***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**

**CALL FOR PRESENTATIONS AND ABSTRACTS FORM**

**(Please complete one per presentation)
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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

If you wish to offer an oral presentation or poster on any topic (Fertility, Egg incubation, Embryonic Development, avian physiology, breeder management) please provide the following details and indicate your form of presentation below.

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| **Author/s:** | **Vitorino Carvalho Anaïs1, Couroussé Nathalie1, Crochet Sabine1, David Sarah-Anne1, Bordeau Thierry1, Godet Estelle1, Piégu Benoît2, Hennequet-Antier Christelle1, Brionne Aurélien1, Noirot Céline3, Bigot Yves2, Pitel Frédérique4, Collin Anne1, Coustham Vincent1**  |
| **Company/Institution:** | 1INRA – UR83 Recherches Avicoles – 37380 NOUZILLY2INRA – UMR85 PRC – 37380 NOUZILLY3INRA - UR875 MIAT – 31326 CASTANET-TOLOSAN4INRA – UMR1388 GenPhySE – 31326 CASTANET-TOLOSAN |
| **Postal Address:** | **INRA Centre Val de Loire** |
|  | **F-37380 Nouzilly** |
|  | **France** |
| **Email-address of the corresponding author :** | vincent.coustham@inra.fr |
| **Preferred presentation format (please tick below)** |
| oral presentation(Powerpoint) | **X** | Poster |  | Oral presentation or Poster |  |
| **ABSTRACT** |  |
| **Title:** Impact of embryonic thermal manipulation on quail transcriptome and methylome**Keywords:** quail, epigenetics, thermal manipulation, DNA methylation, transcriptome**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. To further explore the molecular basis of heat acclimation, we took advantage of an inbred line of Japanese quails (*Coturnix japonica*) 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.  |
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