Proteomics approaches for identification and validation of predictive biomarkers applied to translational systems pharmacology in oncology

The last decade has witnessed significant advances in the development of biomarkers in the oncology arena that enhance our understanding of molecular and cellular mechanisms controlling Tumor initiation, maintenance and growth. Predictive or also called diagnostic biomarkers are helpful in predicting the clinical outcome of patients under immuno-oncology drugs and targeted therapies and in preventing toxicity. Advances in proteomics methodologies have tremendously helped in the advancement of translational systems pharmacology in cancer therapy through the increased identification and validation of molecular predictive biomarkers. Some good examples of proteomics based identification and validation of predictive biomarkers being used in the daily clinical oncology practice are: Estrogen and progesterone receptors to predict sensitivity to endocrine therapy in breast cancer, HER2 to predict sensitivity to Herceptin treatment and KRAS mutation to predict resistance to epidermal growth factor receptors (EGFR) antibody therapy. In this symposium the latest progress on proteomics approaches applied to quantitative protein and signalling event characterization in cancer therapy will be reviewed and examined. A discussion on how these technologies have been successfully applied in both discovery research and clinical studies for Signalling pathway dissection, Proteomic biomarker assessment, Targeted treatment evaluation and quantitative proteomic analysis will be held. Lastly, a comparison of the different proteomics technologies with other conventional platforms will be performed.

Biography

Sihem Bihorel has joined the Department of Pharmaceutics at the University of Florida as an Assistant Professor. Her laboratory is located at the Center for Pharmacometrics and Systems Pharmacology in Lake Nona, Orlando. Her research interests are in the areas of preclinical and clinical pharmacokinetic and pharmacodynamic (PK/PD) analysis, Omics, PK/PD modeling and simulation, systems pharmacology and population modeling, large molecule therapeutics (proteins, monoclonal antibodies), liposomes, targeted therapeutics and anti-angiogenic therapeutics. She utilizes quantitative systems pharmacology approaches to guide the development of new therapies and the identification of promising combination therapies as well as of novel biomarkers in oncology. She integrates quantitative systems pharmacology with PK/PD modeling and simulation to advance drug discovery and development and leverage the understanding of drugs action which holds great promise to facilitate translational research. Her research is also focused on investigating how priming solid tumors with a pro-apoptotic agent then combining a subsequent large therapeutic with anti-angiogenic agent can defeat drug resistance in cancer and further enhance the efficacy of targeted anticancer agents and translating these findings toward clinical settings.

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