

DIFFERENTIAL EXPRESSION ANALYSIS IN SPINAL MUSCULAR ATROPHY PATIENTS

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Spinal muscular atrophy (SMA) is a recessive disorder involving the degradation and subsequent loss of motor neurons from the spinal cord. The main cause of SMA is related with the absence of the functional form of the survival motor neuron (SMN) gene (SMN1). This gene presents a telomeric (SMN1) and a centromeric (SMN2) copies that differ in 5 nucleotides. This mutation produces an alternative splicing of SMN2 giving rise to a truncated protein with reduced functionality (1,2). All the SMA patients have at least one copy of the SMN2 form that is necessary for survival, and disease severity depends primarily on the number of SMN2 gene copies. However, the number of SMN2 copies doesn't explain completely the different severity of the disease observed in SMA patients.

In this work we compared by 2DE the fibroblasts proteomic patterns corresponding to several members of a SMA-carrier family (four sisters and their mother) and a group of four controls.

Among the family members, the four sisters have the same genotype but show different levels of disease severity (one of them is asymptomatic). The mother is heterozygous and thus asymptomatic. The analysis revealed the presence of 42 differential proteins between controls and patients with the SMA phenotype. Two other proteins were found differential between symptomatic and asymptomatic members of the family. A biological process analysis of the identified proteins reveals a high percentage of proteins classified as stress response and protein metabolism and modification. The functional implications of these proteins will be evaluated in future studies.

1. Lefebvre, S. (1995). "Identification and Characterization of a Spinal Muscular Atrophy-Determining Gene." *Cell* **80**: 155-165.
2. Sumner, C. J. (2007). "Molecular Mechanisms of Spinal Muscular Atrophy." *Journal of Child Neurology* **22**: 979-989.