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Microbial Diversity and Bioinformatics

The Impact of Chronic Pain on the Structure and Stability of Gut Microbial Community in Mouse Models

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Host: Dr. Ying-Ru Chiang 江殷儒副研究員

Online Doctoral Dissertation Defense Presentation

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Abstract

The gut microbiota, a complicated and highly dynamic ecosystem, consists of microorganisms that live within the gastrointestinal tract of its hosts and its structure and stability is relevant to the host health. The gut-brain axis of vertebrates is a bi-directional integrated system composed by immune, endocrine, and neuronal components by which the knowledge regarding the interactions between the gut microbiota and the nervous system (e.g., brain) is lacking. For example, the influence of chronic muscle pain with or without peripheral nerve injury on gut microbiota has not been extensively addressed. Here we used spared-nerve injury (SNI) model that mimics neuropathic pain and acid-induced muscle pain (AIMP) model that mimics fibromyalgia to investigate the link between chronic muscle pain and the dynamics of gut microbiota in C57BL/6 mice. We cut the peripheral nerves for SNI model and performed repeated muscle insult on the left gastrocnemius muscle using acidic saline for AIMP model, evaluated with pain behavioral test, and collected multiple fecal samples to generate time-series data. High-throughput amplicon sequencing coupled with mothur identified certain bacteria genera such as *Adlercreutzia*, *Bifidobacterium*, *Muribacullum*, *Oscillospira*, *Staphylococcus*, and *Erysipelatoclostridium* significantly affected by the chronic pain treatments. Microbial interaction network analysis based on generalized Lotka–Volterra (gLV) equations with multiple simulations showed the instability of gut microbial community when the mice were exhibiting chronic pain. Moreover, the metagenome imputation shed light on the functional profiles of gut microbial communities. Altogether, our bioinformatic analyses of mice gut microbiota indicated the impact of chronic pain on the structure and stability of gut microbial community in vertebrates.