Title: PHYLOGENETIC GROUP DETERMINATION OF ESCHERICHIA COLI ISOLATED FROM ANIMAL SAMPLES

Authors Fernanda Morcatti Coura¹, Soraia de Araújo Diniz¹, Marcos Xavier Silva¹, Silvia Minharro Barbosa², Jamili Maria Suhet Mussi¹, Andrey Pereira Lage¹, Marcos Bryan Heinemann³*

Institutions ¹ UFMG - Universidade Federal de Minas Gerais, Escola de Veterinária (Av. Antônio Carlos, 6627, CEP30123-970, Belo Horizonte, MG), ² UFT - Universidade Federal do Tocantins, Escola de Medicina Veterinária e Zootecnia (Avenida NS, 109 Norte, 77001-090, Palmas, TO), ³ USP – Universidade de São Paulo, Faculdade de Medicina Veterinária e Zootecnia (Av Prof Orlando Marques de Paiva, 87, CEP 05508-270, São Paulo, SP)

Abstract:

Escherichia coli is a Gram-negative, fermentative, rod-shaped bacterium and is the major facultative anaerobic bacterium in the intestinal tract of most animal species. E. coli cause enteric and extraintestinal diseases in animals. Escherichia coli strains can be assigned to one of the seven phylogenetic groups. Phylogenetic studies are important to improve the understanding of E. coli population and the relation of strains and its hosts and disease. This study aims to analyze the occurrence and distribution of phylogenetic groups of Escherichia coli isolated from different domestic animals. Escherichia coli were isolated from fecal samples from cattle and water buffalo. The samples from poultry were collected in a slaughterhouse with federal inspection service and were obtained from the respiratory tract with signs of airsacculitis, liver and heart suspected of colibacillosis and carcasses with no clinical alteration. E. coli strains were tested by PCR for characterization of phylogenetic groups A, B1, B2, C, D, E and F. The Shannon and Simpson diversity indexes were calculated. Identification of phylogroups A (P < 0.001) and phylogroup F (P = 0.002) were associated with E. coli strains isolated from poultry, phylogroups B1 (P < 0.001) and E (P < 0.001) were associated with E. coli strains isolated from cattle, and phylogroups B2 (P < 0.001) and D (P = 0.007) were associated with E. coli strains isolated from water buffalo. Our results indicate that B1 is the main phylogroup of E. coli isolated from domestic animals, followed by phylogroup A. The diversity indices (Shannon and Simpson index) show that there is greater diversity in E. coli strains isolated from poultry then water buffalo and cattle. The results of chi-square test and the Correspondence Analysis agreed and showed that phylogroups B1 and E are associated with Escherichia coli strains isolated from cattle and phylogroups A and F with poultry. However, E. coli strains from water buffalo were associated with phylogroups B2 and D in the chi-square but the CA showed no clear association. In our study, most phylogroups were detected in all the three hosts studied, however, the chi-square test and the CA model indicates some host-specificity and can be used for molecular epidemiology studies.

Keywords: Escherichia coli; phylogroups; correspondence analysis; cattle; poultry; water buffalo

Acknowledgment: CNPq, FAPEMIG