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¹H-NMR metabolite profiling of broiler breast meat affected by muscular abnormalities

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Nuclear Magnetic Resonance (NMR) spectroscopy represents a versatile technique that allows gathering, in a single spectrum, quantitative and qualitative information on the metabolic profile of a tissue. In the present study, ¹H-NMR was applied to quantify free amino acids, histidine compounds and metabolites involved in energy-generating pathways in *Pectoralis major* muscles affected by growth-related abnormalities (White Striping – WS, Wooden Breast – WB and Spaghetti Meat – SM). The study was conducted on a single flock of 48 days old broiler chickens (Ross 308, females, average live weight 2.8 kg) classified into the following groups: Normal (NORM), WS, WB and SM. The increased ($p < .001$) concentration of free amino acids observed in WS, WB and SM likely results from the degenerative processes taking place within these muscles as well as from a concurrent attempt of the tissue to overcome necrosis and repair the damaged fibres. This is corroborated by the significantly higher ($p < .001$) glutamine and glutamate content found in WS, WB and SM previously observed in *mdx* mice and dystrophic muscles and hypothesised to be related to the intense regenerative processes associated to these conditions. In addition, significantly higher ($p < .001$) glycine and branched amino acids (namely valine, leucine, isoleucine and proline) were found in WS, WB and SM thus suggesting an increased collagen synthesis and an intense extracellular matrix remodelling within these muscles. With regard to the histidine compounds, the lower ($p < .001$) levels of anserine and carnosine found in abnormal muscles confirms that oxidative stress can contribute to the aetiology of breast muscle abnormalities in broilers. Besides, WS, WB and SM exhibited significant variations in the metabolites involved in energy-generating pathways (lower lactate, creatine and inosine-5-monophosphate) thus supporting the assumption of metabolism perturbations associated to the development of these conditions. However, since no distinctive metabolites were found, similar causative mechanisms leading to WS, WB and SM can be hypothesised. In conclusion, the adoption of ¹H-NMR spectroscopy allowed to corroborate earlier findings (i.e. oxidative stress and perturbation of energy metabolism) and provide novel insight (i.e. higher content of free branched amino acids) into metabolic pathways

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involved in the development of growth-related abnormalities which are nowadays of great importance for the broiler industry.

ANIMAL BREEDING AND GENOMICS – SMALL RUMINANTS GENETICS

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VarGoats international initiative, a 1000 goat genomes project

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Goats were domesticated ~10,000 years ago from their bezoar wild ancestor *Capra aegagrus*. These founder animals spread out from domestication centres in Europe, Asia, and Africa during the next few thousand years, which resulted in many populations becoming locally adapted to diverse environmental constraints such as heat, altitude, disease resistance, etc. After a very long period of soft selection for production traits, the situation changed dramatically with the emergence of the breed concept about 200 years ago. Selection pressure was strongly increased, and gene flow between populations (or newly formed breeds) was seriously reduced, leading to the fragmentation of the initial gene pool. Currently, there are more than 1000 goat breeds worldwide, 18% of which are either threatened or already extinct.

Through the generation of domestic breeds sequence data and their analysis together with existing data of domestic and wild animals, VarGoats collaborative project aims at becoming the first step of a 1000 goat genomes project. VarGoats Consortium is coordinated by the Institut National de la Recherche Agronomique INRA (France), and includes an international team of partners (Laboratoire d'Ecologie Alpine, France; Parco Tecnologico Padano, Italy; Agricultural Research Service, USDA, USA; International Goat Genome consortium; African Goat Improvement Network; Roslin Institute and the Centre for Tropical Livestock Genetics and Health, UK). At present, a dataset containing 829 goat