10.3 The Natural Antibiotic Resistome

Antimicrobial biosynthesis and the associated evasion mechanisms are common in bacteria that coexist in a given microbial habitat (D'Costa et al. 2007). Antibiotic resistance is a natural property of bacteria, hypothetically favored in nature to cope with microbial community members that naturally produce antibiotic residues. Hence, resistance mechanisms may be regarded as survival traits in bacteria thriving in natural communities, being observed in bacteria that were never exposed to antibiotics of anthropogenic origin (Allen et al. 2010). The natural antibiotic resistome, i.e. the whole set of genes that contribute to cope with the presence of antibiotics, encodes possibly a wide panoply of functions that can span from microbial cell defense, inhibition of competitors growth, to biochemical signals, modulators of metabolic activity, or even natural substrates (Davies et al. 2006; Dantas et al. 2008; Martinez 2009). Remarkably, the soil natural resistome has been one of the most studied, with genetic determinants of resistance evidencing either high or low resemblance with the resistance determinants observed nowadays in clinically relevant bacteria (Riesenfeld et al. 2004; D'Costa et al. 2006; D'Costa et al. 2011; Forsberg et al. 2012). The diversity of the natural resistome is also evidenced by the fact that it is probably spread over the whole domain *Bacteria*, with frequent descriptions of occurrence in members of the phyla *Actinobacteria*, *Proteobacteria*, or *Bacteroidetes* (Riesenfeld et al. 2004; D'Costa et al. 2006; D'Costa et al. 2011; Forsberg et al. 2012).

10.4 The Contaminant Resistome

Due to the widespread dissemination in the environment, ARB and ARG are nowadays considered environmental contaminants (Pruden et al. 2006; Berendonk et al. 2015). Contaminant ARB and ARG are emitted by a wide diversity of sources, mainly human and animal excreta. Hence, domestic and animal farm effluents as well as animal manure are the major sources for ARB and ARG, which continuously enrich what has been called the contaminant resistome (Vaz-Moreira et al. 2014; Manaia 2017).

The human impact on the dissemination of antibiotic resistance is demonstrated by the observation of a direct correlation between human intervention and abundance and diversity of ARB and ARG. For example, studies with wildlife species, such as small mammals, gulls and birds of the prey, iguanas, or permafrost soils, show the wide dissemination of antibiotic resistance and, eventually, the effects of the continuous exposure of the biota to antibiotics and some pollutants (Thaller et al. 2010; D'Costa et al. 2011; Vredenburg et al. 2014; Furness et al. 2017). The risks that new resistance determinants jump from the natural resistome to clinically relevant bacteria, jeopardizing the efficiency of antibiotics still regarded as valuable therapeutic tools, exist and have