crosstalk with the human cells is essential to maintain the nutritional balance, stimulate gut cell maturation and proliferation, protect against enteric or opportunistic pathogens, and modulate the host immune system.

It is well established that changes in our diet alter the composition and metabolic output of the human gut microbiome (Sonnenburg and Bäckhed 2016), and it is not surprising that broad-spectrum antibiotic uptake also induces collateral damages in this community, altering the gut ecosystem (Dethlefsen and Relman 2011). Either diet- or antibiotic-induced microbiome perturbations can result in transient or permanent changes, spanning from days up to years. This imbalance in a normal healthy microbiome composition, termed dysbiosis, has been linked to many pathologies including inflammatory bowel disease (IBD), diabetes, obesity, colon cancer, allergies, and infectious diseases (Honda and Littman 2016; Thaiss et al. 2016).

The widespread antibiotic (mis)use is creating a heavy selective pressure in the gut microbiome, forcing the propagation of super-resistant strains. In addition, the correlation between antibiotics consumption and the growing onset of several pathologies from nosocomial resistant infections to chronic and autoimmune conditions, not only in adults but also in infants of increasingly low ages, is raising concern (Francino 2016; Langdon et al. 2016).

Due to the decreased usage of AGAs, their impact on human microbiome has not been as explored as for other antibiotic classes (Rafii et al. 2008; Langdon et al. 2016) (information on AGAs is summarized in Table 1.1). However, the renewed interest in the AGAs and their known role in antibiotic resistance makes it imperative to assess their specific impact and raise awareness to the need of more AGA-targeted studies. Here, we revise the main features of what is known for the general impact of antibiotics, establishing comparisons and particularizing for the AGAs whenever possible. We give an overview of the effect of altered gut microbiome function and composition and of antibiotic-induced alterations on host health and homeostasis and in the accumulation and spread of resistances, which is of major relevance concerning the usage of AGAs. Alternative strategies to modulate human microbiome responses to antibiotics are also discussed.

### 1.4.1 The Effect of Antibiotic-Induced Alterations

In the crowded gut environment, commensals, opportunists, and pathogens continuously struggle and compete for resources and attachment sites (Human Microbiome Project Consortium et al. 2012). In return for food and shelter, bacteria provide many advantages for the host by producing important metabolites and modulating the immune system. Alternative glycan sources used as microbial substrates will result in the production of short-chain fatty acids (SCFAs) such as butyrate, propionate, or acetate (Hamer et al. 2008). Human nutrition and glycan uptake are factors shaping the microbiota (Sonnenburg