ANTIMICROBIAL RESISTANCE IN BACTERIA ISOLATED FROM TROPICAL COASTAL WATERS OF PENINSULAR MALAYSIA

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ABSTRACT   Thirty three heterotrophic bacteria isolated from tropical coastal waters in Peninsular Malaysia were tested for susceptibility to 15 different antibiotics representing nine different classes of antimicrobial agents. We found that tetracycline, sulfonamide, mecillinam, sulfamethoxazole, erythromycin, and streptomycin resistance were predominant among the bacterial isolates. Resistance to chloramphenicol, ampicillin, vancomycin, norfloxacin, ofloxacin and trimethoprim/sulfamethoxazole were less common. All of the bacterial strains were susceptible to meropenem, imipenem, and ciprofloxacin. Approximately 70% of the isolates were resistant to two or more structural classes of antibiotic. Findings from this preliminary study indicated the prevalence of antibiotic resistance bacteria in the coastal waters of Penisular Malaysia.

ABSTRAK   Kerentanan tiga puluh tiga bakteria heterotrofik yang diasingkan dari perairan pantai tropika di Semenanjung Malaysia telah diuji terhadap 15 antibiotik yang mewakili sembilan kelas agen antimikrobial. Kami mendapati bahawa ketahanan terhadap tetracycline, sulphonamide, mecillinam, sulfamethoxazole, erythromycin dan streptomycin adalah predominan di antara bakteria isolat. Resisten terhadap chloramphenicol, ampicillin, vancomycin, norfloxacin, ofloxacin dan trimethoprim/sulfamethoxazole adalah kurang lazim. Semua strain adalah peka terhadap meropenem, imipenem dan ciprofloxacin. Sekitar 70% daripada bakteria strain adalah resisten terhadap dua atau lebih struktural kelas antibiotik struktural. Penemuan kajian preliminari ini menunjukkan kelaziman resistensi bakteria di perairan pantai Semenanjung Malaysia terhadap antibiotik.

(Keywords: marine bacteria, antibiotic, multidrug resistance, coastal waters)

INTRODUCTION

Antibiotics are used intensively and widely as medicines and growth promoters in agricultural industries. However, these chemical compounds receive little attention as pollutants in the aquatic environment [1]. The persistence and elevated concentrations of antibiotics pose some risks to the aquatic ecosystems, in particular microorganisms. Recent findings show that antibiotics can have deleterious impacts on denitrifying bacteria, eventually affecting the nitrogen cycle [1,2]. This initiated the idea that the persistence and elevated concentrations of antibiotics in environment could have the potential to disrupt biogeochemical processes in the biosphere.

Elevated concentration and persistence of antibiotics in aquatic ecosystems also generate new selective pressures on natural bacterial populations, and hence antibiotic-resistant bacteria are selected from the indigenous communities [3]. The high prevalence of indigenous antibiotic-resistant bacteria could present a potential health risk because the antibiotic resistance genes could be transferred to human microflora via food-borne or environmental bacteria [4,5,6,7]. The report by Dantas *et al*. [8] have also shown that environmental bacteria act as reservoir of antibiotic resistance genes and are a source of novel resistance genes for clinical pathogens.

Despite many studies to date that have examined the prevalence of antibiotic resistance in environmental bacteria and the mechanism of antibiotic resistance, studies from the aquatic environment in the South East Asia region are relatively scarce. As antimicrobial resistance genes and resistant bacteria in the environment are increasingly seen as an ecological problem [9,10], there is a need to carry out this study. In this paper, we present preliminary data on