INTRODUCTION

Differential proteome analysis of the cerebrospinal fluid (CSF) of normal and equine protozoal myeloencephalitis (EPM) affected horses using two-dimensional fluorescence difference gel electrophoresis (2D DIGE) and mass spectrometry (MS) is a powerful tool to identify proteins that differentiate diseased from healthy samples. This technique is critical for understanding the pathogenesis of EPM, a significant disease affecting horse health.

RESULTS

Fig. 1: Experimental design for CSF proteome analysis study.

Fig. 2: 2D maps of horse CSF proteins labeled with CyDyes. CSF proteins were electrophoresed, labeled with CyDyes DIGE, scanned on Typhoon (A and B) and the images were analyzed with DeCyder 2-D differential analysis software. The yellow and red spots were differentially expressed. Cy3 (B) and Cy5 (A) difference gel images with spot excision for mass spectrometry analysis are compared to normal CSF for identification of differentially expressed proteins.

Table 1: Identification of differentially regulated proteins. The identified proteins that were found to be differentially expressed may lend insight into the pathogenesis of EPM.

CONCLUSIONS

The EPM decrease in serum albumin, apolipoprotein E, and apolipoprotein A-I compared to the CSF of normal horses. The above proteins, including the isoforms, may be associated with EPM, and the proteins that were found to be differentially expressed may lend insight into the pathogenesis of EPM.

ACKNOWLEDGMENTS

Discovery Park, and the School of Veterinary Medicine Purdue University for financial assistance.

REFERENCES