

Ecological Study of *Escherichia coli* Isolates with Phylogenetic Grouping, Antibiotic Resistance, and Virulence Gene Profiling

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Total 1729 *Escherichia coli* isolates were obtained from feces of 138 humans, 376 domesticated animals (chicken, duck, beef cattle, dairy cattle, and swine), and 24 wild geese, including 96 isolates from the Yeongsan River in Jeonam Province, Korea. Genotypically unique strains were indicated using Horizontal fluorophore-enhanced rep-PCR DNA fingerprinting (HFERP) [1]. Multiplex PCR analysis done for phylogenetic grouping [2] indicated that none of the strains belonged to *E. coli* phylogenetic group B2. In contrast, phylogenetic group B2 strains were detected in about 17% (8 of 48 isolates) from 24 wild geese feces and in 3% (3 of 96) isolates obtained from the Yeongsan River. The distribution of *E. coli* strain in phylogenetic groups A, B1, and D varied depending on the host examined. Another multiplex PCR analysis was done for virulence gene detection targeting *eaeA*, *hlyA*, *stx1*, *stx2*, *est*, *elt* and *ipaH* [3, 4]. Subsequently, the distribution of *E. coli* virotypes of Enteropathogenic *E. coli* (EPEC), Enterohemorrhagic *E. coli* (EHEC), Enteroinvasive *E. coli* (EIEC) and Enterotoxin producing *E. coli* (ETEC), were determined. Total 89 unique strains were assigned to the 4 virotypes as follows: EHEC (18 strains), EIEC (41 strains), EPEC (9 strains) and ETEC (14 strains). Virulence genes were most frequently present in the phylogenetic group B1 strains isolated from beef cattle. Taken together, results of these studies indicate that *E. coli* strains in phylogenetic group B2 were rarely found in humans and domesticated animals in Korea and that the majority of strains containing virulence genes belonged to phylogenetic group B1 and were isolated from beef cattle. In addition to these, antibiotic resistance tests were conducted with 15 antibiotics (Ampicillin, Carbenicillin, Cefazolin, Cefoxitin, Ceftazidime, Chloramphenicol, Ciprofloxacin, Gentamicin, Kanamycin, Piperacillin, Streptomycin, Sulfamethoxazole, Tetracycline, Trimethoprim, and Tobramycin) coupled with PCR targeting integrase. Overall, high percentage of antibiotic resistant strains were observed in Tetracycline, Streptomycin, and Sulfamethoxazole (average 54.7%, 36.0%, and 34.4%, respectively), while swine isolates showed the highest percentage at average 38%, followed by chicken (26.2%) and beef cattle (15.2%). Moreover, total 208 strains were found to carry integrase gene. The highest percentage of integrase holding strains were observed in swine isolates at 46.1%, followed by chicken and duck isolates (26.0% and 25.3%, respectively). To date, our study is the first to describe the *E. coli* ecology in Korea with virulence gene profiling, phylogenetic grouping, and antibiotic resistance.

References

- [1] Johnson, L. K., M. B. Brouwn, *et al.* *Appl Environ Microbiol* , **70**, 4478, 2004.
- [2] Clermont, O., S. Bonacorsi, *et al.* *Appl Environ Microbiol* , **66**, 4555, 2000.
- [3] Paton, A. W., and J. C. Paton, *Journal of Clinical Microbiology* **36**, 598, 1998
- [4] Toma, C., Y. Lu, *et al.*, *Journal of Clinical Microbiology* **41**, 2669, 2003