Metabolomics Study of Premature Labor: Combined Supercritical Fluid Chromatography and Liquid Chromatography Coupled with Ion Mobility-Mass Spectrometry

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Yearly, 15 million babies are born preterm, for which complications are the leading cause of death for children under 5 years of age (~1 million in 2013)[1]. However, the complete understanding of preterm birth still remains unknown. Risk factors (maternal age and infections) can have an influence, but alone, do not have the predictive power to apply necessary measurements for prenatal care. The discovery by metabolic signatures associated with preterm birth has the potential of not only predicting but also understanding the complexity of pregnancy where two organisms are in constant symbiotic interaction. Several omics methodologies have been previously utilized to study and predict preterm risk with positive outcomes[2]. Even though the study of the pregnancy metabolome been of interest for decades, these studies are relatively new with state-of-the-art high throughput technology available today[3].

A significant consideration in mass-spectrometry based untargeted metabolomics studies is the coverage of different biomolecular classes when utilizing only one separation technique prior to ionization. Reversed-phase liquid chromatography (RPLC) is usually the technique of choice by most studies despite limitations with polar molecules. By combining different separations, such as supercritical fluid chromatography (SFC), higher metabolome coverage can be attained, increasing the number of features detected, thus increasing the probabilities of detecting features significantly different in abundance between sample groups.

Herein we present the analysis of amniotic fluid samples of term and preterm pregnancies with both traditional and non-traditional techniques. RPLC and SFC coupled to ion mobility-mass spectrometry (IM-MS) provide the great advantage of higher metabolome coverage since separations are based upon different physicochemical properties. A self-organizing maps (SOM) software (MEDI, Molecular Expression Dynamics Investigator), which compares and groups up-

and down-regulated metabolites was employed to prioritize differences between term and preterm metabolome [4]. MEDI images show significant differences between the metabolome of term and preterm amniotic fluid samples for both separation techniques.

References

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