PROTEOMICS & SEPSIS–NEW AVENUES FOR DIAGNOSIS

AJC Soares[1,3], MF Santos[1,3], J Chung[1,3], LM Albuquerque[2,3], MRO Trugilho[2,3], AGC Ferreira[2,3], J Perales[2,3] and GB Domont[1,3]

[1]Laboratório de Química de Proteínas, Depto de Bioquímica, Instituto de Química, UFRJ, [2]Laboratório de Toxinologia, IOC, Fiocruz, [3]Rede Proteômica do Rio de Janeiro

Sepsis is a major healthcare problem from the perspective of mortality and economics. In this study 2-D electrophoresis profiles of plasmas from 10 patients with sepsis caused for gram-negative bacilli, *Acinetobacter baumannii*, admitted in the Hospital de Força Aérea do Galeão (2006, RJ) and 10 healthy donors were compared. Plasmas were depleted of the 6 most abundant proteins using the multiple affinity removal column (Agilent Technologies0, followed by the multiplex analysis of the samples using the DIGE technique and the DeCyder® 5.0 software. Protein spot detection and quantitation were performed using the Differential In-gel Analysis module. To match protein spots on different gels and perform statistical analysis (paired Student's T test) of the data the Biological Variation Analysis module was used. Several lower abundant proteins were differentially expressed between the two experimental groups ($p < 0.01$). These proteins were identified by MALDI-TOF/TOF after total protein visualization with colloidal Coomassie stain. This multiplex approach significantly reduced experimental variability, allowing confident detection of small differences in protein levels among several biological samples. Hence, this may help us to identify proteins important in the pathogenesis of sepsis, contributing for a better understanding of the disease. **Acknowledgements**: Fiocruz, FAPERJ, CNPq, CAPEs and UFRJ