

Presentation preference: Oral

Presenting author: Wei Zhang, PhD student

Title: Capillary electrophoresis-mass spectrometry for metabolic profiling of low numbers of mammalian cells

Sponsor of the project: the Vidi grant scheme of the Netherlands Organization of Scientific Research (NWO Vidi 723.016.003)

Capillary electrophoresis-mass spectrometry for metabolic profiling of low numbers of mammalian cells

Wei Zhang^a, Faisa Guled^a, Thomas Hankemeier^{a,b}, Rawi Ramautar^a

a. Division of Systems Biomedicine and Pharmacology, Leiden Academic Centre for Drug Research, Leiden University, the Netherlands

b. Netherlands Metabolomics Centre, Leiden, the Netherlands

Metabolomics studies using a small amount of cells may save time and money, while in some cases (e.g., profiling pathogenic cells in an early-stage tissue), only a small number of cells are accessible for analysis. The analysis of small amounts of biological samples challenges the analytical toolbox used in present-day metabolomics studies, and a significant number of crucial biological questions cannot be properly addressed. To allow metabolic profiling of limited sample amounts, the potential of capillary electrophoresis-mass spectrometry (CE–MS) using a sheathless porous tip interface has been assessed using HepG2 cells in starting amounts of 500 and 10,000 cells as a model system in this work. It is shown that highly efficient and information-rich metabolic profiles for cationic metabolites at low-pH separation conditions could be obtained by sheathless CE–MS using an injection volume of only circa 42 nL, which equals to the content/aliquot of circa 0.25 and 5 HepG2 cells, respectively. With as little as the content of 0.25 cell injected, more than 24 cationic metabolites could be identified. A further improvement of sample preparation and/or the injection part is required in order to effectively analyze the compounds of interest in very low sample amounts by sheathless CE–MS. However, the results obtained so far clearly indicate the strong potential of the proposed method for metabolic profiling of limited sample amounts.