

Assessment of the Tick Gut Metabolome Composition

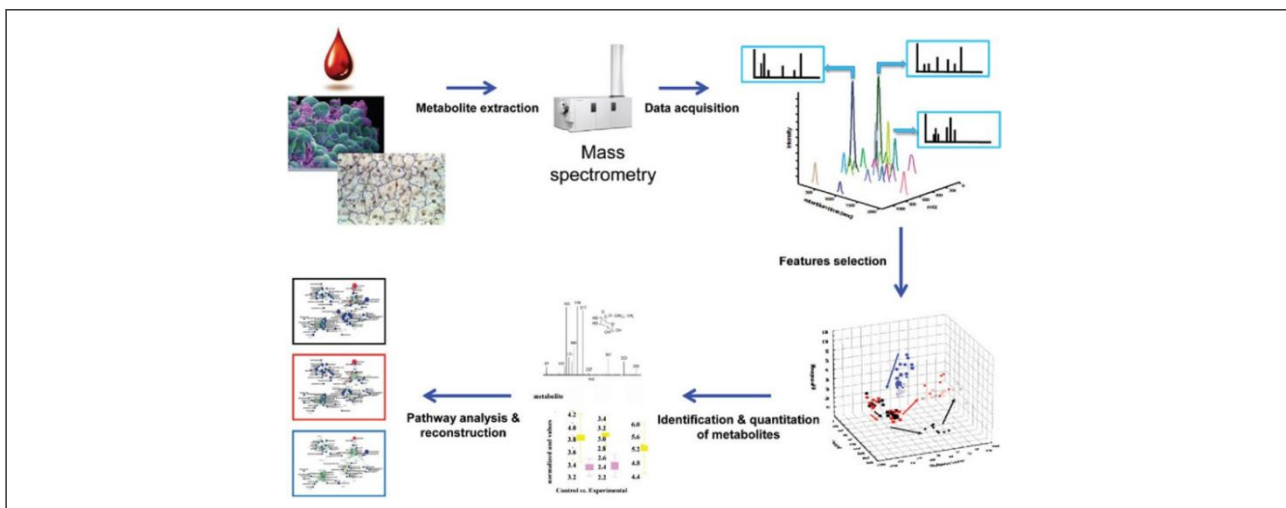
The gut microbiome is involved in the regulation of various metabolic pathways in the host. Some metabolites that are generated and released by the gut microbiota play a vital role in host metabolism, signaling, and immunity. Creative Proteomics provides untargeted metabolomics service to help you analyze the composition of intestinal microbial metabolites.

Metabolomic Profiling

Untargeted Metabolomics

The Lyme disease agent, *Borrelia burgdorferi*, colonizing the gut of the tick *Ixodes scapularis*, can transmit pathogens to vertebrate hosts including humans. *B. burgdorferi* colonization increases the expression of several tick gut genes including *pixr*. Abrogation of PIXR function in vivo alters the gut microbiome, metabolome and immune responses. Changes in the gut microbial members is likely to influence the metabolome of the tick gut due to differences in the metabolic functions unique to the specific bacteria genera. Changes in the composition of intestinal metabolites can be analyzed by means of untargeted metabolomics

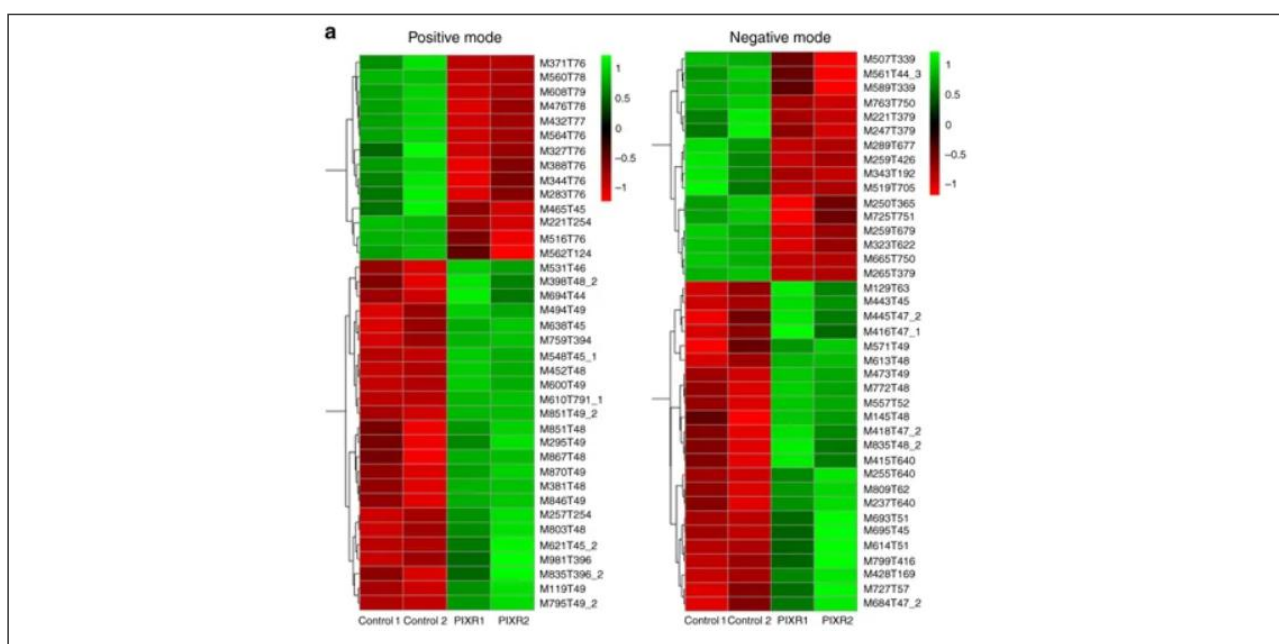
ASSAY OVERVIEW



Extract intestinal metabolites. The analysis is carried out using ultra performance liquid chromatography and quadrupole time-of-flight mass spectrometry (UPLC-Q TOF). 2-Chloro-L-phenylalanine (Sigma) is used as an internal standard. The raw data of the MS is processed and verified. Data obtained from the LC-Q TOF MS system are filtered for denoising

to remove compounds. The filtered data are standardized by peak area normalization and processed with the SIMCA.

DATA OVERVIEW



A total of 59 metabolites were identified on Positive mode (73 hits in total), and 64 metabolites were identified on Negative mode (85 hits in total). At least 38 and 39 differentially represented metabolites were identified under positive and negative mode, respectively, between the guts of ticks fed on PIXR-immunized or ovalbumin-immunized mice and is shown graphically by hierarchical clustering to heatmap.

Features

- Fully automatic, high-throughput, one-stop full-spectrum metabolomics service
- UHPLC-QTOF-MS (Agilent 1290) and UHPLC + AB QTOF 5600(ACQUITY UHPLC) can be used for analysis.
- Quick turnaround time.

Applications

- Development and validation of metabolite-related disease diagnostic markers.
- Mechanism of metabolite related signaling pathway study.

Reference:

Narasimhan S, Schuijt T J, Abraham N M, *et al.* Modulation of the tick gut milieu by a secreted tick protein favors *Borrelia burgdorferi* colonization. *Nature communications*, 2017, 8(1): 184.