knowledge regarding DBD transmission and prevention. This moderate understanding helps keep the spread of DBD relatively low. However, the environmental conditions, both inside and outside the homes, are not ideal, which poses challenges.

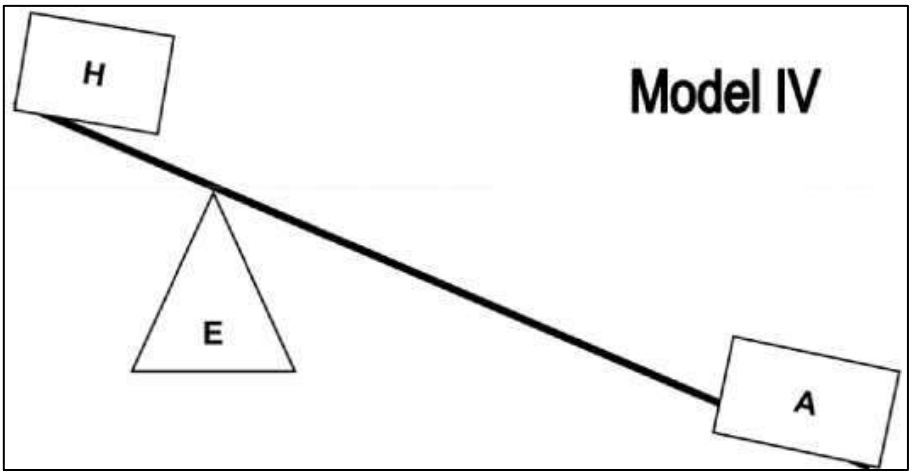

Figure 10. Model Interaction Diagram

Disussion

Based on the research findings, several important conclusions emerge regarding the impact of host factors on the spread of dengue hemorrhagic fever (DHF) in North Sumatra Province.

First and foremost, host factors significantly influence the transmission of DBD. The study reveals that the knowledge, attitudes, and actions of individuals play a crucial role in shaping the dynamics of dengue transmission. High levels of awareness about the disease can effectively mitigate its spread. When the community possesses a solid understanding of transmission methods and prevention strategies, the risk of dengue outbreaks diminishes significantly.

Additionally, environmental conditions in the region have a noteworthy impact on DBD transmission. The findings indicate that the physical environment—both inside and outside homes—falls into a less favorable category. Poor environmental conditions can facilitate the spread of the disease, highlighting the necessity for better management of living spaces. The surrounding environment profoundly influences the incidence of DBD, underscoring the need for community-level interventions aimed at improvement.

Furthermore, the role of vector factors cannot be overlooked. The study underscores that the proliferation of mosquitoes, the primary carriers of dengue, is a critical determinant of transmission levels. Effective vector management strategies are essential in controlling the incidence of DBD, as the health of the community is closely tied to the presence and breeding habits of these insects.

In light of these findings, it is imperative for the community to take proactive measures in enhancing their environmental conditions. Efforts should focus on creating healthier living spaces through regular maintenance and improvement of homes, which can significantly reduce the risk of dengue transmission.

Moreover, government initiatives are vital in providing support and guidance to communities facing challenges related to their environment. By promoting education on dengue prevention and effective environmental management, authorities can empower individuals to take control of their health and reduce the burden of this disease.

Finally, addressing host variables, improving environmental conditions, and managing vector populations are key steps in slowing the spread of dengue hemorrhagic fever in North Sumatra Province. We can reduce the incidence of this disease and improve public health outcomes for the population by putting community and government suggestions into action.

Declaration of conflicting interests

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

Funding

The author(s) received no financial support for the research, authorship, and/or publication of this article.

Reference

[1] Chandra, B., 2007. Pengantar Kesehatan Lingkungan P Widyastuti, ed., Jakarta: EGC.

[2] Chandra, P.K. (2009) Aboriginal Uses and Management of Ethnobotanical Species in Deciduous Forests of Chhattisgarh State in India. Journal of Ethnobiology and Ethno Medicine, 5, 1-9.

[3] Rajab, W. 2009. Buku Ajar Epidemiologi untuk Mahasiswa Kebidanan: Jakarta. Penerbit Buku Kedokteran EGC

[4] Timmreck, TC, 2005, Epidemiologi Suatu Pengantar Edisi 2, EGC, Jakarta

[5] Wijanto, S.H. 2008. Structural Equation Modeling dengan LISREL 8.80: Konsep dan Tutorial. Yogyakarta: Graha Ilmu..