POSTER SESSIONS 1 AND 2 – Monday and Tuesday – all odd number posters will be on display.
POSTER SESSIONS 3 AND 4 – Wednesday and Thursday – all even number posters will be on display.

*AWARD WINNERS

BIOMEDICAL

P-103 Is there a metabolomic signature indicative of human urine specimen degradation? A systematic review

PRESENTING AUTHOR: ***Ana Rosen Vollmar, Yale School of Public Health, United States***

CO-AUTHORS: ***Caroline H. Johnson***

With metabolomics increasingly used to investigate the exposome, interest is growing in using biobanked samples and other specimens in long-term storage. Specimen quality can vary due to handling procedures, storage conditions, and freeze-thaw cycles. We conducted the first systematic review of whether there is a metabolomic signature of human urine specimen degradation. Using controlled vocabulary terms and text words, studies were identified through PubMed and Web of Science. Seventeen studies met the inclusion criteria of using human urine, and comparing conditions of storage time, temperature, and freeze-thaw cycles. We developed a study quality rating system based on the Metabolomics Standards Initiative. Study quality varied but was generally moderate to high, lending support to our findings. While targeted analyses found significant metabolite changes across comparison groups, untargeted analyses found no meaningful changes in the global metabolomic profile, with biological variability the primary source of variability between specimens rather than handling and storage conditions. More than 2-3 freeze-thaw cycles may alter metabolite composition in targeted studies, but untargeted analyses are robust to even 9 freeze-thaw cycles. Minimal difference was observed between specimens stored at -20 °C and -80 °C. Specimens remained stable for 6 months at -25 °C or -80 °C, but no studies examined storage longer than 6 months. A total of 90 metabolites associated with handling and storage conditions were identified across all studies, with 19 identified by at least 2 studies, indicating there is not yet a clear metabolomic signature of urine degradation, but offering directions for future research.

P-104 Sugars and derivatives in the human metabolome: what they can tell us

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Sugar compounds (mono- and disaccharides, polyols and sugar acids) are part of the metabolome. Although numerous sugar compounds occur in nature, mostly only a very few common and well-known compounds are analyzed. Metabolomics often requires a compromise between detecting as many different metabolites and substance classes as possible, and satisfactory separation of compounds within each substance class. Sugars with their high structural similarity present a particular challenge with usually insufficient chromatographic and mass spectrometric separation. More comprehensive and highly selective methods to assess the diversity of the human body fluid sugar profile are thus needed because sugar compounds may serve as markers of dietary intake and may act as reporter molecules of the health status. We developed a semitargeted GC-MS based profiling method enabling detection of known and unknown sugar compounds in urine and plasma. 24 h urine samples of the observational Karlsruhe Metabolomics and Nutrition study with 300 healthy participants were analyzed and markers for dietary intake were identified amongst the sugars, such as mannoheptulose and perseitol for avocado consumption. In an additional intervention study including an oral glucose tolerance test, plasma samples of healthy, prediabetic and diabetic participants were analyzed and revealed, next to glucose, a variety of sugars and derivatives with marked postprandial differences dependent on health status, such as trehalose. Overall, the application of the sugar profiling in these human studies revealed a more complex sugar profile than described or expected so far with potential for finding novel markers.

P-105 Metabolic phenotyping of individuals in baseline and repeat surveys of Tohoku Medical Megabank Cohort Project

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Tohoku Medical Megabank (TMM) Project operates prospective cohort studies for more than 150,000 individuals in Japan. We have finished baseline surveys and are now conducting repeat surveys. We are also operating genome and omics analyses for the cohort participants and have already collected whole genome sequences data from more than 5,000 participants and the metabolome data from more than 10,000 participants. We have released these results as a database, Japanese Multi Omics Reference Panel (jMorp), which is freely available on the web site (https://jmorp.megabank.tohoku.ac.jp/). In this conference, we report recent progress of our metabolome analyses in the TMM project. We expanded our metabolome analysis and will release NMR metabolome data from more than 15,000 participants at the baseline survey this year. We also quantified more than 1,000 participant's plasma metabolites by means of LC-MS/MS and will also release these results. On the other hand, we have performed metabolome analysis for participants at the repeat assessment survey and will show the changes of metabolic phenotypes of individuals between the baseline and repeat surveys. We are also performing metabolome genome-wide association study (MGWAS) and other association studies. We suggest the importance of the long-term examination of metabolome analysis for the large scale prospective cohort studies.