colleagues demonstrated that supplementation with pectin and inulin could ameliorate the effect of gentamycin and ampicillin uptake in an *in vitro batch* culture of human gut samples (Johnson et al. 2015). Knowing the substrate specificity of each microbiome strain and how the glycans are recognized and shared by the community is central to design novel prebiotics. This will open endless possibilities to recover from dysbiosis and fight infections by increasing the growth of specific competitors or simply by limiting the growth of targeted pathogens (nutrient depletion).

Combined therapeutics with prebiotics and fecal microbiota therapy (FMT) have shown some promising results in treating or ameliorating *C. difficile* chronic infections and IBD (Colman and Rubin 2014; Moayyedi et al. 2015). Despite the intrinsic resistance to AGAs, *C. difficile* is a reservoir of mobile elements and genetic mutations, hence a menace to increasing antibiotic resistance (Johanesen et al. 2015). The FMT is a crude form of probiotic administration enabling delivery of unknown strains that are thought to suppress *C. difficile* infection by competing for the same niche. The study of FMT can give rise to tailored microbial preparations of defined composition to treat any dysbiosis scenario.

Other approaches to modulate the human gut microbiome include the production of anti-quorum sensing drugs to disrupt bacterial communication and consequently virulence in *P. aeruginosa* (Starkey et al. 2014); antitoxin or small molecule inhibitors of type II–IV secretion systems, the major virulence systems in *Bacillus anthracis*, *Shigella flexneri*, or *Brucella* spp. (Felise et al. 2008; Smith et al. 2012); and anti-biofilm compounds to block biofilm formation, a mechanism of resistance to AGAs (Poole 2011).

1.5 Conclusions and Outlook

In this chapter, an overview on AGAs was made highlighting important aspects related to their historical clinical use as effective antibacterial drugs and their structural motifs and the action of AGA-modifying enzymes and other mechanisms causing bacterial resistance. In recent decades, there has been a renewed interest from the scientific community and the pharmaceutical industry on this well-studied broad-spectrum class of antibiotics. It is also worth mentioning that the study of AGAs as ribosome-targeting antibiotics has been crucial to the elucidation of the bacterial ribosome and to understand at molecular level the fidelity and efficiency of the translation process. The knowledge gained from the structural studies, concerning their mode of action and on resistance mechanisms applied by bacteria, has hinted into new strategies to fine-tune the action of AGAs and their pharmacological profiles. In a recent review by Thamban Chandrika and Garneau-Tsodikova (2018), the authors provide a comprehensive analysis on strategies (synthetic and chemoenzymatic) developed by different groups for generation of novel aminoglycosides and