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Antibiotics susceptibility of *Burkholderia* species of Sarawak origin

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ABSTRACT

Aims: The *Burkholderia* species is comprised of more than 70 members which co-exist in the same ecological niche including *Burkholderia pseudomallei,* which causes fatal melioidosis infections in humans and animals. Many of the members of the *Burkholderia* species share similarities in their biochemical and morphological profiles. *B. pseudomallei* is intrinsically resistant to a myriad of antibiotics and hence, the treatment of melioidosis involves various types of antibiotics with prolonged prescription. Apart from *B. pseudomallei* which has been widely described due to its clinical importance, little is known about the antibiotics mechanisms and susceptibility profile of *Burkholderia* species. This leads to the question of whether the antibiotics susceptibility profile of the *Burkholderia* species is similar to that of *B. pseudomallei*.
Methodology and results: In this study, *Burkholderia* species isolated from environmental samples were tested for their susceptibility against gentamicin, ceftazidime, cotrimoxazole (trimethoprim/sulfamethoxazole) and azithromycin using the disk diffusion test method. The antibiogram profiles *Burkholderia* species isolates tested in this study suggested that the antibiogram profile of *Burkholderia* spp. resembles that of *B. pseudomallei* for some antibiotics while totally different for other antibiotics.
Conclusion, significance and impact of study: The actual mechanisms which render these observations and whether the interaction of these subspecies within the same ecological niche attribute to these observations warrant further investigation.

Keywords: Antibiotics susceptibility, *Burkholderia*, *Burkholderia pseudomallei*

INTRODUCTION

Burkholderia species is a Gram-negative bacilli bacterium with over 70 types of subspecies found in a wide range of ecological niches, many of which share similarities in their biochemical and morphological characteristics (Coenye and Vandamme, 2006). Some of the *Burkholderia* spp. are pathogenic to plants (Stoyanova *et al*., 2007), while others such as *Burkholderia pseudomallei* which causes melioidosis and *Burkholderia mallei* which causes glanders, are both pathogenic and potentially fatal to humans and animals (Wiersinga *et al*., 2012). Apart from that, *Burkholderia cepacia* has been reported to cause opportunistic infections in individuals suffering from cystic fibrosis and chronic granulomatous disease (Coenye and Vandamme, 2006).

Burkholderia pseudomallei is inherently resistant to myriad antibiotics such as β-lactams, aminoglycosides and macrolides, conferred through various mechanisms including inactivating enzymes, cell exclusion, and broad-range efflux pumps (Dance *et al.*, 1989; Simpson *et al.*, 1999; Jenney *et al.*, 2001). However, unlike what has been reported in other melioidosis endemic countries, over 80% *B. pseudomallei* strains in Sarawak were found to be susceptible towards aminoglycosides and macrolides (Podin *et al.*, 2014). Apart from a previous report of *B. cepacia* being resistant to tobramycin (Kennedy *et al.*, 2015), there is little knowledge on the antibiotics susceptibility profile of other *Burkholderia* spp.

It has been previously established that recombination and lateral gene transfer may occur between *B. pseudomallei* and other *Burkholderia* spp. that are sharing the same ecological niche which have led to greater intra-species diversity (Kim *et al.*, 2005; Tuanyok *et al.*, 2007). This brings about the question of whether such intra-species interactions include the antibiotics susceptibility mechanisms and whether there are similarities of antibiotics susceptibility profile between *B. pseudomallei* and other *Burkholderia* spp. Hence, the objective of this study is to investigate the antibiotics susceptibility profile of *Burkholderia* spp. isolates of Sarawak origin.

MATERIALS AND METHODS

Bacterial strains

Burkholderia spp. isolates, some of which were archival from a previous study, were used for this project. The

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