The human gut microbiome, including the microorganisms, their genomes, and the surrounding environment in the gut, has received unprecedented attention over the past decade. Mounting evidence is suggesting that the metabolic activities in the gut microbiome are profoundly intertwined with human health and disease. Owing to its crucial role in human fitness, the gut microbiome is now considered as a new organ in the human body. It is unequivocal that the gut microbiome functions properly on the premise that a normal gut microbial homeostasis is maintained. However, the constitution and functionality of the gut microbiome can be readily influenced by diverse intrinsic and extrinsic factors, which are linked to elevated disease risks. As such, gut microbiome modulation with predictable and desirable outcomes is an attractive approach to promote health and prevent disease. This seminar shows how we examined the role of a black raspberry-based gut microbiome-modulation approach using a mouse model. The functional repertoire and metabolic profile of the mouse gut microbiome were characterized after treatment of a standardized black raspberry-rich diet. Moreover, the effects of this approach on intestinal inflammation were determined. Mice fed this way showed less severe inflammation in the colon, and higher levels of aryl hydrocarbon receptor (AHR) activation in the gut microbiome. Given the importance of AHR in intestinal homeostasis, the ameliorating effects may result from increased microbiome-derived AHR ligands in the black raspberry-modulated gut microbiome.