CHAPTER 1

INTRODUCTION

1.1 Problem Background

The rapid rise in bacterial resistance towards most antibiotics has become a global threat. The evolution of antibiotics runs parallel with the development of this resistance, reducing their efficacy significantly. This phenomenon is a result of two major factors which are the lack of development and inappropriate use of antibiotics. Lack of regulation causes the exploitation of antibiotics. They are cheap and excessively accessible leading to overuse. This inconsiderate consumption of antibiotics in many countries causes the survival of resistant bacteria and allowing them to inherit their resistance gene or pass it on via horizontal gene transfer (Ventola, 2015).

Staphylococcus aureus is one of the most common antibiotic resistant bacteria, causing 11,285 deaths in the United States alone (Ventola, 2015). In 2010, 28% of hospitals in Indonesia and Hongkong, and 70% in Korea had reports of Methicillin-Resistant *Staphylococcus aureus* (MRSA) (Chen & Huang, 2014). Another study assessed the prevalence of MRSA in between the period of 2010-2014 in Dr. Saiful Anwar General Hospital Malang. Their studies revealed that out of 772 *Staphylococcus aureus*, 38.2% were MRSA. Moreover, between the years 2010-2014, the incidence of MRSA was highest in 2012 with 45.3% (Erikawati, Santosaningsih, & Santoso, 2016). This resistance has even worsened in which new strains of resistance such as Vancomycin-*resistant S. aureus* (VRSA) has also now been reported (Dulger & Dulger, 2014). Due to their elevated morbidity and mortality rate, WHO has considered Methicillin-resistant and Vancomycin-resistant *Staphylococcus aureus* as a high priority. Therefore, an antibiotic with distinct mode of action that is effective towards these bacteria must be identified (WHO, 2015).

The emergence of antibiotic resistance bacteria has shifted much attention to the use of natural resources as a source of novel antibiotics. Natural resources hold infinite amount unexplored sources for pharmacological substances ranging from antiviral, anticancer, anti-inflammatory and

antibacterial potentially with much higher efficacy, abundance, and safety. With the current knowledge and technological advancements, structural modifications or even novel chemical entities could be identified from natural resources and be the key to countering this resistance (Karnchanatat, 2012).

Marine biodiversity is often overlooked when compared to terrestrial diversity. The fact is that the ocean is a habitat for more than 5 million species of living organism, accounting for 30 phyla as opposed to 17 phyla from land. Also, marine organisms offer metabolites that differ structurally from the terrestrial organism in which most antibiotics are based (Doshi, Aggarwal, Martis, & Shanbhag, 2011). Marine organisms develop multiple metabolites which are a result of evolution and adaptations against harsh conditions including environmental and biological pressures such as competition for space from other organisms. Consequently, these metabolites have pharmacological activities including anti-cancer, antimicrobial, antifungal, antiviral and anti-inflammatory (Pérez, Falqué, & Domínguez, 2016). Among these marine organisms, algae represent one of the highest diversity which makes up approximately 30,000 to a million species; with brown algae accounting for 1792 of those species (Guiry, 2012). Brown algae have high potential as an antibacterial agent. Aside from their abundance, they belong to a taxonomically diverse group and possess multiple metabolites responsible for pharmacological activities. It was reported that brown algae contain secondary metabolites with potent antimicrobial activity (Stengel & Connan, 2015).

Sung-Hwan Eom carried out research in which they assessed the antimicrobial activity of different extracts of Brown algae (*Eisenia bicyclis*) against *Staphylococcus aureus* (Eom *et al*., 2011). Amel Ismail *et al*. assessed the antibacterial activity of *Padica pavonica* species of brown algae against 12 species of pathogenic bacteria including *Staphylococcus aureus* (Amel Ismail *et al*., 2016). Sarah Saleh Abdu-llah Al-Saif *et al*. compared the antibacterial capacity of different extracts of marine algae against different strains of bacteria including *Staphylococcus aureus* (Al-Saif, Abdel-Raouf, El-Wazanani, & Aref, 2013). All of these experiments exhibited that brown algae showed high antibiotic activity against *Staphylococcus aureus*.

More than 150 species of marine algae have been reported to have antibacterial activity towards multiple pathogenic bacteria. However, it is important to note that different algae offer different antibiotic capabilities. In fact, the antibacterial activity of each alga is dependent on their species, location, season, growing conditions and equally important, the extraction methods (Al-Saif, Abdel-Raouf, El-Wazanani, & Aref, 2013; Rajasulochana, Dhamotharan, Krishnamoorthy, & Murugesan, 2009). Furthermore, to fully understand the potential of brown algae, it is also essential to assess the mechanism of action by which they work. Some of the possible mechanisms of action include inhibition of biofilm formation, oxidative phosphorylation, increase in membrane permeability, protein leakage and binding to DNA (He, Yang, Yang, & Yu, 2010). Therefore, this project aims to assess whether brown algae from Pari Island, Indonesia has the antibacterial potency towards *Staphylococcus aureus*.

1.2 Hypothesis

Brown algae *Sargassum* species posses antibacterial activity towards *Staphylococcus aureus*

1.3 Research Objective

- Investigation of antimicrobial activity of brown algae from Pari Island, Indonesia
- Perform multiple extraction techniques on crude extract of brown algae in order to identify the most optimal condition for their antibacterial activity
- Assess antibacterial activity of each extraction methods by performing disc-diffusion assay against *Staphylococcus aureus*

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