Differentiation of Escherichia coli from Different Animal Sources Using PCR-based Techniques. (A05-fiser180714-Poster)

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Abstract:

Fecal contamination is a threat to water quality, and the sources of contamination must be determined before they can be managed. Several methods have been suggested for source tracking of Escherichia coli based on genetic fingerprinting, including rep-PCR. Before its potential for source tracking can be determined, the variability of E. coli populations in hosts must be known. For this study, manure samples were taken from fifteen pigs, ten cows, ten chickens, other poultry, and wildlife. Between ten and fifteen E. coli isolates were taken from each animal. Rep-PCR fingerprints were generated with REP and BOX primers for each isolate. Results using the REP primers indicate that one fingerprint pattern is dominant in each animal, and animals from different facilities had the same dominant pattern. A single fingerprint type was observed for most animals. The dominant REP pattern observed in pigs was seen in cows at a lower frequency. The BOX primer produced a wider variety of fingerprint types, but most animals still had one dominant type. Several dominant types were found among animals from the same facility, and some fingerprint types were seen in both cows and pigs.

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