

*紅柳翳穹隙*科技活动月研究成果展

Synbiotics inhibits gut microbiome perturbation-caused prolongation of migraine-like pain by restoring short-chain fatty acid signaling

背景介绍

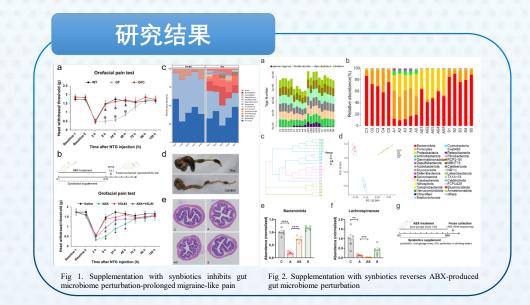
Migraine is the most common disabling primary headache disorder with a high incidence of pain hypersensitivity. However, its exact pathogenesis remains unclear. The gut-brain axis mediates the communication between gastrointestinal (GI) tract and brain through neural, endocrine, metabolic, and immune pathways. Accumulating evidence has suggested that gut microbiome plays an important role in the pathogenesis of migraine. However, how gut microbiome is involved in migraine remains to be investigated. Synbiotics facilitate the production of gut metabolites including SCFAs that regulate the interactions of central nervous system, peripheral nervous system and enteric nervous system, and SCFAs receptors are expressed broadly in these nervous systems. However, which SCFA receptor mediates such effect is still unknown. In the present study, we investigated the effect of synbiotics supplementation on the gut microbiome perturbation-caused prolongation of migraine-like pain and examined whether SCFA signaling contributes to the underlying mechanism.

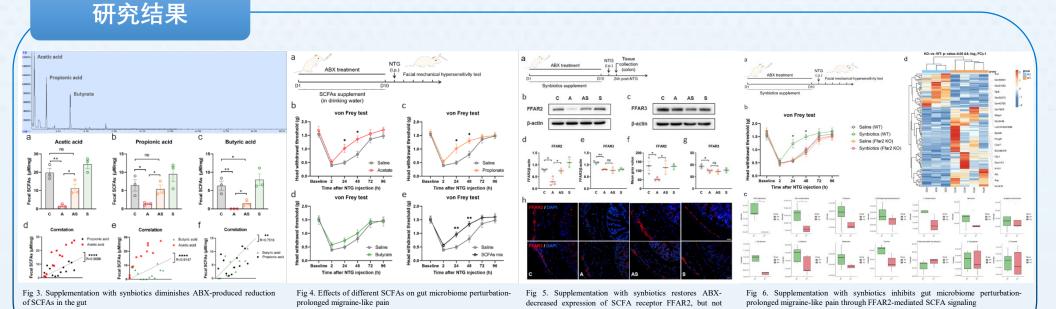
研究方法

- 1. Animals: C57BL/6 wild-type mice and Ffar2 knockout mice were used.
- 2. Nitroglycerin-induced migraine mouse model
- 3. Antibiotics treatment and synbiotics supplementation
- 4. Facial mechanical hypersensitivity test
- 5. 16S rRNA sequencing
- 6. Fecal SCFA measurement
- 7. SCFA treatment
- 8. Histomorphological evaluation
- 9. Western blotting
- 10. Immunohistochemistry
- 11. mRNA sequencing experiment
- 12. Metabolite extraction and UPLC-MS/MS analysis

作者简介

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结论

In conclusion, our results demonstrate that gut SCFAs, especially acetic acid and propionic acid, as well as SCFAs-FFAR2 signaling are critical for migraine pain chronification, and that the supplementation of synbiotics or relevant SCFAs can be developed into an alternative therapy for chronic migraine pain. Future studies could focus on FFAR2 downstream pathways to identify more specific molecular targets for this pain condition.

致 谢

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代表作

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