CHAPTER I

INTRODUCTION

I.1 Background

Indonesia belongs to the tropics and is one of the countries with high level of biodiversity. This nation has various plants of biological origins that can be used as traditional medicinal ingredients and a ripe discover for a novel compound. There is a favorable association between collected knowledge and the capacity to identify new medication in all other therapeutic domains. Antibiotics are chemotherapeutic drugs used to treat bacterial illnesses clinically since the 1940s. Antibiotics attacks bacterial physiology and biochemistry, causing a cell to dead or halting its expansion. Most of the antibiotics on the market right now are usually generated through microbial fermentation or semi-synthetic approach by employing the existing antibiotic backbone structure, modifying the existing scaffolds (Sengupta et al., 2013). Historically, most scaffolds originated from the Waksman platform. Antimicrobials have made a lasting impact on human and even animal wellbeing.

Unfortunately, Antimicrobial Resistance (AMR) has been spreading. The increase in drug-resistant pathogens is a result from multiple factors, including but not limited to high rates of antimicrobial prescriptions, antibiotics mismanagement in the form of sold-medication, or interruption of therapy (da Cunha et al., 2019). Simultaneously, the number of new compounds in antiinfection screening is decreasing. Unexploited fungus and bacteria genera became the promise for new chemicals with a fundamental structure and various mode of action. Secondary metabolite new compounds with varied structures are known to be produced by fungi or natural sources. Antimicrobial Resistance (AMR), predicted to cause ten million annual deaths by drug-resistance infectious by 2050, has emerged and is currently growing, endangering this advancement (Booton et al., 2021).

To find new sources of plant drugs, number of plants has been screened for wide range of biological activity in various research institutions. Plant-based antimicrobials represent a vast untapped source for medicines by possessing enormous therapeutic potential. They are effective in treating infectious diseases while simultaneously mitigating many of the side effects often associated with synthetic antimicrobials (Paritala et al., 2015).

Varieties of secondary metabolites have antibacterial or antifungal actions (Liu et al., 2017). The complex structures of microbial secondary metabolites encompass practically all functional groups in organic chemistry and are usually inaccessible by synthetic libraries and other approaches. Antimicrobial activities of plant constituents such as phenol, quinines, flavones, flavonoids, tannins, terpenoids, essential oils and alkaloids have been reported by several authors (Valentin Bhimba et al., 2010). The genus Aglaia is a rich source of compounds of different kinds with often interesting biological activities such as bisamides, lignans, aromatic derivatives of the benzofuran series, and tetracyclic triterpenes (Hutagaol et al., 2021).

The genus of Aglaia has been known as a rich compound of different kinds with often interesting biological activities. Bisamides, lignans, aromatic derivatives of benzofuran series and tetracyclic triterpenes have known to be found as interesting biological activities in the genus Aglaia (Hutagaol et al., 2021). Silvestrol is a natural compound of the rocaglate family that can be isolated from the plan Aglaia foveolata. Silvestrol is also known to exhibits anti-tumor activity in many pre-clinical models without showing significant toxic side effects (Elgner et al., 2018). Aglaia foveolata is described as a highly efficient, non-toxic, and specific inhibitor of the DEAD-box RNA helicase elF4A, a eukaryotic initiator factor 4A that functions as a subunit of the initiation factor complex elF4F, which mediates the binding of mRNA to the ribosome (Todt et al., 2018).

As a result, antiinfection screening was performed. Aglaia foveolata bark was isolated in order to get a pure compound. Multidrug Resistance (MDR) are tested against the extract to find new peaks of action by using the Minimum Bactericidal

Concentration (MBC) and Minimum Inhibitory Concentration (MIC). From the MBC and MIC carried, the extract showed which fractions has antibacterial activity against the pure extract. The pure compound was analyzed using Liquid Chromatography High Resolution Mass Spectroscopy (LC-HRMS), 1D-NMR, 2D-NMR, FTIR, and UV-Vis Spectrophotometry then compared to the current public database for already existing compounds.

I.2 Research Purposes

This research has a purpose to isolate secondary metabolite from the bark of *Aglaia foveolata*; to identify the bioactivity of the isolated secondary metabolite from the bark of *Aglaia foveolata* against *Klebsiella pneumoniae* MDR, *Pseudomonas aeruginosa* MDR, *Staphylococcus aureus* MDR, *Bacillus subtilis* MDR, and *Escherichia coli* MDR; and to obtain the structure elucidation of the pure compound with active antibacterial agent.

I.3 Research Benefits

This research expected to provide information about the secondary metabolite from the bark of *Aglaia foveolata* isolated along with its bioactivity against the MDR bacteria, which in this research were *Klebsiella pneumoniae* MDR, *Pseudomonas aeruginosa* MDR, *Staphylococcus aureus* MDR, *Bacillus subtilis* MDR, and *Escherichia coli* MDR. This research is also expected to provide insight into the future research regarding secondary metabolite isolations.