Communicating between CNS and gut microbiota in a viral model for multiple sclerosis

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Abstract

While the immune system eliminates extracellular viruses, altering proteomics, immune response, or immune responses, in our present study, various strains of influenza viruses (H1N1, H3N2, and H1N2), Newcastle disease virus (NDV), and Sendai virus (SV) were used to infect mice. The mice were then sacrificed at 3 days post-infection (dpi), and the brains were removed and fixed to analyze the expression of immune-related genes. The results showed that the expression of immune-related genes was downregulated in the brain tissues of infected mice compared to control mice. In addition, the expression of immune-related genes was upregulated in the gut tissues of infected mice compared to control mice. These findings suggest that the immune system is regulating immune responses to eliminate extracellular viruses. Furthermore, the expression of immune-related genes in the brain tissues of infected mice was downregulated compared to the expression of immune-related genes in the gut tissues of infected mice. These findings suggest that the immune system is regulating immune responses to eliminate extracellular viruses.

Results

In the liver, the expression of immune-related genes was downregulated in the brain tissues of infected mice compared to control mice. In addition, the expression of immune-related genes was upregulated in the gut tissues of infected mice compared to control mice. These findings suggest that the immune system is regulating immune responses to eliminate extracellular viruses. Furthermore, the expression of immune-related genes in the brain tissues of infected mice was downregulated compared to the expression of immune-related genes in the gut tissues of infected mice. These findings suggest that the immune system is regulating immune responses to eliminate extracellular viruses.

Pattern matching identifies the genes that significantly correlate with gut microbiota changes

In the CNS, the expression of immune-related genes (T cell and antibody) genes starts on day 7.

CNS transcriptome

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Fecal microbiome

In the phylum level, the phylum Tenericutes is decreased on day 35 of TMEV infection.

Bacterial diversity of fecal microbiome is increased in TMEV-infected mice on day 35

In the genus level, chronic TMEV infection decreases the genus Anaeroplasma and increases the genera of family Tenericutes.

Principal component analysis (PCA) distinguishes microbiome patterns depending on the time points

Conclusion

TMEV infection changes relative abundance of five bacterial genera. Immuno-activated microbiota may contribute to the pathogenesis of multiple sclerosis in the CNS. TMEV infection increases the diversity of the gut microbiota. Influenza, seasonal, and avian influenza viruses affect immune responses.

References


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The study was supported by the Ministry of Education, Culture, Sports, Science, and Technology of Japan. The authors declare no competing interests.

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