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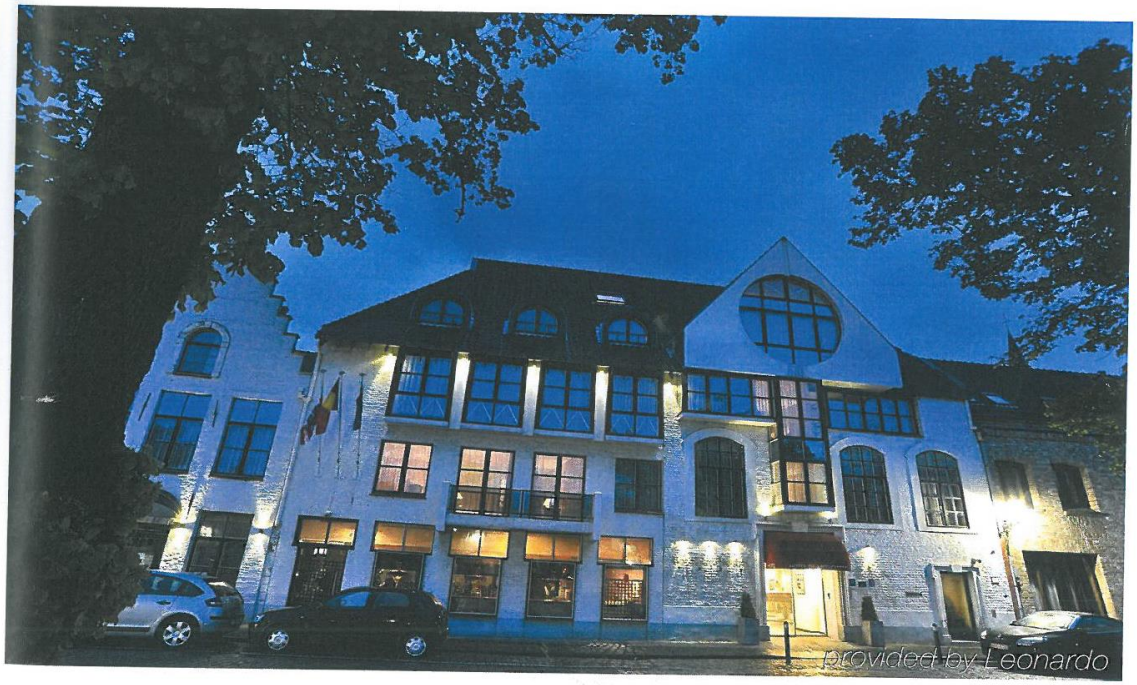

Impact of embryonic heat acclimation on histone post-translational modifications in chicken

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Chickens that have been genetically selected for growth performance are challenged by temperature variations. Considering the problem of global warming, embryonic heat treatment was proposed to acclimatize chicken to heat in the long term. The embryonic thermal manipulation (TM) consists of a cyclic increase of egg incubation temperature from the embryonic day E7 up to E16 associated with an increase of the relative hygrometry (HR) (from 37,8°C and 55% HR to 39,5°C and 65% HR for 12h/d). This change in early environment has little effect on hatching and improves the survival rate of chickens when exposed to a HS at slaughter age (i.e. 5 weeks of age post-hatching). This increased thermotolerance is associated with physiological, metabolic and genes expression changes at slaughter age.

We hypothesized that the change in gene expression observed in TM chickens could be the result of epigenetic alterations established during the treatment that persist throughout development. Indeed, early environmental exposure to pollutants, drugs, diet and other factors, is able to change genes expression in the long term through epigenome alterations. For instance in Drosophila melanogaster the exposure to a heat shock (HS) during the embryogenesis leads to long-lasting epigenetic reprogramming mediated by the Polycomb Repressive Complex 2. This complex is involved in the establishment of the tri-methylation of the lysine 27 on the histone H3 (H3K27me3) which is known to play a part in the memory of a repressive state under the influence of the environment. To investigate the potential epigenetic mechanism involved in heat acclimation we performed an unbiased analysis of two histone post-translational modifications (HPTM). We analyzed H3K27me3 associated with repression of gene expression and the tri-methylation of the lysine 4 on the histone H3 (H3K4me3) associated with gene expression. The distribution of these modifications were studied by ChIP-seq on hypothalamus, the regulatory center of thermotholerance, of TM and control chicken at slaughter age. Based on the recommendations of the Encyclopedia of DNA Elements (ENCODE) we profiled both marks on four individuals per treatment (4 TM and 4 control). We performed a bio-informatic analysis to detect peaks with PePr followed by a bio-statistical analysis with DESeq2 to detect and validate differential peaks.