PROTEOMICS: A POWERFUL TOOL TO DEEPEN THE MOLECULAR MECHANISMS OF ISCHEMIC STROKE

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Ischemic stroke (IS) is characterized by the sudden loss of blood circulation to an area of the brain originated as an occlusion of a cerebral vessel. In industrialized countries stroke is the major cause of death and long-term disability in adults.

Its consequences impose a burden on patients, payers, and society in terms of cost of care and lost productivity. Taking into account that his burden is expected to rise over the coming decades due to number of elderly people are increasing in industrialized countries.

Currently, the diagnosis relies on neurological assessment of the patient and neuroimaging techniques. A clinical goal for decades has been the identification of biomarkers of impending stroke in asymptomatic subjects and clinical prognosis in stroke patients. One of the potential of the proteomics is to detect novel drug targets and diagnostic markers, useful for disease detection, in easily obtained body fluids, like plasma or urine.

The aim is to identify and to validate plasma proteins associated with IS phenotypes in order to find potential biomarkers disease and therapeutic targets to assist in the development of rapid diagnostic tests.

5 IS patients and 5 healthy volunteers as controls were studied. Plasma samples were fractioned by depletion using the affinity column MARS-14 (Agilent technologies). Proteomic analysis was performed of fractionated plasma by 2D-DIGE, seeking to identify low dynamic range proteins involved in the disease process.

40 spots with altered expression levels (average ratio≥1,5) were found and identified by MS/MS. We expect that this analysis provides additional information to enable us to deepen our knowledge of physiology and etiology of the disease, and the identification of proteins with possible diagnostic and therapeutic value.