

## Clinical proteomics in Cancer: Lessons from patient samples of glioma and leukemia

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Proteomics is one of most complex field, and new technologies and strategies appear every year. Cancer development is caused by the accumulation of DNA changes in genes, but genomic analyses do not accurately unravel the situation at the protein levels, and cancer is increasingly recognized as a proteomic disease, so that, proteomics represent a short cut between genome mutation and cancer development. We used proteomics approach based on protein separation by 2D gel electrophoresis and mass spectrometry analysis to perform analysis of clinical relevant samples. We analyzed 14 CLL and 20 glioma patient samples. In CLL, we found 26 spots differentially abundants ( $\pm$  2 times), 17 proteins differentially abundant in stage C of Binet: heterogeneous nuclear ribonucleoprotein A2/B1; 14-3-3 Protein zeta/delta, profilin-1, and decreased levels of S100-A8. Proteins of 14-3-3 family bind to phosphorylated BAD and they inhibit apoptosis which is one of the hallmarks of CLL (accumulation of mature B lymphocytes). In glioma, we investigated by 2D gel, 15 patient tumor samples classified as grade II, III and IV (WHO) compared to 5 non-neoplastic brain tissue samples surgically removed from epileptic patients as control. Thirteen proteins differentially abundant were detected. Six protein were detected more abundant than control, and five proteins were detected as lower abundant than control. Among of 13 protein spots 6 were increased in GBM: annexin A1, annexin A5, triose-phosphate-isomerase, peptidyl prolyl-cis-trans isomerase, alpha-crystalline chain B and nucleophosmin. Five proteins were less abundant and they correspond to creatine kinase chain B, HSP70, RKIP, CRMP2 (all of them were statistically significant,  $p < 0.005$ ). They are involved in protein translation, RNA biogenesis, genomic stability, and energetic metabolism. Proteomics in patient sample represents the opportunity to better understanding cancer progression and to detect proteins that could be useful for early diagnostic and therapy target.

FAPESP, FINEP and FAEPA.