Chapter 1

Introduction

1.1 Introduction

In the majority of human history, acquiring bacterial infections are deadly. This was the case in the black death, a disease caused by *Yersinia pestis*, which saw total mortality rates up to 41%, with infant deaths making the largest contribution at about 30% in France alone (Benedictow & Benedictow, 2004); and the 1831-1866 cholera epidemics of Europe. The epidemics were significant; a death toll of 605 within four months of December 1848 in the city of Bergen in Norway (Oending, 1992) was found, while the disease was also known to have killed as much as a million people between 1847 and 1851 in the entirety of Russia (Hosking, 2001). These statistics are most likely because once bacteria, or any other infectious agents for that matter, penetrate the immune system enough to cause symptoms; the human host must adapt to survive, often without the help of effective, selective drugs. It is therefore of no surprise that infections are a major cause of death in the pre-antibiotics age (Zaffiri, Gardner & Toledo-Pereyra, 2012). The discovery and subsequent usage of antibiotics led to the marked decline of fatalities caused by infections. However, it also brings with it the advent of antimicrobial resistance; this problem was noticed as early as the 1940s when penicillin resistance was first described in *Escherichia coli* species (Abraham & Chain, 1940). In Europe, an estimated 33,000 people were killed as a result of antibiotic-resistant bacterial infection. 39% of the death toll is estimated to result from infections of bacteria resistant to last-line antibiotics such as carbapenem and colistin (European Centre for Disease Prevention and Control, 2018). The presence of antimicrobial resistance, coupled with the unceasing demands for better and more effective

antimicrobial agents, means that the discipline of drug discovery is a flexible one, and also one that requires a very large “net” for identifying antibiotic candidates on various natural sources.

The discovery and use of antibiotics is a modern approach to curing infectious diseases while the use of natural products, such as herbs and mushrooms to combat infectious diseases, is ancient. One of the earliest evidence of herbal medicine was found in a mummy preserved from 5300 years ago from Tyrol, Italy, where they found *Piptoporus betulinus* among his corpse, which is a fungus that has laxative and antibiotic activity against mycobacteria while simultaneously toxic to metazoans as well (Capasso, 1998). Natural medicine employs sophisticated recipes used to treat various ailments centered on plants, with the earliest records coming from the Mesopotamia region at around 2600 BC, which makes use of about 1000 substances derived from plants (Newman, Cragg &Snader, 2000). Herbs are therefore an obvious source to develop new antimicrobials, as attempts to isolate active antimicrobial components are more likely to be successful on already tried-and-tested plant sources that demonstrate antimicrobial activity.

Laportea decumana is a member of the*Urticaceae* family. As their name suggests, most members of this family possess urticating, or stinging hairs on their bodies, which serves to defend themselves against herbivores. *Laportea decumana* is relatively known locally in Maluku, Papuan province, and in Papua New Guinea as an anti-inflammatory agent and effective painkiller. A preliminary study conducted by Simaremare (2014) indicated the presence of alkaloids, glycosides, and steroids in *Laportea decumana*. There has also been a recent study on *Laportea decumana* on its purported antimicrobial activity conducted by Simaremare et al (2020), stating both the activity of Laporteadecumana against *Escherichia coli* and *Staphylococcus aureus*; and the toxicity of the polar, semi-polar, and non-polar fraction of *Laportea decumana*. This is the first study about *Laportea*

decumana antimicrobial activity, and no further studies were found that could corroborate this result yet. However, *Laportea aestuans* which coexist in the same habitat with the *Laportea decumana* species has recently been validated to contain significant antimicrobial activity; it has shown significant activity at 50-200 mg/mL when tested in agar diffusion assays against *Klebsiella pneumoniae, Salmonella typhi, Candida albicans, Rhizopus stolon,* and *Aspergillus niger* (Oloyede, 2016). A review on its genetic relatives could therefore be constructed to provide more data that would help support this result, by identifying antimicrobial activity and possible biochemicals on *Laportea aestuans* and *Laportea crenulata*. The data can then be used to point out the possible biochemicals or activity against certain bacteria that can also be present on *Laportea decumana* owing to its genetic similarity, hence supplementing lacking data on the *Laportea decumana* antimicrobial activity

1.2 Objectives

The objective of this study is to systematically review the possibility of antimicrobial activity against pathogenic bacteria from different solvent polarities of *Laportea decumana* plant extract, by way of a direct search on *Laportea decumana* antimicrobial activity and inference on its genetic relatives which are *Laportea aestuans* and *Laportea crenulata*. A second objective of the study will be to analyze the extraction efficiency of *Laportea decumana* on different solvent polarities. On a PICO format: the objective of the thesis is,"What phytochemicals are present in *Laportea aestuans* and *Laportea crenulata*that may also be present in *Laportea decumana*a nd be responsible for *Laportea decumana* antimicrobial activity?". The population for the study is "*Laportea aestuans* and *Laportea crenulata* and *Laportea decumana*", the intervention is "extract type", the comparison will be "antibiotic type", and lastly, the outcome is defined as "*Laportea decumana* possible antimicrobial activity"