

C-009

### The genetic of welfare: gene expression and heat stress in chicken

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High environmental temperature is one of the most important stressors associated with economic losses to the poultry industry. It causes poor growth performance, immunosuppression, and high mortality, contributing thus to a production decrease. Broilers are in general more sensitive to high environmental temperatures than other domestic animals but the responses to heat differ between different chicken genetic backgrounds. We used One Step Taqman real time RT-PCR technology to evaluate the effect of heat stress on the expression of six genes codifying for the antioxidative enzymes (SOD and CAT), heat shock protein (HSP) 70 and HSP90, glucocorticoid receptor (NR3C1), and Caspase 6 (CASP6) in the liver of two chicken strains: Red JA Cou Nu Hubbard (CN) and Ross 508 Aviagen (RO). A total of 120 RO and 120 CN broilers, 4 weeks of age, were divided into 4 groups of 60 animals, which were then reared for 4 weeks at two different environmental temperatures: 34°C and 22°C. Corticosterone (CORT) concentration was measured in blood samples using enzyme immunoassay method. We also analyzed the association between transcriptomic response and specific SNPs in each genetic strain of chickens. The results demonstrated that there was both a genotype and a temperature effect on the chickens' growth, given that a different trend was seen in the four combinations genetic strain-environmental temperature from the 6<sup>th</sup> week to the end of the experiment. Chronic heat stress caused a significant increase in CORT levels due to activation of the hypothalamic-pituitary-adrenal axis in both genetic strains. Carcass yield at slaughter were similar in all groups, ranging from 86.5 to 88.6%, whereas carcass weight was negatively influenced by heat stress in both breeds. Heat stress affected the expression of quite all target genes and the differences found in the mRNA copies of two (CASP6 and HSP70) out of the six genes could be partly explained by SNPs. In particular, we found three SNPs for the HSP70 gene (HSP70-3, -7, -9) with different allelic frequencies between the two target breeds, and a SNP polymorphism in the CASP6 gene (CASP6-9). The evidence

given in this study, on gene expression and genome polymorphisms will be useful in the future marker assisted selection of chickens more tolerant to heat stress.

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C-010

### Broiler *Pectoralis major* muscle affected by emerging abnormalities: histology and gene expression

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In the last few years, modern chicken hybrids selected for an increased breast muscle weight exhibited new breast muscle myopathies, termed "wooden breast" and "white-stripping", which impair product appearance and quality properties. This study is aimed to preliminarily analyse the genomic basis of wooden breast and white striping (WB/WS) abnormalities using Affymetrix expression array. For this purpose, 10 normal (NORM) and 10 WB/WS *Pectoralis major* muscles were obtained from the same flock of heavy broilers (males, slaughter weight of 3.8kg) slaughtered on a single day under commercial conditions. Furthermore, a second sample was collected for histological analysis to be stained with Masson's trichrome. Comparing the expression profiles obtained for WB/WS and NORM samples, 226 differentially expressed genes (DEG) were found, 114 up- and 112 down-regulated. A functional classification was carried out using DAVID tools. The significant ( $P < 0.05$ , Benjamini corrected) functional categories represented by the up-regulated genes are: regulation of organismal growth and cellular developmental processes related to skeletal muscle, activation of polysaccharide metabolism (extra cellular matrix and collagen), calcium and sodium metabolism. The down-regulated genes did not show any specific clustering. The histological analysis revealed the presence on WB/WS samples of an intense proliferation of the perimysial collagen (fibrosis) in respect to the muscular fibers that appear decreased both in number and in diameter and, in some cases, degenerate (necrosis). In many cases, these degenerative lesions were accompanied by attempts of muscle tissue to replace the necrotic fibers with adipose tissue manifested with an abnormal increase of intramuscular fat. On the whole, these functions seem to indicate the alteration of several cellular