Recently, there were dramatically increased interests on human microbiome research worldwide. Human microbiome has been considered as the second genome in addition to our own genome and played very crucial roles in maintaining human health. Human microbiota typically reside on the surface of epithelial cells and play various biological roles ranging from metabolism, immune development, mental health, and to organ development. Since 2008, we have determined the diversity of Korean microbiome and determined the genes and pathways of gut microbiome using Korean Twin Cohort. The specific aims of this presentation are 1) to determine and characterize the composition of human microbiome as related to clinical biomarkers, 2) to investigate the effects of host genetics and gut microbiota on metabolic syndrome. We find that the abundance of numbers of OTUs is strongly correlated with BMI, HOMA index, and triglyceride levels. Interestingly, among the gut microbes associated with MetS status, Actinobacteria to which the Bifidobacterium belong, had the highest heritability. Even after adjustment for MetS status, reduced abundances of Actinobacteria and Bifidobacterium were significantly linked to the minor allele of specific SNP, which is associated with triglyceride level and MetS. Our data suggest that specific OTUs in the gut may contain metabolic genes the characteristics of which differ according to host genetic background and/or diet. Our research will help us to understand the association between human microbiome and diseases and to improve human health by intervening both human microbiome and diets.