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Identification of sources of Salmonella in watersheds and characterization of multiple antimicrobial resistant strains

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Abstract Text:

More than 56,000 acres of shellfish beds along coastal NC are closed to harvesting due to elevated levels of bacteria. Bacterial contaminations, primarily by zoonotic pathogens such as Salmonella result from human activities such as farming, forestry, and factors associated with urbanization. Strains with resistance to multiple antimicrobials are also of major public health concern. The objective of the study is to determine and compare the sources of Salmonella contamination for watersheds using phenotypic and genotypic approaches. Samples were collected from four different water shed systems: urban, crop farming, animal agriculture (swine farm) and natural forest. Water specimens were cultured for Salmonella and further tested for antimicrobial susceptibility using Kirby-Bauer disc diffusion approach. More than 100 isolates were tested by serotyping by the USDA-NVSL. DNA fingerprinting is currently being processed using pulsed-field gel electrophoresis (PFGE). Highest prevalence of Salmonella was detected from residential (35%) followed by the swine production (29%). More than a quarter of the samples from the natural forest (26%) were also positive. Serotyping results revealed the diversity of Salmonella serotype with the majority being Anatum, Gaminara and Inverness (18% each) and serotypes of high public health significance were also detected at moderate levels: Muenchen and Newport (8% each), Bredeney (7%), Montevideo (6%) including some other serotypes. We detected differential translocation of the serotypes as all Newport were detected from Crop agriculture, which may be associated with spraying cattle manure onto crop fields. Also, Gaminara and Inverness were predominantly detected from residential and natural forest but not the other two locations. Antimicrobial susceptibility testing also demonstrated 15 various antimicrobial resistance patterns with the majority being pan-susceptible (67.3%). The most highly multi-drug resistant strains were detected from water shed associated with the swine farm: AmStTeAxChKmGm+ (n=5). Genotyping using PFGE is currently underway. The study revealed that all the various areas including the natural forest could be important contributors of Salmonella contamination of waterbeds. Serotypes of high public health significance and resistant to multiple antimicrobials are also of significant concern.

Impact Statement:

The dry weather screening program provides assistance to BCSWD to detect illicit and/or inappropriate connections to the storm drainage system. It provides a foundation for the reduction of discharge of pollutants and increased water quality protection.