

Characterization and Antimicrobial Susceptibility of Extra-intestinal Pathogenic Escherichia coli in Healthy Camel in South Tunisia

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ABSTRACT

Escherichia coli (*E. coli*) besides being a normal inhabitant of the intestinal tract of all mammals, is one of the most important zoonotic pathogens which are responsible of many diseases affecting livestock and has been subjected to extensive studies in developing countries. The aim of this study was to characterize extra-intestinal pathogenic *Escherichia coli* (ExPEC) strains isolated from healthy camel in south Tunisia. A total of 36 fecal samples were collected from healthy camel in south Tunisia and assayed by PCR for the presence of *E. coli* virulence genes associated with extra-intestinal *Eschericha coli*. Among the 9 virulence genes of ExPEC tested in this study, prevalence of *iroN* (72.2%), *iucd* (41.6%), *papC* (27.7%), *sfa* (13.8%) and *afa8* (13.8%) were most frequent in camels. Analysis of PCR results were done for determination of phylogenetic groups which showed that the most abundant phylogenetic group in the *E. coli* isolates collection were B1 (50.5%) and B2. No isolate was identified in groups D and E. Serogroups most frequently detected was O123. All isolates were sensitive to amoxicillin/Clavulanic acid, cefoxitin and gentamicin whereas the highest frequency of resistance was observed to tetracycline 55%. The high prevalence of *iucd*, *papC*, *sfa*, *afa8* and *iroN* suggest that healthy camel may constitute an important natural reservoir of ExPEC strains.

Keywords: E. coli, virulence genes, serogroups, antimicrobial susceptibility, PCR.