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Agilent Technologies Lunch Presentation

Metabolomics 2024

Event Details

Metabolomics 2024

Lunch Session

Date | 18 June , 2024

Time | 12:20 – 13:20

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Title : Development of CE-MS metabolomics and its application in cancer

Speaker : Tomoyoshi Soga, Institute for Advanced Biosciences, Keio University

Metabolomics has become an essential tool in many fields, including biological, medical, clinical, microbial, plant, and food studies. Despite their importance, no analytical method has been developed that fully encompasses all metabolites. This is primarily because more than 1,000 metabolites, with similar to different physical and chemical properties, coexist in the cell, complicating their analysis. Almost all of the metabolites of key pathways in the central carbon metabolism are polar and charged species, e.g., phosphorylated saccharides, phosphorylated carboxylic acids, carboxylic acids, amino acids, nucleosides, and nucleotides. Focusing on this characteristic, the authors proposed the first CE-MS method for global metabolomic profiling in 2003 [1,2]. CE-MS shows advantageous features as an analytical tool for metabolomics, such as high resolution, very low sample consumption, and the possibility to easily detect charged compounds. Moreover, CE-MS has demonstrated its better quantification accuracy and reproducibility compared with other analytical platforms.
Recently, we have reported a high-throughput metabolite profiling method based on multiple sample injection capillary electrophoresis triple quadrupole tandem mass spectrometry (CE-MSI-MS/MS), which allows sequential 40-sample analysis in a single run.
In this seminar, I will present two examples of the application of CE-MS metabolomics to colorectal cancer research. One is to answer the question of when colorectal cancer metabolism occurs and what are the regulatory molecules that reprogram colorectal cancer metabolism, which is the focus of much attention in cancer metabolism [3], and the other is on the development of a high-throughput screening method for colorectal cancer [4].

References

1. Soga T, et al. J. Proteome Res. 2, 488-494, 2003.
2. Soga T, et al. J. Biol. Chem. 281, 16768-16776, 2006.
3. Satoh K, et al. PNAS 114, E7697-E7706, 2017.
4. Igarashi K, et al. J. Chromatogr. A 1652, 462355, 2021.

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