antibiotics

MDPI

Article

Plasmid-Mediated Antibiotic Resistant *Escherichia coli* in Sarawak Rivers and Aquaculture Farms, Northwest of Borneo

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Abstract: Background: The emergence of plasmid-mediated antibiotic resistance in *Escherichia coli* in water resources could pose a serious threat to public health. The study aims to investigate the dispersion of plasmid-mediated antibiotic-resistant *E. coli* from six rivers in Sarawak and two aquaculture farms in Borneo. Methods: A total of 74 water samples were collected for the determination of their bacteria colony count. An IMViC test identified 31 *E. coli* isolates and tested their susceptibility against twelve clinically important antibiotics. The extraction of plasmid DNA was done using alkali lysis SDS procedures. Characteristics, including plasmid copy number, molecular weight size, resistance rate and multiple antibiotic resistance (MAR), were assessed. Results: Our findings revealed that bacterial counts in rivers and aquaculture farms ranged from log 2.00 to 3.68 CFU/mL and log 1.70 to 5.48 cfu/mL, respectively. Resistance to piperacillin (100%) was observed in all *E. coli*; resistance to amoxicillin (100%) and ampicillin (100%) was observed in *E. coli* found in aquaculture farms; resistance to streptomycin (93%) was observed in *E. coli* found in rivers. All *E. coli* were resistant to ≥2 antibiotics and formed 26 MAR profiles, ranging from an index of 0.17 to 0.83, indicating that there are high risks of contamination. Some (48.4%) of the *E. coli* were detected with plasmids (1.2 to >10 kb), whereas 51.6% of the *E. coli* did not harbor any plasmids. The plasmid copy numbers reported were one plasmid (n = 7), two plasmids (n = 4), ≥ two plasmids (4). *E. coli* isolated from the Muara Tuang River showed the highest-molecular-weight plasmids. A statistical analysis revealed that there is no significant correlation (r = 0.21, p = 0.253) between the number of plasmids and the MAR index of the tested isolates. Conclusion: The distribution of MAR in *E. coli* from rivers is higher compared to the aquaculture environment. Our study suggests that MAR in isolates could be chromosome-mediated. Our results suggest that riverbed sediments could serve as reservoirs for MAR bacteria, including pathogens, under different climatic conditions, and their analysis could provide information for public health concerns.

Keywords: drug resistant; aquaculture; extrachromosomal; *Escherichia coli*; water source; plasmid

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1. Introduction

The occurrence of antibiotics in the aquatic environment, especially in aquaculture farms and rivers, has been viewed as one of the major threatening issues causing environmental pollution worldwide. Aquaculture is a fast-growing food-production industry, supplying 30.1 million tons of aquatic plants, 80 million tons of total food fish and 37,900 tons of non-food products [1] to the growing world population. The usage of antimicrobial agents in aquaculture has increased exponentially, accounting for 63,151 tons in 2010, and is expected to increase to 67% by 2030 [2]. Brazil, Russia, Africa and India are the countries recorded with the highest global antimicrobial consumption [3]. Most farmers do not use antibiotics appropriately and responsibly, especially in raising fish and shrimp either in