

ABSTRACT

Antibiotic resistance has been a major threat to human and animal health because pathogenic microorganisms are becoming resistant to the most commonly prescribed antibiotic treatments, leading to prolonged illness and greater risk of death. However, the detection of antimicrobial resistance in nonclinical settings has been receiving little focus in research. This may be because antibiotic concentrations in these settings are generally very low. Of special interest are aquatic environments because, water, which provides easy access to dissolved nutrients, as well as protection from desiccation and UV light, is an ideal medium for bacterial life. Furthermore, both freshwater and marine systems act as a sink for bacteria that enter aquatic systems via treated and untreated sewage, hospital waste, agricultural run-off, and other anthropogenic sources, all of which can harbor different levels of antibiotic resistance and virulence. Reports of antimicrobial resistance in marine animals are fewer compared to terrestrial animals, but these studies are significant in relation to marine mammal stranding and rehabilitation activities, and dissemination of resistant bacteria in the environment. This study generally aims to determine the antibiotic resistance patterns and detect virulence factors of bacteria isolated from cetaceans that stranded in the Philippines during the year 2018. Specifically, this study aims to (1) confirm the phenotypic and molecular identifications of Gram-negative bacteria from the stranded cetaceans; (2) test the susceptibility of bacterial isolates to 15 antibiotics representing 7 antibiotic classes; (3) detect target virulence factors in selected bacterial groups; (4) find significant association between stranding event parameters (e.g., age, sex, species, stranding location, stranding season, and sea-surface temperature) and antibiotic resistance patterns as well as presence of virulence factors in bacterial isolates. Bacteria that were isolated from the stranded cetaceans will be identified phenotypically with the use of Gram-staining, morphological description, and biochemical reactions with the aid of VITEK Identification System. As supplement to phenotypic identification, molecular identification will also be confirmed through amplification and sequencing of the universal 16S rRNA gene. Testing of sensitivity to different antibiotics will be done by automated antibacterial susceptibility assay using VITEK 2. Associations between patterns of antibiotic resistance or virulence and stranding event parameters will be determined using regression analysis and spatial modeling.