



HMT Newsletter

Dear colleagues and friends,

Welcome to our February newsletter. In our featured article this month, Prof. Brian Van Tine found that pharmacologically induced arginine depletion caused increased serine biosynthesis, glutamine anaplerosis, oxidative phosphorylation, and decreased aerobic glycolysis, effectively inhibiting the Warburg effect in ASS1 deficient cells. Co-authored by Kami Kenjiro and Laura Shelton from HMT, Dr. Van Tine has again demonstrated the value of CE-MS in measuring cancer metabolism.

Another one from Dr. Matsumoto used CE-MS to identify low molecular weight metabolites that are transported from colon lumen to colonocytes and somatic blood. Dr. Yamamoto's paper addresses a systematic approach to broadening our annotation list using the unique attributes of CE separations combined with our accurate mass measurements to predict the identify of unknown metabolites.

Alexander Buko, PhD
Vice President
Human Metabolome Technologies America

HMT Updates

2017 New Year's campaign

17% off for new metabolomics projects

- Start the new year with Metabolomics -

Basic Scan: Untargeted global profiling by unique CE-MS
C-SCOPE: Absolute quantitation of 116 key metabolites
Minimum study size: 6 samples
Quick turnaround - 4-8 weeks data delivery
Offer expires on **February 28, 2017**

Featured articles

Arginine Deprivation Inhibits the Warburg Effect and Upregulates Glutamine Anaplerosis and Serine Biosynthesis in ASS1-Deficient Cancers.

Kremer J. C., Van Tine B. A., *et. al.*, *Cell Reports*, **18**, pp. 991-1004.

Recent studies have revealed cooperative modulations of metabolic pathways in tumorigenesis, but the complex relationship dependent upon nutrient availability is still unclear. Prof. Brian Van Tine's group in the Division of Hematology and Oncology at the University of Washington, St. Louis, revealed that pharmacologically induced arginine depletion results in metabolic changes that effectively inhibit the Warburg effect. From the metabolic profiling, they identified an increase in serine biosynthesis accompanied by the suppression of glycolysis. Furthermore, ¹³C labeling analysis confirmed these changes in metabolic flux along with changes in glutaminolysis. These results identify key pathways for new pharmaceutical targets in combination with arginine depletion.

Colonic Absorption of Low-Molecular-Weight Metabolites Influenced by the Intestinal Microbiome: A Pilot Study.


Matsumoto M. et al., *PLoS One*, **12**: e0169207.

The metabolic communication between intestinal microbiota and host is involved in a variety of disease including obesity and cancer, but the identification of factors intermediating the signal is still remained. Dr. Matsumoto's group employed metabolomics to evaluate the correlation of metabolic pools among feces, colon tissue and blood to identify small compounds transporting the pathway. They assessed about 200 metabolites and categorized them based on the potential capability in host body. This is the first case to report the transportation of small compounds from the colonic lumen to blood *in vivo*, and provide criteria to clarify host-intestinal bacterial interactions.

Metabolomics-based approach for ranking the candidate structures of unidentified peaks in capillary electrophoresis time-of-flight mass spectrometry.

Yamamoto H. et al., *Electrophoresis*, in press.

The identification of unannotated peaks in metabolomics data is one of the biggest issue for the discovery of novel biomarker and metabolic mechanism. Dr. Yamamoto and his colleagues, a researchers of HMT, established the new approach to provide the ranking of candidate chemical structures of peaks detected by CE-MS platform. The method include the employment of information about the known metabolites detected in target samples and also three discrete steps. This novel approach is expected to broaden our target space of metabolome.



2017 New Year Campaign

CARCINOSCOPE or BASIC SCAN - 17% OFF from 6 Samples

Contact us for details - Offer ends Feb 28, 2017

HMT is a leading company providing metabolomic profiling based on unique and high performance CE-MS technology. We complete over 400 projects a year and our technology has contributed to the advancement of research in a variety of scientific areas.

Edited by Takushi Oga, PhD

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