**OVERVIEW**

We employed a 'label-free' mass spectrometry-based approach to discover proteomic and metabolomic profiles from CSF samples from healthy subjects and healthy controls. Partial least squares discriminant analysis showed a highly significant separation of the metabolomic profiles between schizophrenia patients and healthy controls. In the metabolomics study, potential metabolomic biomarkers contributing to the separation were identified. In the proteomics study, putative peptide biomarkers were identified and quantified. The results indicate a potential association between specific CSF metabolites and CSF proteins.

**RESULTS**

The PLS-DA scores plots (Figure 1a and 1b) show that the data from both the proteomics and metabolomics studies are clearly separated, with the control samples clustering in the lower left corner and the schizophrenia samples in the upper right corner of the plots, indicating a significant separation between the two groups.

**CONCLUSIONS**

- A total of 118 different proteins were identified with expression changes, 18 were up-regulated and 16 were down-regulated in the schizophrenic samples.
- The PLS-DA scores plots (Figure 1a and 1b) show that the data from both the proteomics and metabolomics studies are clearly separated, with the control samples clustering in the lower left corner and the schizophrenia samples in the upper right corner of the plots, indicating a significant separation between the two groups.
- The quantitative data set was processed using Waters Protein Expression software for further analysis.

**METHODS**

1. **LC CONDITIONS**

   - For the metabolic study: 5 µL of neat CSF sample was analyzed. For the proteomic study: 75 µL aliquots of each CSF sample were analysed.
   - Table 1. Comparison of identified proteins

2. **PROTEOMICS**

   - Proteins were identified from a database search using PLGS software for further analysis.
   - The EMRT components responsible for any clustering or separation within the data can be readily determined from the associated weightings plot. The compounds responsible for the clustering were primarily amino acids and lipids. In addition, the clustering were principally amino acids and lipids. In addition, the clustering were principally amino acids and lipids. In addition, the clustering were principally amino acids and lipids.

3. **METABOLIC STUDY**

   - The data was deconvoluted and aligned using the MarkerLynx™ application manager within MassLynx™.
   - The table of MS/MS retention time pairs with associated intensities generated was analyzed. For the proteomics study: 75 µL aliquots of each CSF sample were analyzed. For the metabolic study: 5 µL of neat CSF sample was analyzed. For the proteomics study: 75 µL aliquots of each CSF sample were analyzed.

**REFERENCES**

1. Thérèse McKenna1, Hilary Major1, Jan Claerbeaut3, Jennifer Burgess1, Christopher Hughes1, Jeffrey T.-J. Huang2, Sabine Bahn2, and James Langridge1

   APPROACH TO BIOMARKER DISCOVERY FOR A COMBINED PROTEOMIC AND METABONOMIC STUDIES

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   **OVERVIEW**

   Schizophrenia is a common, chronic disabling neuropsychiatric disorder which is characterized by hallucinations, delusions, inappropriate affects and bizarre or inappropriate behaviors. Approximately 1% of the population will be affected during their lifetime and as diagnosis of schizophrenia relies on a large number of symptoms, making diagnosis at the individual level difficult.

   **METHODS**

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