



HMT Newsletter

Season Greetings to all our subscribers,

2016 was a particularly great year for HMT and for the field of metabolomics. We saw significant growth of metabolomics applications in food, nutrition, and health research and an expanding literature base! Over 3,200 publications in metabolomics sets a new record; that is more than 250 per month! At HMT we enlarged our publication base by over 20% as our Boston-based business continues to grow in North America and Europe.

This year, as before, we saw great progress in the field with the development of new computational tools, algorithms, and software for metabolomics data analysis and data handling. Several computational tools including data sharing and standardization protocols have been organized with an increasing number of metabolite standards available for metabolite validation. At HMT, our PEA biomarker for Major Depressive Disease continues to fast track to commercialization with the release of a new beta version assay and an increasing patient enrollment for true validation studies. We continue to add additional value to our pipeline with our work in liver and kidney disease.

As the field continues to grow at a rapid rate, HMT is planning for an exciting 2017 by expanding our current platforms and area of expertise. As always, we appreciate your collaboration and look to you, our clients and partners, to work with us to provide the finest metabolomics support. Lastly, we wish you all a safe and happy holiday season.

Alexander Buko, PhD
Vice President
Human Metabolome Technologies America

HMT Updates

News release

Next Generation MDD Diagnostic Assay Kit for Clinical Validation

On November 24, 2016 Human Metabolome Technologies Inc. (HMT) announced for our clinical collaborators in Japan the availability of our clinical enzymatic assay kit for PEA (Phosphoethanolamine) for the diagnosis of major depressive disorder (MDD). From these validation studies using this newly released beta version PEA kit, HMT will obtain clinical feedback to define the suitability of the assay kit and analytical protocols. The commercial release of the final PEA assay kit is scheduled for 2018 in Japan.

Featured articles

2016 - Making Strides with Personalized Medicine

Patient phenotyping, the growing story of the health influence from our microbiome and comprehensive computational modeling are helping to drive metabolomics toward a game-changing status. While metabolomics has already established itself in diabetes, kidney disease, liver disease and many others, in 2016 we saw an upswing in interest showing the role of metabolomics in immunological diseases.

In today's issue, Dr. Fujii's paper on brain metabolism of patients with schizophrenia and Dr. Miyamoto's paper on serum metabolomics in osteoporosis, represent metabolomics growing role in personalized medicine, which combined with basic research, provide a better understanding of human disease.

Metabolic profile alterations in the postmortem brains of patients with schizophrenia using capillary electrophoresis-mass spectrometry.

Fujii T. *et al.*, *Schizophrenia Research*, in press.

We aimed to find the alterations in the profiles of low-molecular-weight metabolites in the brains of schizophrenia patients that may reflect the pathophysiology of the disorder. Human postmortem brain tissues from the frontal cortex (15 schizophrenia patients and 15 controls) and the hippocampus (14 schizophrenia patients and 15 controls) were obtained from the Stanley Foundation Neuropathology Consortium. We analyzed ~300 metabolites, using capillary electrophoresis with time-of-flight mass spectrometry.

A serum metabolomics-based profile in low bone mineral density postmenopausal women.

Miyamoto T. *et al.*, *Bone*, **95**, pp. 1-4.

Osteoporosis is characterized as a metabolic disorder of bone tissue, and various metabolic markers are now available to support its diagnosis and evaluate treatment effects. Substances produced as end products of metabolic activities are the correlated factors to the biological or metabolic status, and thus, metabolites are considered highly sensitive markers of particular pathological states, including osteoporosis. Here we undertook comprehensive serum metabolomics analysis in postmenopausal women with or without low bone mineral density (low BMD vs controls) for the first time using capillary electrophoresis/mass spectrometry.

Biotic Interactions Shape the Ecological Distributions of Staphylococcus Species.

Kastman E. K. *et al.*, *MBio*, **7**: e01157-1116.

Many metagenomic sequencing studies have observed the presence of closely related bacterial species or genotypes in the same microbiome. Previous attempts to explain these patterns of microdiversity have focused on the abiotic environment, but few have considered how biotic interactions could drive patterns of microbiome diversity. We dissected the patterns, processes, and mechanisms shaping the ecological distributions of three closely related *Staphylococcus* species in cheese rind biofilms.

CARCINOSCOPE
C-SCOPE
Absolute quantitation of
116 primary metabolites

HMT target-based analysis

- Quantitative profiling for essential metabolic pathways
- Glycolysis, TCA cycle, Pentose-P pathway, Amino acids, etc.
- Report with statistical analyses and interpretation by biochemist

F-SCOPE
13C labeling analysis for
metabolic flux

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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