International conference dedicated to 10th anniversary of Center for Life Sciences
"MODERN PERSPECTIVES FOR BIOMEDICAL SCIENCES: FROM BENCH TO BEDSIDE"

National Laboratory Astana, NAZARBAYEV UNIVERSITY

GUT MICROBIOME ALTERATIONS IN SENIORS SUFFERING FROM ALZHEIMER'S DISEASE

Sholpan Askarova, Aiym Kaiyrlykyzy, Samat Kozhakhmetov, Madiyar Nurgaziyev and Almagul Kushugulova

Center for Life Sciences, National Laboratory Astana, Nazarbayev University, Nur-Sultan, Kazakhstan; Kazakhstan Society of Human Microbiome, Nur-Sultan, Kazakhstan

shaskarova@nu.edu.kz

Keywords: gut microbiome, Alzheimer's disease

Introduction: One of the important factors influencing human health and attracting increasing attention of scientists during the last two decades is gut microbiome. It has been demonstrated that the links exist between gut microbiome density and composition and a number of pathological conditions including diabetes, obesity and cardiovascular diseases. These diseases, in turn, are the established risk factors for the development of Alzheimer's disease (AD). Moreover, there is data indicating that gut microbiome can directly affect brain functions. However, only few studies have characterized the human gut microbiome communities associated with AD. Therefore, more research is needed in order to reveal the relationships existing between gut microbiome and brain functions and their influence on the development and progression of AD.

Material and methods: Stool samples were obtained from patients with AD (n =11) and cognitively normal age- and sex-matched participants (n =13). The composition of gut microbiome was characterized by 16S ribosomal RNA MiSeq sequencing. Data analysis was performed using an independent computational pipeline, less OTUs scripts (LotuS) [Hildebrand, F., 2013], SILVA reference database were used as reference for 16S rRNA alignment. Statistical analyses were performed using R version 3.0.2.

Results: Our preliminary results demonstrated that gut microbiota of AD individuals had overall higher α-diversity compared to healthy controls, although this difference was not significant, while β-diversity analysis has revealed statistical significance (R-squared: 0.075975; p-value <0.033). Among bacterial genera, microbiome of AD participants was characterized by a preponderance of *Eubacterium copros*, *Lachnospiraceae NK*, *Rikenellaceae RC9*, *Christensenellacea*, *Prevotella*, *Ruminococcus torgue*, *Parabacterides*, *Coprococcus* and *Corynebacterium* (LDA score [log10] > 3), whereas the healthy microbiome was characterized by a preponderance of *Lactobacillus*, *Holdemania*, *Holdemanella*, *Granucatella* (LDA score [log10] > 3). The relative abundances of *Lachnospiraceae*, *Lactobacillus*, *Eubacterium*, and *Odoribacter* were significantly different in AD patients compared to healthy participants (p < 0.01). Our data are consistent with the results of Vogt et al. (2017) showing that in patients with AD the dominant families were *Lachnospiraceae* and *Ruminococcaceae*.

Conclusion: Distinct microbial communities were associated with patients with AD when compared with cognitively healthy seniors. However, more data is needed to ascertain our findings.