FOODS FOR HEALTH

Graduate Student Awards

Recipients of Foods for Health Graduate Student Awards are funded for 50% support for the academic year to work on a transdisciplinary, collaborative project that uses metabolomics to address a relevant problem in the food-nutrition-health axis, with mentoring by two or more affiliates in the Foods for Health initiative.

2017 Awards

Combined proteomics and metabolomics profiling of KLB1 mutant NSCLCs cells to characterize the deregulation of metabolism and pathways contributing to tumorigenesis

Awardee: Bernice Agana, Major: OSU Biochemistry Program
Mentors: Vicki Wysocki, Dept. of Chemistry and Biochemistry; Ken Riedl, Nutrient Phytochemical Analytics Shared Resource; Morgan Cichon, Foods for Health

Lung cancer is the leading cause of cancer mortality in the United States with non-small cell lung cancer adenocarcinoma being the most common histological type. The advancements in next-generation sequencing technology and other high-throughput genomic profiling techniques have enabled the extensive examination of genetic mutations in lung tumors. The tumor suppressor Liver Kinase B1 (LKB1) loss has been reported to occur in about 30% of all cases of non-small cell lung adenocarcinomas. LKB1 is a ubiquitously expressed serine/threonine kinase that regulates cell polarity, energy metabolism, survival, and growth. This study is aimed at understanding the molecular pathways that are altered following LKB1 mutation in non-small cell lung cancer. Such knowledge would be instrumental in elucidating lung cancer signatures as well the identification of the molecular drivers of tumorigenesis., candidate targets of intervention and to aid with diagnosis by identifying candidate biomarkers for clinical use.

Metabolome-based genome-wide association study of innate immunity in rice

Awardee: Pengfei Bai, Major: Plant Pathology
Mentors: Guo-Liang Wang, Dept. of Plant Pathology; Joshua Blakeslee, Dept. of Horticulture and Plant Sciences

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Rice is an important food crop that feeds about half of the world’s population. However, rice yield is threatened by various bacterial and fungal diseases. Among these diseases, rice blast, which is caused by the fungus *Magnaporthe oryzae*, is particularly devastating, routinely causing 10–30% yield losses. Growing rice resistant cultivars has been recognized as a cost-effective approach to disease management which has the potential to contribute to increased crop productivity, while reducing adverse environmental effects and potential for chemical contamination affecting human health. Recent progress in molecular and genetic analyses of rice immune receptors and signaling regulatory proteins has greatly enhanced efforts to genetically engineer disease resistant rice. However, there remains a gap in our current knowledge on the linkage between pathogen-induced changes in gene expression and pathogen-induced shifts in metabolite accumulation which has hindered the successful use of immune receptors and regulators for disease control in rice. Metabolome-based genome-wide association study (mGWAS), the integration of metabolomic data sets (usually shifts in the accumulation patterns of specific metabolites between genetic lines or variants) with genetic polymorphisms, allows for the mapping of the genomic loci responsible for natural variations in metabolism and is a powerful tool which can be used to identify novel genes associated with metabolomic changes under different stress conditions. We aim to profile metabolomic changes in response to *M. oryzae* infection in both resistance and susceptible rice lines, and identify genes associated with key metabolites that are important for rice disease resistance using mGWAS.

**Identification of unknown and known metabolites by SUMMIT MS/NMR: Application to bile**

**Awardee:** Cheng Wang, Major: Chemistry  
**Mentors:** John Gunn, Dept. of Microbiology; Ewy Mathé, Dept. of Biomedical Informatics; Rafael Brüschweiler, Campus Chemical Instrument Center, Dept. of Chemistry and Biochemistry, Biological Chemistry and Pharmacology

Despite ongoing progress in the compilation of ever-larger metabolomics databases, the identification of unknown metabolites remains a major bottleneck in understanding how genetics, diet, lifestyle, and environment influence the transcriptome, proteome and, ultimately, the metabolome. Finding ways to synergistically apply the two primary analytical techniques in metabolomics, namely mass spectrometry (MS) and nuclear magnetic resonance (NMR), to the same problem has been a challenge due to the high complementarity of their information content. *Salmonella* Typhi, the etiologic agent of typhoid (enteric) fever, which is a human systemic disease that is responsible for an estimated 21 million new infections annually, is the cause of approximately 600,000 deaths worldwide. Up to 5% of individuals infected with S. Typhi become chronic carriers, where the prime location of persistent infection is the gallbladder (GB). Identification of unknown and known metabolites in bile extracted from GB plays crucial role in understanding the pathogenic mechanisms or metabolic processes for further therapeutic purposes. We recently introduced an approach that synergistically uses NMR and MS applied to a single sample of a complex mixture (at 13C natural abundance) for the validation of known compounds and the determination of unknowns without the use of NMR or MS spectroscopic databases, termed SUMMIT MS/NMR (for “Structure of Unknown Metabolomic Mixture components by MS/NMR”). We aim to build a fully integrated framework that applies ultrahigh resolution MS and NMR analytical techniques and bioinformatics, metabolomics data to rapidly and accurately identify known and unknown metabolites in bile mixture extracted from GB toward molecular and functional characterization of metabolisms disrupted by Typhoid fever.

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