multiple generations of Japanese quail, resulting from feeding a diet high in methyl donors in only the founder population. Effects of the high methyl diet were observed on egg size in G0 as well as subsequent generations G1 and G2, which were fed a control diet. Differences in DNA methylation were observed across generations G0, G1, and G2 as a result of G0 diet. Differential methylation persists across generations at specific but not all locations within the genome. Specific genomic regions impacted by the G0 diet that persisted across multiple generations include the DNA methyltransferases (DNMT1 and DNMT3) and the vitellogenin gene family (associated with oocyte development). This work demonstrates the importance of considering the transgenerational effects of environment in poultry species and its long-term impact on phenotypes of economic importance.

Keywords: epigenetics, DNA methylation, Methyltransferase, quail

Revealing gene networks in relation to feather pecking behaviour using RNA-sequencing

Joergen B. Kjaer

Institute of Animal Welfare and Animal Husbandry, Federal Research Institute for Animal Health (FLI), Dörnbergstr. 25/27, D-29223 Celle, Germany

Corresponding author: joergen.kjaer@fli.de

Injurious feather pecking behaviour (IFP) is a very serious welfare and production issue world wide in modern intensive egg production systems, inducing risks of high rates of mortality, increased feed intake and reduced egg production.

We developed White Leghorn lines by genetic selection, showing either low (LFP) or high (HFP) levels of IFP in relation to an unselected control line (CON). Using hens from these lines, we aimed at describing transcriptional differences between lines and phenotypes (performers, vs. non-performers).

IFP was observed in mixed line groups of hens at 30-32 weeks of age by direct observation and at 65 weeks-of-age, 36 birds were chosen for RNA-seq. Hen were killed, the whole brain was homogenised and RNA was isolated using Qiagen Rneasy-kits and sequenced on Illumina PE150 (250-300 bp PE) with min. 20 mio. reads per sample.

Preliminary analyses identified around 14000 genes. Within performers, resp. 27, 86 and 10 differentially expressed genes (DEGs) were found between CON-LFP, CON-HFP and LFP-HFP lines. Within non-performers these numbers were 141, 300 and 443 DEGs. Within lines (CON, LFP and HFP resp.) the phenotypes showed a number of 2, 17 and 0 DEGs. The top 40 DEGs were mainly between LFP and HFP non-performers, examples being uncharacterized LOC107049265, Ring finger protein 207, uncharacterized LOC769512, Acylphosphatase 1, Tropomodulin 1, GTPase IMAP family member 8-like 1, uncharacterized LOC107053511, uncharacterized LOC107052719, Zinc finger protein 737-like and Stimulator of chondrogenesis 1. Further GO enrichment and KEGG pathway analysis results will be presented.

Keywords: Injurious pecking, Laying hens, Transcriptomics, Selection, Genomic variation

Analysis of feather pecking behavior, plumage condition and body weight in laying hens

Lina Hattendorf[1], Hanna Iffland[2], Jörn Bennewitz[2]

[1]Lohmann Tierzucht GmbH, Cuxhaven, Germany; [2]University of Hohenheim, Stuttgart, Germany

Corresponding author: lhattendorf@ltz.de

Feather pecking (FP) is a current topic and a multifactorial problem in laying hens. It is difficult to measure and thus breeding against it is challenging. The aim of this study was therefore to find out if plumage condition or body weight might be usable as proxy traits for identifying feather peckers.

Birds of a White Leghorn layer strain were divergently selected for high (HFP) and low (LFP) feather pecking for more than 15 years. At the age of around 32 weeks, feather pecking was recorded for 511 laying hens (282 HFP, 229 LFP), which were held in groups of around 36 animals per pen, for four consecutive days in two experimental runs. Body weight and feather score were recorded one week after observation. All three traits were analyzed in a multi-trait-sire-model and corrected for a fixed effect consisted of the combination of experimental run and pen number. Heritabilities and genetic correlations were calculated based on the variance components estimated in the multi-trait-model. Phenotypic correlations were estimated based on the raw data. HFP and LFP data was analyzed separately.

The results showed no significant phenotypic correlations between the traits plumage condition and feather pecking. Between body weight and feather pecking, significant low phenotypic correlations (HFP: $r_p = 0.12$, LFP: $r_p = 0.16$) could be revealed. To conclude, neither plumage condition nor body weight seems to be usable as a proxy trait for feather pecking in laying hens, despite low to medium heritabilities were found for feather pecking and plumage condition.