become reservoirs of these resistant organisms, including endangered unintentional hosts (Day et al. 2016; Iredell et al. 2016).

In more detail, it is said that the main sources of antibiotic contamination come from medicine practices related with urban and hospital effluents (Freire et al. 2016), pharmaceutical production facilities (Rummukainen et al. 2013; Tang et al. 2016), and wastewater from animal production farms (Van Boeckel et al. 2015). All these lead to a substantial increase of antimicrobial accumulation and their metabolites in the environment (Ulstad et al. 2016). The spread still continues, daily, all around the world, but it is more alarming in developing countries (Sosa et al. 2010; Reardon 2014).

Over the years, new classes of antibiotics were developed, such as erythromycin, tetracycline, and chloramphenicol, in the 1940s with the aim of preventing or treating infectious diseases (Kong 2010). But more recently, these have emerged as new pollutants in the environment, mainly because some metabolites are persistent and localized to groundwater and can even cause problems even at low concentrations (Manzetti and Ghisi 2014).

According to CDC (2015), antibiotics are among the most commonly prescribed drugs used in human medicine. However, up to 50% of the time, antibiotics are not optimally prescribed, with incorrect dosing, improper antibiotic selection, or inappropriate treatment duration, or even wrong prescription in case of nonbacterial problems (Ventola 2015).

This constant use of numerous antimicrobial compounds in different activities enables them to reach easily the environment (Li et al. 2014). Consequently, these drugs suffer transformations that induce the production of active compounds with unknown environmental consequences and the rise of new drug-resistant bacteria (DuPont and Steffen 2016; Manzetti and Ghisi 2014). Furthermore, bacteria have become adaptable and more competent in facing environmental stress (Chen et al. 2016; Planta 2007). So, there are different kinds of resistance mechanisms to counter these drugs (Figure 11.1), classified into four main categories: (i) modification or protection of the target, (ii) enzymatic modification or inhibition of the antibiotics, (iii) active expulsion of the antibiotics (efflux pump), and (iv) alteration of membrane permeability (Spellberg et al. 2011; Tenover 2006).

The increment of drug resistance outpaces the pharmaceutical development of new drugs and, according to Centers for Disease control and Prevention (2013), “the more antibiotics are used, the more quickly bacteria develop resistance.”

The worldwide antimicrobial use is one of the main concerns because it turns this problem as a global menace, but we have to consider, as mentioned previously, the endless inappropriate use, overuse, and negligent disposal (Potter et al. 2016; Righi et al. 2016).

Today, in the twenty-first century, the antimicrobial resistance (AMR) threat continue to be a huge problem for the treatments of many pathogenic microorganisms with expected rise of resistant bacteria and the increase of