environmental exposure and food contamination (Ahmed et al. 2010; Guerrero-Ramos et al. 2016). Nowadays, antibiotics are often used not only for treatments but also for prophylactic purposes, mainly in food animals such as chickens (Saenz et al. 2001) or pigs (Li et al. 2014). A review on antibiotic consumption in the United States showed that 80% of the antimicrobial drugs are widely used in different animal species to prevent infections and also obtain a higher-quality product, as supplements in livestock (Ventola 2015).

The exchange of resistance determinants between bacteria can be majored by the horizontal gene transfer (HGT) via mobile genetic elements such as plasmids, transposons, or integrons (Lupo et al. 2012). Quick mutations cause new drug resistance rates in the microorganism population because of their shorter generation times and larger population sizes (Blair et al. 2015; Woodford et al. 2006). Therefore, MDR is common in pathogens with short life cycles, like viruses, bacteria, and protozoa (Medicine 2013).

11.4 *Enterobacteriaceae*: General Characterization

The GI tract of humans and animals are inhabited predominately by Gram-negative and Gram-positive anaerobes (Centers for Disease control and Prevention 2013). Bacteria within the family *Enterobacteriaceae* includes common *K. pneumoniae, E. coli, Salmonella enterica*, and the rare *Proteus mirabilis, Raoultella planticola, and Citrobacter freundii.* All of these strains are considered important human pathogens in nosocomial and community settings (Hamilton and Wenlock 2016; Ruppé et al. 2015). The work of Burow et al. (2014) reported that commensal bacteria have an important role in the spread of AMR because they can be reservoirs of antibiotic resistance genes and drug-resistant opportunistic pathogens. A recent study done in Bangladesh by Das et al. (2016) showed that *E. coli* (69%) and *Klebsiella* spp. (15%) were the most commonly isolated pathogens present in the urinary tract from children hospitalized with diarrhea.

11.4.1 Escherichia coli

Different commensal bacteria may be reservoirs for MDR determinants. *Escherichia coli* is a rod of *Enterobacteriaceae* family and it is also an inhabitant of intestinal microbiota in warm-blooded animals. *Escherichia coli* strains ferment lactose and has an important role in studies about microbiological safety of food products (Van Boeckel et al. 2015), water (Bulycheva et al. 2014), and environment (Kuhnert et al. 2000). Moreover, this bacterium is a causative agent of diarrhea, neonatal meningitis, pneumonia, and extraintestinal infections (Das et al. 2016; In et al. 2016).

In the European context, Portugal has the seventh prevalence of resistance to fluoroquinolones in *E. coli*, with the highest rate among the 29