
一般口演

[O3-4](+)RNA 8

座長：

水谷 哲也 (東京農工大学 農学部附属国際家畜感染症防疫研究教育センター)

小池 智 (公益財団法人 東京都医学総合研究所)

2019年10月31日(木) 14:30 ~ 15:15 第4会場 (平安)

14:45 ~ 15:00

[O3-4-08]ピコルナウイルス誘導性急性脊髄炎モデルにおける腸内細菌叢と中枢神経遺伝子発現の変化

*佐藤 文孝¹、尾村 誠一¹、朴 雅美¹、藤田 貢¹、Khadka Sundar¹、西尾 和人¹、角田 郁生¹ (1. 近畿大学)

[Objective] While acute flaccid myelitis (AFM) caused by picornaviruses including enterovirus D68 is an emerging infectious disease, its precise pathomechanism is unclear. Although the gut microbiota can affect systemic immune responses, contributing to the pathogenesis of remote organs including the central nervous system (CNS), it is unclear how the gut microbiota, the immune system, and the CNS communicate one another in AFM. Theiler's murine encephalomyelitis virus (TMEV) belongs to the family *Picornaviridae* and causes AFM-like acute encephalomyelitis in the CNS, where active viral replication and inflammation are obvious 4 and 7 days post infection (p.i.), respectively. We aimed to determine whether CNS TMEV infection could induce gut dysbiosis, which in turn may affect immunopathology in the CNS. [Methods] We infected SJL/J mice with TMEV and harvested the CNS tissues and feces 4 and 7 days p.i.. We examined the CNS transcriptome and the fecal microbiome by RNA sequencing and 16S rRNA sequencing, respectively. [Results] On 4 days p.i., we found upregulation of innate immunity-related genes in the CNS. Fecal microbiome showed that the genera *VadinBB60* and *Dorea* were more and less abundant in TMEV-infected mice than in uninfected controls. On 7 days p.i., we found upregulation of acquired immunity-related genes in the CNS as well as an increase of the genus *Marvinbryantia*. Pattern matching between the CNS transcriptome and fecal microbiome demonstrated that on 4 days p.i., a decrease of the genus *Dorea* correlated with 204 genes ($r^2 > 0.64$) including the innate immunity-related gene *Nlrp3*. On the other hand, on 7 days p.i., an increase of the genus *Marvinbryantia* correlated with 233 genes including immunoglobulin and T cell receptor genes. Principal component analysis showed that the increased *S24-7* family and decreased *Anaeroplasm* genus correlated with principal component 2 values reflecting CNS inflammation. [Conclusions] In TMEV infection, altered abundance of distinct bacterial genera could affect expression patterns of immune response genes in the CNS positively or negatively, contributing to the acute CNS pathology.