Exploring the role of gut microbiota in advancing personalized medicine

ABSTRACT

Ongoing extensive research in the field of gut microbiota (GM) has highlighted the crucial role of gut-dwelling microbes in human health. These microbes possess 100 times more genes than the human genome and offer significant biochemical advantages to the host in nutrient and drug absorption, metabolism, and excretion. It is increasingly clear that GM modulates the efficacy and toxicity of drugs, especially those taken orally. In addition, intra-individual variability of GM has been shown to contribute to drug response biases for certain therapeutics. For instance, the efficacy of cyclophosphamide depends on the presence of Enterococcus hirae and Barnesiella intestinihominis in the host intestine. Conversely, the presence of inappropriate or unwanted gut bacteria can inactivate a drug. For example, dehydroxylase of Enterococcus faecalis and Eggerthella lenta A2 can metabolize L-dopa before it converts into the active form (dopamine) and crosses the blood–brain barrier to treat Parkinson's disease patients. Moreover, GM is emerging as a new player in personalized medicine, and various methods are being developed to treat diseases by remodeling patients' GM composition, such as prebiotic and probiotic interventions, microbiota transplants, and the introduction of synthetic GM. This review aims to highlight how the host's GM can improve drug efficacy and discuss how an unwanted bug can cause the inactivation of medicine.