Determining Science-Based Solutions for Emergence of Tetracycline Resistant Bacteria

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Emergence of antibiotic resistant bacteria is a major concern for human health. Identities of the resistant bacteria as well as mechanisms by which they become resistant to antibiotics are largely unknown. This gap in the knowledge base is important because lack of such knowledge is preventing developing effective ways of preventing emergence of antibiotic resistant bacteria. The central hypothesis is that feeding cattle with the antibiotic Tetracycline causes some rumen bacteria to become resistant to Tetracycline, and that these bacteria have diverse genetic mechanisms of resistance to the antibiotic. The objectives of this study were to identify Tetracycline resistant rumen bacteria and determine multi-drug resistance in these bacteria. The approaches included cell culture, streak plating, gram staining, microscopy, and genetic test. The results showed that of the 10 Tetracycline resistant bacteria (that were previously selected using Tetracyline at 12 micrograms/ml), eight were able to grow in nutrient rich media Trypic Soy Broth (TSB) agar supplemented with 25 micrograms/ml Tetracycline and six of these were gram positive. Colony characteristics of the bacteria were as following: 1) Bacteria from samples 1, 2, 3, and 7 were small colonies with whitish grey color, 2) Bacteria from samples 5 and 6 were large colonies with yellowish color, and 3) Bacteria from sample 8 were medium colonies with yellow color. The multi-drug resistance tests showed that all of the bacteria except grew on TSB agars supplemented with Chloramphenicol, Ampicillin and Kanamycin. The bacteria from sample #8 grew on agars containing Chloramphenicol and Ampicillin but not on agar containing Kanamycin. The genetic test using PCRto determine the sequence of the 16S rRNA.

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