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Impact of embryonic thermal manipulation on quail transcriptome and methylome

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Combined Meeting

Incubation and Fertility Research Group (IFRG/Working Group 6)

and of the Fundamental Physiology and Perinatal Development Group (WPSA Working Group 12)

2017 Meeting – Hof van Wageningen

www.hofvanwageningen.nl

August 30 – September 1st

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August 1st 2017

Scientific committee dr. G. Baggott dr. A. Collin, dr. B. Tzschentke, Prof. S. Yahav

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CALL FOR PRESENTATIONS AND ABSTRACTS

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oral presentation (Powerpoint)	X	Poster		Oral presentation or Poster	
ABSTRACT					
<p>Title: Impact of embryonic thermal manipulation on quail transcriptome and methylome</p> <p>Keywords: quail, epigenetics, thermal manipulation, DNA methylation, transcriptome</p> <p>Abstract: Changes in gene activity through epigenetic alterations induced by early environmental challenges during the embryogenesis are known to impact the phenotype, health and disease risk of animals. The epigenome is therefore an essential contributor to phenotypic plasticity, and learning how environmental exposures translate into persisting epigenetic changes may open new doors to improve robustness and resilience of developing animals. Birds are agronomic species of choice to directly manipulate the embryonic environment and study its consequences on the developing animal. We previously showed that the heat tolerance of male commercial chickens was improved by cyclically elevating the egg incubation temperature. This treatment named embryonic thermal manipulation (TM) was associated with changes in gene expression that persisted during the development of chickens and enhanced gene expression response in case of heat challenge at slaughter age, 35 days post-hatch.</p> <p>To further explore the molecular basis of heat acclimation, we took advantage of an inbred line of Japanese quails (<i>Coturnix japonica</i>) to investigate the impact of TM on bird methylome. Among other advantages, quail generation cycle is 3-4 time faster than chicken and the use of an inbred genotype should reduce the phenotype variations associated with genetic variability. A characterization of TM on quail phenotype was performed in interaction with a post-hatch heat stress at the onset of sexual maturity. Notably, we observed an impact of the embryonic treatment on the temperature and the weight of young quails, similarly to what was reported for chicken. Concomitantly we investigated the impact of TM on quail transcriptome by RNA-seq and methylome by whole genome bisulfite sequencing (WGBS) on brain tissues sampled at hatch. Several differentially expressed gene and differential methylation regions were identified. Interestingly, the nature of some transcripts seemed to be affected by the embryonic treatment at both methylation and transcript levels.</p>					