Abstract

Foodborne diseases occur worldwide, including through the consumption of contaminated meat. This study was conducted to investigate the prevalence of *Escherichia coli* contamination in fresh beef, poultry, and pork, and to determine whether any isolated *E. coli* possessed genes associated with pathogenicity. Three thousand meat samples were collected from 2004 to 2006 and were tested for the presence of *E. coli*. Two hundred and seventy-three *E. coli* isolates were obtained from beef, poultry, and pork, resulting in an overall isolation rate of 9.1%. Of these isolates, 201 were obtained from 1350 pork samples (14.9%), followed by 41 of 900 poultry samples (4.6%) and 31 of 750 beef samples (4.1%). A total of 39 pathogenic *E. coli* isolates from the three meat types were categorized into three virulence groups, namely enterotoxigenic *E. coli* (43.6%), enterohemorrhagic *E. coli* (EHEC) (35.9%; 22.6% of beef, 7.3% of poultry, and 2.0% of pork), and enteropathogenic *E. coli* (20.5%). Fourteen strains were identified as belonging to the EHEC, which included O18, O136, O119, O86, O8, O111, O15, O128, and O6. This study demonstrated that pathogenic *E. coli* are found in meat in Korea, and could act as a transmission vehicle for human infection as suggested by the occurrence and classification of pathogenic *E. coli* in retail meats. Furthermore, the data from this study could be used in the risk assessment of foodborne illnesses linked to meat consumption.