

First characterization of the goat mammary gland mitochondrial proteome: A gel based approach on the study of tolerance to weight loss in two breeds from the Canary Islands

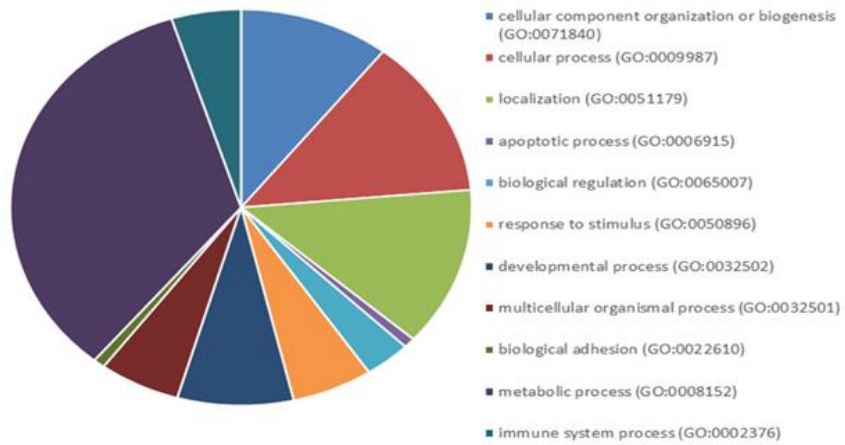
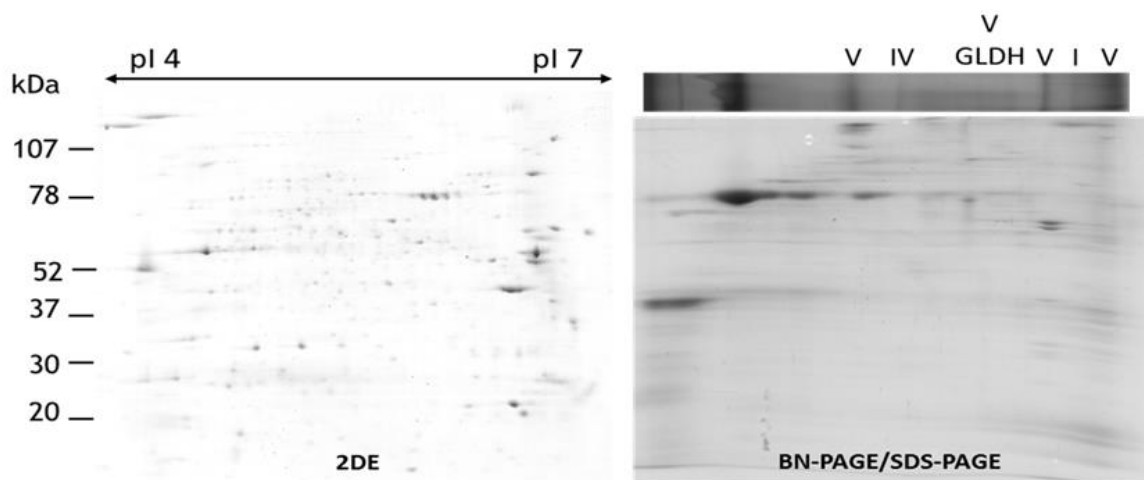
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Seasonal weight loss (SWL) is the most important limitation to animal production in Tropical and Mediterranean regions, conditioning producer's incomes and the nutritional status of rural communities. It is of utmost importance to produce strategies to oppose adverse effects of SWL. Breeds that have evolved in harsh climates have acquired a tolerance to SWL through selection. Most of the factors determining such ability are related to biochemical metabolic pathways and are likely important biomarkers to SWL. In this study, a gel based proteomics strategy (BN: Blue-Native Page and 2DE: Two-dimensional gel electrophoresis) was used to characterize the mitochondrial proteome of the secretory tissue of the caprine mammary gland. In addition, we have also conducted an investigation of the effects of weight loss in two dairy goat breeds with different levels of adaptation to nutritional stress: Majorera (tolerant) and Palmera (susceptible). The study was conducted using 10 Majorera and 10 Palmera goats, divided in 4 sets, 2 for each breed: underfed group fed on wheat straw ad libitum (restricted diet, so their body weight would be 15-20% reduced by the end of experiment), and a control group fed ad libitum on commercial feed. After 22 days, mammary gland biopsies on the animals were conducted following standard procedures and under competent veterinary supervision. The proteomic analysis of the mitochondria of mammary glands, upon organelle isolation, enabled the resolution of a total of 277 proteins, and 184 (66%) were identified by MALDI-TOF/TOF mass spectrometry. Among the proteins identified were subunits of the glutamate dehydrogenase complex and the respiratory complexes I, II, IV, V from mitochondria, as well as numerous other proteins with different functions in: metabolism, development, localization, cellular organization and biogenesis, biological regulation, response to stimulus, among others, that were mapped in both BN and 2DE gels. The comparative proteomics analysis enabled the identification of Succinyl-CoA synthetase, Guanine nucleotide-binding protein, NADH-ubiquinone oxidoreductase, in majorera, and ACTA2 protein in Palmera, as being over-expressed as a consequence of SWL.

Figure: Characterization of the goat mammary gland mitochondrial proteome, using two-dimensional gel electrophoresis and Blue-Native PAGE.



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