PW01-45 - BIOMARKER DISCOVERY FOR PSYCHIATRIC DISORDERS BY STABLE ISOTOPE METABOLIC LABELING AND QUANTITATIVE PROTEOMICS

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Objectives: Biomarkers for psychiatric disorders are critical for patient stratification, premorbid diagnosis and personalized treatment. Our aim is to identify protein biomarkers for anxiety disorders by comparing the synaptic proteomes of a well-established mouse model of high (HAB), normal (NAB) and low (LAB) anxiety-related behavior.

Methods: We have compared protein expression levels using ^{15}N metabolic labeling and quantitative proteomics. Mice were metabolically labeled through feeding with a ^{15}N-enriched diet. Synaptosomes from unlabeled HAB and LAB mice were then compared with synaptosomes from ^{15}N labeled NAB mice by quantitative mass spectrometry. Protein expression differences were validated with Western blots, enzymatic assays and *in silico* pathway analysis.

Results: We have identified numerous protein expression differences between HAB and LAB synaptosome proteomes. We observed alterations in energy metabolism pathways such as the Krebs cycle as well as in mitochondrial function. Furthermore, we detected changes in transport and phosphorylation processes.

Conclusions: We present an accurate proteomics platform for biomarker discovery in psychiatric disorders. We identified candidate biomarkers and pathways involved in anxiety pathophysiology. Our data provide the basis for the establishment of a biomarker panel that will shed light on anxiety pathophysiology and can be applied for optimal therapeutic intervention.