



Optimierung der Zuchtauswahl von Legehennen mithilfe von Sensorsensor-technologie und Datenanalyse zur Verbesserung des Wohlbe-findes in käfigfreien Haltungssystemen

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Key words

hen, welfare, breeding, phenotype, selection

Aim of the study

Current breeding programs for laying hens use groups of less than 50 animals which contribute to behavioral and welfare problems (e.g., toe pecking, keel fractures, etc.) experienced by Swiss producers and other users of cage-free systems. The proposed work expanded on an existing effort using large groups in aviary housing to identify desired health and behaviour phenotypes by employing advanced sensor technology to directly inform breeding selection. The project targeted trait selection using genomic methods (Genome Wide Association Study and causation modeling) and evaluation of candidate gene selection in relation to animal movement patterns. Results are an important first step towards determining use of these movement traits in modern breeding programs for cage-free housing systems.

Material and methods

The hens used in this study were provided by Hendrix Genetics (5831 CK Boxmeer, The Netherlands) and comprised 1,124 white laying hens from 100 known sires. Total daily movement records numbered 230,590 using a custom Radio Frequency Identification system that tracked animals within five zones of the aviary. All birds alive at 30 WOA were genotyped using a proprietary 60K single-nucleotide polymorphism (SNP) panel (Illumina Inc. 60K). For the genotypic quality control, only autosomal SNP markers with call rates greater than 0.95 and a minor allele frequency greater than 0.05 were retained. After filtering for quality control, a total of 40,563 SNP markers with an average call rate greater than 99% remained. To estimate genetic parameters for duration spent in different zones of the aviary, a multivariate mixed model using repeated records was employed. The model procedure was based on the best linear unbiased prediction (BLUP) using genomic information to derive the genomic relationship matrix, as part of a procedure is known as genomic best linear unbiased prediction (GBLUP). The analysis was performed using the restricted maximum likelihood method implemented in ASReml 4.1.

Results and significance

Heritability estimates ranged from 0.05 to 0.28 (0.01–0.03) for duration spent in the lower tier to litter, respectively. For nesting behavior, the heritability for the duration spent in the nestbox tier was estimated to be 0.11 (0.02). Comparatively, Icken et al. (2013) estimated heritability that ranged from 0.00 to 0.56 (0.00–0.12) for duration of stay in the nest using 12 flocks, results in range of the present study. The comparable result between the current and previous studies is interesting as our tracking system did not allow for quantification of important egg production phenotypes such as egg quality. However, the comparable heritability, in combination with a high correlation between our behavioral proxy of egg-laying of the current study and egg production of the simultaneous field tests of Hedrix Genetics suggest our proxy could be a useful trait for breeding purposes.

Single nucleotide polymorphisms and associated regions were identified that linked with collected movement data.

- The SNP HGC003381 was found to be associated with duration in the wintergarden and is located within an intron region of the ALCAM (Activated leukocyte cell adhesion molecule) gene and is upstream of the CBLB (Cbl proto-oncogene B) gene. Both the ALCAM and CBLB genes have previously been related to immune response in poultry.
- The SNPs HGC005373 and HGC005374 were found to be associated with duration in the litter between 25 and 32 weeks of age. Both are found within an intron region of the ATP11A (ATPase phospholipid transporting 11A) gene and are upstream of the gene TUBGCP3 (tubulin gamma complex associated protein 3). The ATP11A gene is part of the efferocytosis pathway, where it has a roll in the transportation of phospholipids and is known to be linked with carcass yield and body size.
- The SNP HGC035687 was found to be associated with duration in the nestbox tier between 45 and 52 weeks of age. It is found downstream of the gene CA15L (carbonic anhydrase 15-like), which is related to the hydration of CO₂ into bicarbonate, a major component in eggshell formation.

A final publication detailing the results of the GWAS and associated SNPs will be submitted in Dec 2024.

Publications, posters and presentations

Makanjuola, B. O., Gebhardt-Henrich, S. G., Toscano, M. J., & Baes, C. F. (2024). Genetic parameter estimates for the use of an aviary with winter garden by laying hens. *Poultry Science*, 103(3), 103369. <https://doi.org/10.1016/j.psj.2023.103369>

Hoeksema, K., Baes, C., Gebhardt-Henrich, S., Petelle, M., Toscano, M., Makanjuola, B. (2023) A genome-wide association study to identify novel genomic regions associated for aviary with winter garden usage by laying hens. EAAP - European Federation of Animal Science annual meeting, Florence, Italy.

Baes, C.F., Gebhardt, S., Toscano, M.J., Makanjuola, B.O. (2023) Future trends in genomic analysis. within the Symposia: Breeding laying hens for a cage-free future, abstract 513S. 109th Annual Meeting of the Poultry Science Association, July 10-13, 2023.

Toscano, M.J., Gómez, Y., Petelle, M.B., Gebhardt, S. (2023) Novel phenotypes in behavior, health and welfare within the Symposia: Breeding laying hens for a cage-free future, abstract 518S. 109th Annual Meeting of the Poultry Science Association, July 10-13, 2023

M. Neuditschko, B. Makanjuola, C. Baes, M. Toscano. (2023) Identification of runs of homozygosity in a commercial laying hen population. 39th International Society for Animal Genetics Conference. Abstract #89730.

Gebhardt-Henrich, S.G., Petelle, Toscano, M.J. (2023) Genetic influences on the use of resources in cage-free housing of laying hens. P 104. 56th Congress of the International Society for Applied Ethology (ISAE), August 1-5th, 2023.

Hoeksema, K. (2023) Behavior as a novel addition to the genome: A GWAS study to identify novel genomic regions linked for hen behavior in a commercial aviary. EU-LI-PHE 1st annual meeting, Bologna, Italy.

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