Differential Effects of Korean vs. American Diet on Gut Microbiota and Metabolic Profiles in Korean Adults: A Randomized Crossover Intervention (P20-004-19)

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Objectives: Habitual diet influences the intestinal microbiota and metabolites profiles, thereby influencing host physiology. In particular, the westernized diet can contribute to the pathogenesis of metabolic disease whereas, traditional Korean (TK) diet which is rich in plant-based products and low in animal fat and protein provides health benefits. However, both from the gut microbial and metabolic point of view, the exact comparing westernized diet and the TK diet in regard to the biological mechanisms of metabolic disease development have not been studied yet. Therefore, the aim of this study was to compare the effect of the TK diet and the western diet on metabolites and gut microbiota profiling in obese and/or overweight volunteers.

Methods: A randomized crossover clinical trial was conducted. Sixty-one subjects were randomly allocated to one of six possible sequential orders for consuming the three diets (traditional Korean (TK) diet, traditional American (TA) diet, recommended American (RA) diet). Each of the three intervention phases was 4 weeks in duration separated by a 2-week. Using 16S rRNA-targeted sequencing as well as serum and urinary metabolomic platforms, we compared gut microbiota and metabolites composition at the time point before and after each diet intervention.

Results: The diversity of gut microbiota was increased by TK diet intervention but not in TA and RA diet intervention. The TK diet consumption subjects had a reduced abundance of *rx4–4*, *Parabacteroides*, and *Lactococcus*, while an increased abundance of *Pyramidobacter*, *Neisseria*, *Lachnospira*, and *Blautia* compared with TA diet. The relative abundance of *Bifidobacterium* was negatively correlated with serum branched-chain amino acid (BCAA) only after TK diet intervention. Also, gut microbial lipid metabolism was positively correlated with serum trimethylamine N-oxide (TMAO), betaine, and choline only after TK diet intervention.

Conclusions: Our observations provide evidence that alteration of metabolites and gut microbiota profiles by dietary patterns would influence host metabolic status, which has relevance for metabolic disease.