

Absence of *Escherichia coli* Phylogenetic Group B2 Strains in Humans and Domesticated Animals from Jeonnam Province, Republic of Korea[∇]

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Multiplex PCR analyses of DNAs from genotypically unique *Escherichia coli* strains isolated from the feces of 138 humans and 376 domesticated animals from Jeonnam Province, South Korea, performed using primers specific for the *chuA* and *yjaA* genes and an unknown DNA fragment, TSPE4.C2, 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) of isolates from feces of 24 wild geese and in 3% (3 of 96) of isolates obtained from the Yeongsan River in Jeonnam Province, South Korea. The distribution of *E. coli* strains in phylogenetic groups A, B1, and D varied depending on the host examined, and there was no apparent seasonal variation in the distribution of strains in phylogenetic groups among the Yeongsan River isolates. The distribution of four virulence genes (*eaеA*, *hlyA*, *stx*₁, and *stx*₂) in isolates was also examined by using multiplex PCR. Virulence genes were detected in about 5% (38 of 707) of the total group of unique strains examined, with 24, 13, 13, and 9 strains containing *hlyA*, *eaеA*, *stx*₂, and *stx*₁, respectively. The virulence genes were most frequently present in 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 Jeonnam Province, South Korea, and that the majority of strains containing virulence genes belonged to phylogenetic group B1 and were isolated from beef cattle. Results of this study also suggest that the relationship between the presence and types of virulence genes and phylogenetic groupings may differ among geographically distinct *E. coli* populations.

Escherichia coli is a normal inhabitant of the lower intestinal tract of warm-blooded animals and humans. While the majority of *E. coli* strains are commensals, some are known to be pathogenic, causing intestinal and extraintestinal diseases, such as diarrhea and urinary tract infections (42). Phylogenetic studies done using multilocus enzyme electrophoresis and 72 *E. coli* strains in the *E. coli* reference collection showed that *E. coli* strains can be divided into four phylogenetic groups (A, B1, B2, and D) (20, 41, 48). Recently, a potential fifth group (E) has also been proposed (11). Since multiplex PCR was developed for analysis of phylogenetic groups (6), a number of studies have analyzed a variety of *E. coli* strains for their phylogenetic group association (10, 12, 17, 18, 23, 54). Duriez et al. (10) reported the possible influence of geographic conditions, dietary factors, use of antibiotics, and/or host genetic factors on the distribution of phylogenetic groups among 168 commensal *E. coli* strains isolated from human stools from three geographically distinct populations in France, Croatia,

and Mali. Random-amplified polymorphic DNA analysis of the intraspecies distribution of *E. coli* in pregnant women and neonates indicated that there was a correlation between the distribution of phylogenetic groups, random-amplified polymorphic DNA groups, and virulence factors (54). Moreover, based on comparisons of the distribution of *E. coli* phylogenetic groups among humans of different sexes and ages, it has been suggested that *E. coli* genotypes are likely influenced by morphological, physiological, and dietary differences (18). In addition, climate has also been proposed to influence the distribution of strains within *E. coli* phylogenetic groups (12). There are now several reports indicating that there is a potential relationship between *E. coli* phylogenetic groups, age, and disease. For example, *E. coli* isolates belonging to phylogenetic group B2 have been shown to predominate in infants with neonatal bacterial meningitis (27) and among urinary tract and rectal isolates (55). Also, Nowrouzian et al. (39) and Moreno et al. (37) reported that strains belonging to phylogenetic group B2 persisted among the intestinal microflora of infants and were more likely to cause clinical symptoms.

Boyd and Hartl (2) reported that among the *E. coli* strains in the *E. coli* reference and the diarrheagenic *E. coli* collections, strains in phylogenetic group B2 carry the greatest number of virulence factors, followed by those in group D. Virulence factors carried by group B2 strains are thought to contribute to

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