

Chapter 1: Introduction

1.1 Background

Dengue is a mosquito-borne infectious disease caused by the dengue virus. Dengue virus is transmitted by both *Aedes aegypti* and *Aedes albopictus* female mosquitoes, the primary and secondary vectors of this disease respectively (Chen & Vasilakis, 2011). The transmission cycle of dengue virus is maintained by the vector mosquitoes and the human amplifier. As with most mosquito-borne diseases, dengue is particularly prevalent in tropical and subtropical areas. Among mosquito-borne viral diseases in the world, Dengue is the fastest spreading, exceeding 100 million cases every year (World Health Organization, 2009). A later study by Bhatt et al. suggests that Dengue cases exceed 390 million humans worldwide annually, more than triple the 2009 estimate provided by the WHO (2013). All dengue virus serotypes, namely DENV-1, DENV-2, DENV-3, and DENV-4, are capable of infecting and causing dengue. Symptoms may range from fever, rashes, and aches during dengue, to dehydration, shock, and organ failure during severe dengue (Heilman et al., 2014; World Health Organization, 2009). There are no available treatments specifically for Dengue virus. Patients suffering from dengue are given supportive care such as antipyretics and rehydration (World Health Organization, 2009).

Dengue, being classified as an NTD, most of the recorded case came from the tropics and came from the lesser developed countries, with rainfall, temperature, urbanisation, and lack of sanitary standards being some of the biggest contributing factors for the spread of the disease (Bhatt et al., 2013, World Health Organization, 2009). Dengue is a major health issue in Indonesia, being among the largest dengue-endemic countries in the world (Haryanto, 2018). Ever since its first reported case in Indonesia as an outbreak in Surabaya and Jakarta in 1968, cases in Indonesia has been steadily increasing (Hotta, Aoki, Samoto, Yasui, & Noerjasin, 1968). Dengue is reported in all provinces in Indonesia year-round and major

outbreaks are common (Graham et al., 1999; Nusa et al., 2014; Sasmono et al., 2019; Suswandono et al., 2006).

All dengue virus serotypes are found in Indonesia (Sasmono et al., 2018; Sasmono et al., 2019). Each serotype is then further divided into numerous genotypes, each of them spread in various regions (Chen & Vasilakis, 2011). Different regions may be predominated with different serotype(s) and genotype(s). Serotypes and genotypes at a specific region can also change on different time points. These changes/shifts may be associated with the severity of the disease and specific outbreaks, thus dengue surveillance or monitoring is crucial to understand the viral dynamics in Indonesia (Graham et al., 1999; Nusa et al., 2014; Sasmono et al., 2018; Sasmono et al., 2019; Suswandono et al., 2006).

Pasuruan is located 60 km southwest of Surabaya. Pasuruan has a large number of dengue cases and cases have been increasing steadily (Dinas Kesehatan Provinsi Jawa Timur, 2015; Dinas Kesehatan Provinsi Jawa Timur, 2016). In addition, Pasuruan has among the highest mortality due to dengue and the region is particularly prone to get infected by dengue virus (Haryanto, 2018). Despite the increasing number of incidences in the Pasuruan, molecular data is lacking, and therefore monitoring serotypic and genotypic shifts in this region is not possible. This study will provide molecular data from Pasuruan isolates, determining serotypes and genotypes that are predominant in Pasuruan.

1.2 Objective

This study determines which antigenically distinct serotypes and genotypes are predominant in Pasuruan.