Muscle proteome changes related to growth and pre-slaughter transport in broiler chickens

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The aim of this research was to define the protein complement of chicken skeletal muscle, as resolved by bidimensional gel electrophoresis in order to study protein expression changes in response to growth and pre slaughter transport duration. The breast muscle of chickens comprises almost exclusively the fast twitch fibers and thus is an ideal tissue system to assess protein expression dynamics. Protein accumulation reflects the balance between two opposing processes of protein synthesis and degradation (Doherty et al., 2004). The protein content of the muscles can also change in response to the biochemical processes that the organism uses to cope with the stress related to transport and handling.

The study was conducted at spring on Ross broiler stocks. Broilers were reared under commercial conditions until they reached to average 1.8 kg and 36 d of age (light) or 2.6 kg and 46 d (heavy). Transport duration to the slaughterhouse was 1.5 h (short) or 3 h (long). A total of 12 carcasses from each group were randomly sampled. Samples of Pectoralis superficialis, collected 15 min post mortem, were used to extract the sarcoplasmic proteins fraction that were analyzed by two-dimensional electrophoresis (two repetitions each bird). Image analysis, followed by statistical analysis through the Wilcoxon-Mann-Whitney test (SAS), enabled to detect qualitative and qualitative differences among individual samples. To focus attention to spots that retain biological relevance, the fold change cut-off was set to 1.5. Interesting spots were excised from gels and MS protein identification was performed. A total of 35 differentially expressed spots were detected with relevance for the weight effect, of which six were significantly different for P<0.05. After visual inspection, two spots were specifically expressed in light birds, and one in the heavy ones. On the other side, 20 differentially expressed spots were detected for the transport effect with fold change ratio < 1.5. After statistical analysis, five spots were significantly different for P<0.05. With a P<0.15 nine more spots were included among the significantly differentially expressed. 26 spots were detected by mass spectrometry; most of them (16) were associated to growth related changes, while 10 were associated to pre-slaughter transport duration. Growth influenced the expression of protein that, although heterogeneous in their functions, are mostly classifiable as enzymes participating in gluconeogenesis and glycolisis, fatty acid synthesis, actin and myosin biosynthesis and regulation different cell functions. Transport duration affected expression of proteins participating in glycolisis and carbohydrate metabolism, lipid degradation, stress resistance, cellular differentiation and apoptosis.

Results evidenced the metabolic pathways that the chicken organism exploits to sustain growth and to cope with stress induced from transport, and support the idea to use selected proteins as markers to test broilers farming conditions and pre-slaughter processing of the birds.