

Characterization and antimicrobial susceptibility of *Escherichia coli* isolated from healthy farm animals in Tunisia

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ABSTRACT

Healthy animals can constitute a reservoir for *Escherichia coli* potentially dangerous for humans. Our objectives were to investigate virulence genes in *E. coli* isolated from healthy animals in southern Tunisia and to determine their resistance to antimicrobials of high importance in humans and animals. 126 fecal samples were collected from healthy animals (cattle, sheep, goats, chicken, camel, bustard and rabbit) and assayed by PCR for virulence genes and by disk diffusion for antimicrobial resistance. STEC were isolated most frequently from goats (27.7%), sheep (20%) and cattle (14.2%). ExPEC prevalence of *iucD* (41.6%), *papC* (27.7%), *sfa* (13.8%), *afa8* (13.8%) and *iron* (72.2%) was highest in camels. Prevalence of the ExPEC associated genes *iss* and *cnf* and the EPEC defining gene *eae* was highest in rabbits (53.3, 13.3, and 53.3%, respectively). The genes defining enterotoxigenic, enteroinvasive and enteroaggregative *E. coli* were not detected and *faeG* was found only in camels (5.5%). The most common phylogenetic groups were B1 (54.5%) and B2 (16.6%). Virulence gene profiles varied greatly between animal species. Overall, antimicrobial resistance was not highly prevalent, the highest resistance being observed against tetracycline, 43.9%.

KEYWORDS

E. coli; virulence genes; serogroups; antimicrobial susceptibility; PCR

Introduction

Escherichia coli is a normal inhabitant of the intestinal tract of all mammals, although certain strains may be zoonotic pathogens or are responsible for various diseases affecting livestock that have been the subject of extensive studies in developing countries.¹ Pathogenicity of *E. coli* has been associated with the production of virulence factors that categorize *E. coli* strains into several pathotypes causing intestinal or extraintestinal disease:^{2,3} enterotoxigenic (ETEC), enteropathogenic (EPEC), enterohemorrhagic (EHEC), enteroinvasive (EIEC), attaching and effacing (AEEC) and necrotoxicogenic (NTEC) and extraintestinal pathogenic (ExPEC). Epidemiological studies have shown that some of these pathotypes occur worldwide and can be found in different sources such as surface water, farm environment, soil, carcasses and are an important cause of many diseases in both humans and animals.⁴⁻⁶

The disease associated with *E. coli* is usually observed in young animals or those with a weak immunological system. The economic consequences

are significant and result in growth retardation and loss of meat and milk due to high morbidity and mortality. The persistence of virulence factors in *E. coli* in adult animals, which are considered as reservoirs, may be transmitted to humans through direct contact with animals or consumption of their contaminated products.^{7,8} Thus, the detection of virulence factors from different sources facilitates the orientation for the implementation of prevention and control strategies such as biosecurity measures and vaccination programs to ensure the safety of animal products.

The massive and uncontrolled use of antibiotics in developing countries is one of the major factors favoring the emergence, selection and spread of resistant strains in animal populations.⁹ Resistant strains can persist for years on farms, representing a direct and indirect source of contamination for animals and humans, respectively.^{10,11} In Tunisia, many studies on antimicrobial resistance in *E. coli* strains isolated from animal husbandry have been published.¹²⁻¹⁵ However, little is known about the association between antimicrobial resistance and virulence genes.