Muscular dystrophies constitute a group of neuromuscular disorder characterized by progressive loss of muscle strength and integrity and degenerative muscle changes. Magnetic resonance imaging (MRI) allows distinguishing different patterns of muscle involvement specific for each muscular dystrophy. Interestingly, some muscles are spared at late stages of the disease regardless of the specific muscular dystrophy (e.g. gracilis). In this study we analyzed the protein expression profile of different normal muscles in order to understand the molecular mechanisms that may be protective for these muscles. We have used two-dimensional gel electrophoresis (2-DGE) combined with mass spectrometry (MS) for this analysis. We were able to perform a reference map of proteins from different muscles obtained from thirty two healthy controls, including: (6) gracilis, (6) semitendinous, (4) tibialis anterior, (4) vastus intermedius, (4) soleus, (4) adductor longus, and (4) adductor brevis.

Proteomic profiling revealed that out of 4411 spots resolved by 2-DGE, 143 proteins exhibited a dramatic change in expression. We found differential expression of proteins involved in muscular contraction, such as troponin, tropomyosin and myosin isoforms we also found proteins important in skeletal muscle metabolism such as aldolase, fatty acid binding protein or triose phosphate isomerase. Finally, we identified proteins that participate in muscle regeneration and repair, sarcomere organization and development and maintenance of Z-disc and ubiquitination such as myozenin-1, and actinin – associated LIM protein (ALP), alphaB-crystallin or TRIMM72. In conclusion, 1) 2-DGE showed a protein expression profile specific for each muscle studied. 2) The specific upregulation of proteins involved in sarcomere stabilization and skeletal muscle remodelling in gracilis and semitendinous muscles, may explain the endurance of these muscles during the process of muscle degeneration in muscular dystrophies.