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Escherichia Coli Phylo-Groups Drug Resistance Pattern

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The paper entitled "Antibiotic Resistance Pattern of *Escherichia coli* Groups A, BI, B2 and D Isolated from Frozen Foods and Children with Diarrhea in Sanandaj, Iran" published in International Journal of Enteric Pathogens. 2013.1(1), is a short, simple article that discusses original research conducted on *E. coli* strains isolated from 125 samples of frozen food from animal sources, and 466 rectal swabs from children with diarrhea. Certainly, such periodic surveys conducted on various samples that may have a major role in the spread of pathogenic bacteria would shed light on the susceptibility of pathogens and help in the containment of spread of infections in hospital environments as well as in the community.

In recent years, the spread and acquisition of antibiotic resistance genes between different species of disease causing bacteria has been on the rise. Among these *E. coli* strains of *E. coli* have gained world wide attention and their pattern of antibiotic resistance has been a subject of controversy among specialists of the field. The existence of four distinct sub-species within *E. coli* has been established; these are designated A, B1, B2 and D (1) that can be divided into seven subgroups (A, A1, B1, B22, B23, D1 and D2), according to the combination of the three genetic markers chuA, yjaA and DNA fragment TspE4.C2 (2). Thus, this study would have been better if they had determined the other three subgroups. Therefore, phylo-group determination can reveal a great deal regarding sub-group membership. Based on the available databases, it has been found that *E. coli* extrapathogenic phylo-group strains are globally disseminated and drug resistant with a broad range of human hosts (3, 4). Further studies are needed to characterize their origins, virulence mode of actions, geographical distribution, clinical associations and modes of dissemination. The findings of the study conducted on frozen food samples of animal origin and rectal swabs from children with diarrhea in the city of Sanandaj by Kalantar et al. are interesting and can be helpful as a reference for future studies for comparative purposes.

References

- 1. Karimi Darehabi H, Naseri MH, Menbari S, Mobaleghi J, Kalantar E. Antibiotic Resistance Pattern of Escherichia coli Groups A, B1, B2 and D Isolated from Frozen Foods and Children with Diarrhea in Sanandaj, Iran. I J Enteric pathogens; 2013; 1(1); 1-4
- Ochman H, Selander RK. Standard reference strains of Escherichia coli from natural populations. J Bacteriol. 1984;157(2):690-3.
- Carlos C, Pires MM, Stoppe NC, Hachich EM, Sato MI, Gomes TA, et al. Escherichia coli phylogenetic group determination and its application in the identification of the major animal source of fecal contamination. *BMC Microbiol*. 2010;**10**:161.
- Gordon DM. The influence of ecological factors on the distribution and genetic structure of Escherichia coli. In: Neidhardt F editor. *Escherichia coli* and *salmonella typhimurium*: cellular and molecular biology. Washington, DC, USA: American Society for Microbiology. 2004.
- Johnson JR, Delavari P, Kuskowski M, Stell AL. Phylogenetic distribution of extraintestinal virulence-associated traits in Escherichia coli. *J Infect Dis*. 2001;183(1):78–88.

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Article Commentary