Oral Presentation HUPO 2019 - 18th Human Proteome Organization World Congress

Days

Saturday, 14th …

Sunday, 15th Se…

Monday, 16th S…

Tuesday, 17th S…

Wednesday, 18t…

Thursday, 19th …

Search

Speakers (http:…

Phenotyping of multiple biofluids for liquid biomarkers for diagnostics and personalized medicine (#224)

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Background & Significance
Inflammatory and autoimmune diseases include multifactual pathomechanisms and systemic responses. Advances in high-throughput molecular technologies have increased investigations into the utility of transcriptomic, proteomic and metabolomic approaches as diagnostic tools for precision medicine (1). Although more commonly diagnosed in adults, all of above diseases can manifest in childhood as early as infancy (2). Thus, Intrauterine bacterial infection predisposes to preterm birth and is associated with dysregulated development of several organs, including gut, lungs and brain. Basic blood tests include inflammatory markers and autoantibodies, however, now analysis speed and robustness allow more readily clinical insight biofluids. We present recent concepts and studies investigating early life inflammatory diseases as well as low grade inflammatory diseases in different biofluids from plasma to CSF accessing causalities leading to inflammation and pain.

Methodologies
Plasma, CSF, synovial fluid and urine samples were investigated in multiple pathologies (Arthritis, sepsis etc.), before and after treatment in patients (biologics; intraarticular gold) or in neonates as well as pig as model animal for neonate conditions. Plasma and urine may be available from the HUPO hPOP project. Deep proteome, PTM and EV profiling were accomplished using quantitative proteomics approaches using quantitative mass spectrometry-based analysis by DIA/PASEF followed by deep datamining (3,4). PTM profiling were evaluated by 4D CCS based feature finding.

Results and Conclusion

Discovery of biomarkers and/or inflammatory signatures through integration of multi-omic data has potential to stratify patients or neonates with sepsis for improved treatment and prognosis. Firstly, our data using next generation proteomics approaches alleviates many pitfalls of missing values and poor proteome coverage including unbiased PTM profiling without enrichment strategies. Next, investigating neonates and molecular ontogeny of newborns revealed distinct immune immunomodulatory and inflammatory profiles readily correlated by cross-species pig studies. Low grade inflammation and treatment regimens are more readily addressed comparing multiple biofluids.

1. 1. Ng S, Strunk T, Jiang P, Muk T, Sangild PT, Currie A. Precision Medicine for Neonatal Sepsis. Front Mol Biosci 2018;5:70.
2. 2. Lee AH, Shannon CP, Amenyogbe N, Bennike TB, Diray-Arce J, Idoko OT, et al. Dynamic molecular changes during the first week of human life follow a robust developmental trajectory. Nat Commun 2019 10(1):1092.
3. Meier F, Beck S, Grassl N, Lubeck M, Park MA, Raether O, et al. Parallel Accumulation–Serial Fragmentation (PASEF): Multiplying Sequencing Speed and Sensitivity by Synchronized Scans in a Trapped Ion Mobility Device. J Proteome Res. 2015 12):5378–87.
4. Claridge B, Kastaniegaard K, Stensballe A, Greening DW. Post-translational and transcriptional dynamics – regulating extracellular vesicle biology. Expert Rev Proteomics 2019 Jan 2 16(1):17–31.