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Distribution and prevalence of antibiotic resistant bacteria in fish farms in East Malaysia

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ABSTRACT

Aims: Aquaculture has grown tremendously in Malaysia over the past decades. However, guaranteeing aquaculture sustainability is a big challenge in terms of maintaining continuous output with a safe environment. Furthermore, the cultured species should be free from antibiotic resistance bacterial and antibiotic residue. This study aimed to monitor the existence and prevalence of antibiotic resistant bacteria associated with aquaculture farms in Sarawak.
Methodology and results: Samples of water, sediment and fish were collected from five aquaculture farms within Sarawak. The samples were plated on trypticase soy agar and incubated at 28 °C for 24 h. A total of 204 bacterial isolates were isolated and analysed by (GTG)$_5$-fingerprinting to determine genetic similarity among the bacterial isolates, so that representatives could be selected from similar clonal isolates. Based on the (GTG)$_5$ profiles, 50 representative isolates were chosen for species identification using 16S rRNA sequencing. The identified bacteria were tested against 25 antibiotics using standard disk diffusion method. The 16S rRNA analysis revealed that the isolates constitute of 14 genera of bacteria including *Bacillus* (38%), *Exiguobacterium* (16%), *Enterobacter* (14%), *Aeromonas* (6%), *Acinetobacter* (4%), *Citrobacter* (4%), *Staphylococcus* (4%), *Achromobacter* (2%), *Chitinophaga* (2%), *Fictibacillus* (2%), *Plesiomonas* (2%), *Pseudomonas* (2%), *Pseudoxanthomonas* (2%) and *Stenotrophomonas* (2%). The antibiotic resistance analysis revealed that the highest percentage of resistance was recorded against streptomycin (75.0%), followed by ampicillin (66.0%), ceftriaxone (50.0%), rifampin (43.3%), aztreonam (36.8%) and ceftazidime (31.6%). Resistance to more than two antibiotics was observed in 40.0% of isolates with an overall multiple antibiotic resistant (MAR) index ranging from 0 to 0.79.
Conclusion, significant and impact of study: The variability of antibiotic resistance patterns exhibited by different bacterial species suggests a dependence on selective pressures exhibited in different geographical locations. Our results show that the occurrence of MAR bacteria in an aquaculture environment with unknown history of antibiotics usage in the aquaculture system is possible, indicating a need to continuously monitor the presence of antibiotic resistant bacteria in the aquaculture system.

Keywords: Aquaculture, bacteria, 16S rRNA, antibiotic resistant

INTRODUCTION

Since the first antibiotic discovery by Alexander Fleming in 1928, many different classes of antibiotics have been developed and concurrently bacteria have slowly developed resistance towards those antimicrobial agents (Paulson *et al.*, 2016). Now, the phenomenon of antibiotic resistance is a global problem in every sector including aquaculture and agriculture (Radhouani *et al.*, 2014; Done *et al.*, 2015). In Malaysia, multiple resistance bacteria and resistance genes have been reported to be present in the aquaculture and its surrounding environments (Samuel *et al*., 2011; Abdullahi *et al*., 2013; Kui Soon *et al.*, 2014; Ng *et al.*, 2014; Seng Chiew *et al*., 2018).

There have been continuous efforts in searching for

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