

Perspectives

Antibiotic “resistomes” in non-healthcare environments: An understudied phenomenon in Brunei Darussalam

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The issue of antibiotic resistance is still present today and poses a global threat to the community. The golden age of antibiotics has long passed since the novel discovery of penicillin in 1929¹. With time, bacteria have grown to become more sophisticated, building up resistance to many antimicrobial drugs and transferring genes between humans, animals, other bacterial species and the environment². The ever-mounting frequency of antibiotic resistance among pathogenic, commensal, and environmental bacteria to a variety of different clinically useful antibiotics, such as vancomycin, methicillin and penicillin, has become a worldwide public health threat. The rapid evolution of antibiotic-resistant bacteria has greatly outpaced the development of novel and effective antibiotic treatments and management strategies. Thus many common infectious diseases caused by bacteria, which were once easily treatable with antibiotics, have now become more difficult or near impossible to treat and are a leading cause of deaths throughout the world due to antibiotic resistance. Discovery of new antimicrobial drugs has been posed as a worldwide importance in dealing with the ever-growing issue of drug resistant bacteria such as methicillin-resistant *Staphylococcus aureus* (MRSA)³.

The environment houses a unique niche of a variety of bacteria. Indiscriminate use and misuse of antibiotics, as mentioned earlier, is a primary contributing factor that

leads to the evolution and continued emergence of antibiotic-resistant environmental bacteria (4). Although bacterial antibiotic resistance will occur eventually as a result of natural selection and random mutations, it is greatly accelerated by strong selection pressure exerted by the widespread use of antibiotics in both human and veterinary medicine in agriculture. In addition, the selection pressure has also facilitated the emergence and spread of resistant bacteria beyond the healthcare and farm settings and into the natural environments including water, soil, and the community⁴. Under strong antibiotic selective pressure, environmental bacteria that are able to mutate their DNA to become resistant to antibiotics will be selected and allow to thrive. Over time, there will be a differential survival as susceptible environmental bacteria are more likely to die than those bacteria that could evolve and become antibiotic-resistant. Having a more selective advantage over other non-resistant bacteria, the antibiotic resistant bacteria are able to survive and propagate in the environment by passing on the unique resistant allele to their progeny⁵. Antibiotic resistance genes or determinants could also be transferred horizontally to other environmental bacteria, which can quickly lead to emergence of a large population of antibiotic-resistant bacteria within that environment and cause widespread dissemination of resistance determinants in many environments. The complete and diverse pool of antibiotic

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resistance genes in the entire community of microorganisms, which include the medically important bacteria, the commensal bacteria of humans and animals, and the environmental bacteria is termed as antibiotic “resistome”⁶. The possibility of gene transfer between the environmental and clinical “resistomes” and that the environmental bacteria could be the antibiotic resistance gene reservoir for the pathogens found in clinics have been postulated^{7,8}.

Staphylococci bacteria are common commensal bacteria present on human skin and mucous membranes and usually do not cause disease under normal circumstances. They are also found in the nasopharynx, respiratory tract, urogenital tract, gastrointestinal tract, mouth and conjunctiva which are constantly exposed to the external environment⁹. Additionally, staphylococci bacteria are also found to inhabit the urogenital tract, gastrointestinal tract, mouth and skin of both companion and livestock animals, such as cats, dogs, chickens, rabbits, sheep, horses, cattle and pigs¹⁰. Staphylococci bacteria can survive for months in dry and hostile environments including various environmental surfaces, thus creating a risk for environment-to-people transmission. Although much is known about the incidence of drug-resistant staphylococci bacteria in the healthcare environment, there is growing evidence to suggest the presence of these bacteria in non-healthcare environments. The presence of drug-resistant staphylococci bacteria in the environment poses a potential risk for serious and life-threatening infections in humans and possibility of resistant genes transfer among the bacterial species.

Until only recently¹¹, the carriage of drug resistant staphylococci outside the healthcare setting was virtually

unknown in Brunei Darussalam. Majority of studies conducted in Brunei have only investigated human carriage of staphylococci, in both the non-health care and health care settings. Bacteria not commonly associated with hospital settings can carry resistance determinants. Non-hospital environments such as public transport systems, parks and gyms are a source of antibiotic resistant staphylococci. Our group was the first to show the existence of bacterial “resistomes” in non-health care environments in Brunei Darussalam¹¹. The presence of antibiotic resistance found in staphylococci samples that we collected from different environments in the Brunei-Muara district indicate that some environments may accelerate the spread of antibiotic resistant strains. More attention should be paid to the inspection and control of antibiotic resistant strains in these environments in Brunei Darussalam as this has major implications in the issues of public health and safety. By knowing the type of drug resistant staphylococci circulating in the community, we can devise measures to control the spread of these drug resistant staphylococci. Given that the environment harbors a vast and diverse reservoir of antibiotic resistance genes that could freely propagate into human commensals and pathogens, a more comprehensive and integrated understanding of the environmental antibiotic “resistome” is crucial as it will not only facilitate future development of novel, effective antibiotics, but will also be useful for future prediction of microorganisms' novel resistance mechanisms to antibiotics that could potentially become major clinical and public health problems. Although our work provided the first-ever evidence of drug-resistant staphylococci in the non-hospital environment in Brunei Darussalam, further research into this area in other districts in the country is warranted.

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