

Powerful integration of lipid metabolic profiling with gene expression analysis

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A recently published research article in the *Journal of Proteome Research*, authored by researchers from the Nestlé Research Center, Genomatix Software GmbH, Rosetta Inpharmatics LLC, CXR Biosciences Ltd, the Cancer Research UK Molecular Pharmacology Unit demonstrates the synergisms and enhanced analytic power of the combination of thorough metabolic profiling with the unique and proprietary microarray analysis methods of Genomatix Software GmbH.

The study elucidated the effects on Mouse lipid metabolism by the disruption of hepatic Cytochrome P450 reductase (POR) in a POR deficient knock-out mouse model. It clearly could demonstrate that though gene expression and lipid metabolism in extrahepatic tissues being sensitive to hepatic POR functionality, the lipidome in general is only minimally affected.

Analysis of regulatory pathways and networks, observed expression changes and lipid profiling led to the conclusion that POR can be considered an enzyme critical for the proper functioning of lipid mobilization and metabolism predominantly within the mouse liver with only minor effects on lipid metabolism in the biological system at large.

The concordance between the two analytical platforms (Genomatix transcriptomic vs lipidomic) in the liver was excellent, and serves as a demonstration for the valid approach for generating novel hypotheses to unravel protein function that cannot be accomplished with as much confidence using either platform individually.

“I am very excited about the possibility to overlay metabolic profiles with expression data and pathway information. We see the strategies applied in this study as a prototype for further analyzes bringing together metabolomics and expression analysis in a multiple lines of evidence manner. “ says Dr. Martin Seifert, co-author of the study and Vice President Microarray Business and Collaborative Research at Genomatix.

Source: Genomatix Software GmbH

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