OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference and Exhibition on
Metabolomics & Systems Biology

March 24-26, 2014 San Antonio, USA

Kinetics and data normalization: Can we avoid being misled by "omic" investigations?

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Abstract

Omic-type analyses allow one to cast a sizeable net in terms of assessing analytes. For example, it is possible to readily characterize and/or quantify large numbers of molecules in targeted and/or untargeted modes. Clearly, scientific revolutions are being driven by advances in novel high-throughput sample preparation techniques along with the development ofmore sensitive hardware (e.g. mass spectrometers) and powerful data processing technologies. Although a central goal of any "omic" investigation is to determine differences between groups, it is often not possible to explanation the nature of any differences. Our first objective here is to consider the use of isotope tracers in parallel with omic-type analyses. We demonstrate the need to simultaneously consider static and kinetic profiles in order to fully appreciate phenotypic differences. This is clearly seen in examples taken from studies surrounding dyslipidemia. Our second objective here is to consider the impact of data normalization on the interpretation. For example, it is possible to develop contradictory conclusions if one examines the concentration of a circulating biomarker(s) in the absence of any consideration for a target tissue(s). We demonstrate an example surrounding the regulation of triglyceride flux in adipose tissue by insulin and/or epinephrine. In total, we believe that omic-type analyses can facilitate the development of novel hypotheses surrounding physiological systems, however, one should exercise caution when drawing conclusions as some observations may be counterintuitive and/or misleading.

Biography

Dr. Stephen F. Previs is currently director at Merck. He worked as Assistant/Associate Professor Nutrition and Medicine Case Western Reserve University during 1999-2009. He did his Post Doctoral from Yale University. Dr. Stephen F. Previs research interests are Analytical chemistry, Biomarkers, Drug discovery, Drug metabolism, LC-MS.

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