1. No.
   2019G036

2. Title
   Interaction between Smoking and Gut Microbiome in the Development of Atherosclerotic Disease: A Large Metagenomic Analysis of Japanese Population

3. Period
   2019-2022

4. Summary
   We hypothesized that gut microbiota may interact in the pathogenesis of "smoking and atherosclerosis. To this end, we elucidate the relationship between smoking-induced microbial changes and atherosclerosis through comprehensive analysis of fecal metagenomics. We performed shotgun metagenomic analysis of feces and constructed a dataset of 2,500 Japanese individuals. Smokers relative to non-smokers significantly differed in gut microbial diversity, suggesting that smoking altered the composition of gut microbiota. Bacterial species that varied significantly in smokers included *Megamonas, Fusobacterium, Prevotella, and Actinomyces* spp, which were known to cause inflammation, but have also been reported to increase abundance in atherosclerotic diseases. In contrast, *Akkermansia* spp and short-chain fatty acid-producing bacteria were significantly decreased in smokers. Next, the functional genes of the microbiota were examined, and a significant and marked increase in Lipopolysaccharide (LPS) was observed in smokers. Taken together, the unique changes in the gut micobiota and their functions with smoking suggest a mechanism that triggers chronic inflammation through increased intestinal permeability. Our data underscores that smoking-induced microbial changes play a crucial role in the pathogenesis of atherosclerotic diseases.