High diversity and abundance of antibiotic-resistant \textit{Escherichia coli} isolated from humans and farm animal hosts in Jeonnam Province, South Korea

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\section*{ABSTRACT}

The spread of antibiotics resistance among bacteria is a threat to human health. Since South Korea uses approximately 1.5 times more antibiotics than do other OECD countries, this is likely to impact the numbers and types of antibiotic-resistant bacteria found in the environment. In this study we examined feces from domesticated animals and humans for the diversity and abundance of antibiotic-resistant \textit{Escherichia coli}. Abundant antibiotic-resistant \textit{E. coli} were isolated from all the tested animals and humans and were examined by horizontal, fluorophore-enhanced, rep-PCR (HERP) DNA fingerprint analysis. A total of 793 unique, non-clonal \textit{E. coli} isolates were obtained from the 513 human and animal hosts examined. Antibiotic resistance analysis, done using 14 antibiotics, indicated that 72.3\% of the isolates (573 of 793) were found resistant to more than one antibiotic. The \textit{E. coli} isolated from swine were resistant to the greatest number of antibiotics. Tetracycline resistant \textit{E. coli} were routinely isolated from all animal hosts (36 to 77\% per host), except for dairy cattle (9.3\%). Twenty-nine \textit{E. coli} isolates from all hosts, except for duck, were resistant to more than 10 antibiotics. Gene transfer and southern hybridization studies revealed that resistance to 13 of the antibiotics was self-transmissible, and likely mediated by plasmids and integrons. Since genetically diverse and numerically abundant antibiotic-resistant \textit{E. coli} were consistently recovered from chicken, swine and other domesticated animals in South Korea, our results suggest that the use of sub-therapeutic levels of antibiotics for disease prophylaxis and growth promotion should be curtailed.

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1. Introduction

Antibiotics are commonly used to control infectious diseases and to promote growth among farm animals. However, it is well documented that the use of antibiotics can subsequently cause intestinal microorganisms to become resistant to antimicrobial agents (Aarestrup and Wegener, 1999; von Baum and Marre, 2005). Common pathogens, such as \textit{Pseudomonas aeruginosa} and \textit{Staphylococcus aureus} have been shown to acquire resistance to antibiotics when these agents are applied to the host for extended periods (Damas et al., 2006).

Previously, it was reported that South Korea consumes about 1.5 times greater amounts of antibiotics, as compared to other countries belonging to the Organization for Economic Cooperation and Development (Park et al., 2005). Kim et al. (2008) detected diverse veterinary pharmaceuticals and antibiotics in aquatic environments in South Korea, addressing the importance of routine monitoring for antibiotics, such as amoxicillin and oxytetracycline in water and fauna. Not surprisingly, antibiotic-resistant pathogens have been frequently isolated from animals and humans in South Korea. Approximately 85\% of \textit{Salmonella} isolated from foods in South Korea were shown to be resistant to antibiotics (Chung et al., 2003), and greater than 90\% of \textit{Campylobacter jejuni}, which have been found in 37.7\% of raw chickens in South Korea, were resistant to nalidixic acid, ciprofloxacin, and tetracycline (Han et al., 2007). Furthermore, 70\% of 45 \textit{E. coli} O157 strains that were isolated from 33 farms in South Korea were found to be resistant to at least one antibiotic and more than 60\% were resistant to four or more antibiotics; a rate described by the authors as the highest in the world (You et al., 2006). The past excessive use of antibiotics in South Korea may partially be responsible for the high incidence of the antibiotic-resistant bacteria. However, to our knowledge, there have never been intensive studies

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