Chapter 1

Introduction

1.1 Background

Dengue is an infectious disease transmitted by *Aedes aegypti* mosquitoes, specifically caused by the dengue virus (DENV), which is classified as a single-stranded RNA virus belonging to the Flaviviridae family and the Flavivirus genus. DENV comprises four unique serotypes (DENV-1 to DENV-4). An infection with one serotype provides lifelong immunity to that specific type but only short-term protection against the others. The presence of partial immunity heightens the risk of severe illness in subsequent infections through a process known as antibody-dependent enhancement (ADE) (Kularatne & Dalugama, 2022; Steindorf et al., 2022).

Dengue infections cause a wide range of clinical symptoms, from mild fever to severe illnesses, such as dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS). Evidence suggests that severe symptoms are highly related to primary infections involving distinct serotypes, highlighting the need for serotype-specific research in predicting disease severity (Shih et al., 2024; Narvaez et al., 2024). This situation renders dengue a significant public health concern globally, particularly in tropical and subtropical regions (Wang et al., 2020; WHO, 2024).

Dengue fever has been an endemic problem in Indonesia since it was first reported back in the 1960s. The country consistently recorded one of the highest case rates with all four of its serotypes (Mamenun et al., 2024). Based on a statistical study conducted by Malavige et al. (2023), dengue outbreaks have been observed to have a "three-year cycle," in which every 3 years the cases and deaths increase significantly. For instance, in 2019, there were 138,127 cases and another surge after three years to 143,000 cases.

North Sulawesi is among the provinces that are most affected by dengue in Indonesia. Over the past five years, it has reported persistent issues with 6,130 cases and 74 deaths. The incidence rate in Manado, North Sulawesi, is notably high, positioning it 6th out of 34 Indonesian provinces, with an incidence rate of nearly 95 per 100,000 population and a case fatality rate of about 1.13%, which shows that it exceeds the national goal to keep it low (Tampang, et al., 2022).

It is crucial to identify the dominant serotype during an endemic period, as individuals who have not previously been infected with that specific serotype may have an increased risk of developing a severe disease, particularly severe outcomes associated with secondary infections (Masyeni et al., 2023). This underscores the critical importance of evaluating the impact of dominant serotypes on clinical manifestations, directing public health initiatives aimed at managing transmission of dengue in Manado, and providing insights into serotype distribution.

1.2 Objective

The main objectives of this study are to determine the prevalence of dengue virus serotypes in Manado, Indonesia, and analyze their serotype distribution. This study also aims to assess the relationship between various dengue serotypes and clinical symptoms in infected patients. The findings will contribute to improving surveillance of dengue virus transmission and aid public health efforts in controlling dengue as a public health problem.

1.3 Hypothesis

1. Prevalence Hypothesis:

The prevalent dengue virus serotype in Manado is predicted to be DENV-3, similar to its predominance during the 2019 outbreak.

2. Clinical Hypothesis:

Different serotypes of the dengue virus are associated with certain clinical symptoms.