Comparative analysis of antibiotic resistance and phylogenetic group patterns in human and porcine urinary tract infectious Escherichia coli

Urinary tract infections (UTIs) are one of the most common infectious diseases in humans and domestic animals such as pigs. The most frequent infectious agent in such infections is Escherichia coli. Virulence characteristics of E. coli UTI strains range from highly virulent pyelonephritis strains to relatively benign asymptomatic bacteriuria strains. Here we analyse a spectrum of porcine and human UTI E. coli strains with respect to their antibiotic resistance patterns and their phylogenetic groups, determined by multiplex PCR. The clonal profiles of the strains differed profoundly; whereas human strains predominantly belonged to clonal types B2 and D, these were not seen among the porcine strains, which all belonged to the E. coli clonal groups A and B1. Contrary to the human strains, the majority of the porcine strains were multidrug resistant. The distinct profiles of the porcine strains suggest selective pressure due to extensive antibiotic use.

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