13th
European Symposium on Poultry Genetics

October 8-10, 2025, Gdańsk, Poland

ABSTRACT BOOK

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Working Group 3
Breeding and Genetics
of the European Federation
of the World's Poultry
Science Association

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The Polish Branch
of the World's Poultry
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WELCOME LETTER

Dear Colleagues and Friends,

It is our great honor and pleasure to welcome you to the 13th European Symposium on Poultry Genetics in Gdańsk (Poland). The main organisers of the Symposium are Working Group 3 Breeding and Genetics of European Federation of World's Poultry Science Association and the Polish Branch of WPSA.

Meetings of poultry geneticists and breeders have a long and illustrious history. It has been a platform for fruitful debates between academia and industry. The first European Symposium on Poultry Genetics was held in Mariensee (Germany) in 1999 and was a good example of Europe coming together. Subsequent symposia were held in Gödöllö (Hungary), Wageningen (The Netherlands), Dubrovnik (Croatia), Brædstrup (Denmark), Będlewo (Poland), Peebles (United Kingdom), Venice (Italy), Tuusula (Finland), Saint-Malo (France), Prague (Czech Republic) and Hanover (Germany). These symposia have established a strong tradition of an intensive and highly scientific program. This is due to the very effective work of the Scientific Committee, especially its Chairman, Prof. Dr. Steffen Weigend, who has held this position for 25 years. We thank him for his great creative commitment. The success of previous meetings is also due to the high quality of the papers and reports presented.

We are delighted to welcome delegates from both the academia and industry to Gdańsk. We believe the Symposium is an excellent opportunity to learn and exchange the latest advances in genomics, genetics and poultry breeding. We are particularly pleased that the delegates include young scientists. The submitted abstracts were of a high standard and the Scientific Committee faced a challenging task. We extend our heartfelt congratulations to the PhD Award winners.

The Symposium is only possible with the collaboration of many people who were dedicated to do their best to make this event happen. We would like to thank all members of the Scientific Committee for the preparation of the programme and the Polish Branch of WPSA for the involvement in the organization of this meeting. We sincerely would like to aknowledge all financial support provided by Poznań University of Life Sciences, Polish Academy of Sciences, World's Poultry Science Association, European Federation of WPSA and all sponsors of this Symposium. Finally, we would like to thank the team of Symposium Cracovience for the excellent collaboration.

We hope that Gdańsk – one of the most beautiful cities in Poland, a city with a deep history, renowned for dialogue and known as the City of Solidarity and Freedom – will be a valuable venue for exchanging experiences, sharing knowledge and enjoyable meetings.

Martino Cassandro
Chair of the Working Group 3
Breeding and Genetics EF WPSA

Tomasz Szwaczkowski
Chair of the Organising Committee

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PROGRAMME

WEDNESDAY, OCTOBER 8, 2025

12:00-13:00 Registration and welcome refreshments

13:00-13:10 Opening ceremony

Martino Cassandro
Chair of WG3, University of Padova, Italy

13:10-13:15 In memory of Professor Stanisław Wężyk (1934-2024)

Tomasz Szwaczkowski
Chair of Organising Committee, Poznań University of Life Sciences, Poland

13:15-16:15 Session 1: Animal/poultry model and gene editing for animal health

Chairs: Klaus Wimmers *(Germany)*, Piotr Pawlak *(Poland)*

13:15-13:45 GenoPHEnix: European research infrastructure for animal phenotyping and animal biobanking

Emily Clark
European Bioinformatics Institute, Hinxton, United Kingdom

13:45-14:15 Bridging the gap between genomics and phenomics: advancing sustainable and welfare-oriented animal breeding

Klaus Wimmers
Research Institute for Farm Animal Biology, Dummerstorf, Germany

14:15-14:45 Genetic engineering in poultry

Mike McGrew
University of Edinburgh, United Kingdom

14:45-15:00 General discussion

Short oral presentations

15:00-15:15 Genetic analysis of keel bone fractures in laying hens housed in a commercial aviary

Pascal Duenk
Wageningen University and Research, The Netherlands

15:15-15:30 Genomic selection on live radiographic phenotypes to improve laying hen bone health

Martin Johnsson
Swedish University of Agricultural Sciences, Uppsala, Sweden

15:30-15:45 Metagenomic survey on the influence of humus additives to bedding during broiler chicken rearing

Piotr Pawlak
Poznań University of Life Sciences, Poland

15:45-16:00 Update on the Chicken Genome Diversity Consortium

Michéle Tixier-Boichard
Université Paris-Saclay, INRAE, Jouy-en-Josas, France

16:00-16:15 General Discussion

16:15-16:45 Coffee Break

16:45-18:00 Poster Session

Chair: Steffen Weigend *(Germany)*

18:15-21:30 Poster viewing and welcome reception

THURSDAY, OCTOBER 9, 2025

9:00-10:45 Session 2: Social debate on genetic engineering

Chairs: Ian Dunn *(United Kingdom)*, Michèle Tixier-Boichard *(France)*

9:00-9:30 New developments in biotechnology applied to farm animals: EFSA 2025 assessment.

Ana Granados Chapatte
European Forum of Farm Animal Breeders-Farm Animal Breeding and Reproductive - Technology Platform, Brussels, Belgium

Short oral presentations

9:30-9:45 Optogenetic spatiotemporal control of gene expression in avian embryos using the magnet-cre system

Enbal Ben-Tal Cohen
Institute of Animal Science, Poultry and Aquaculture Science Department, Agricultural Research Organization, The Volcani Institute, Israel

9:45-10:00 Current performance of *in-ovo* sexing through PCR analysis: the Seleggt process

Jeroen A.M. Snijders
HatchTech, The Netherlands

10:00-10:15 Exploring allelic variants in pHu divergent lines of chicken by RNA-sequencing in *Pectoralis Major* and *Jejunum* tissues

Antoine Clément
Université Paris-Saclay, INRAE, Jouy-en-Josas, France

10:15-10:30 Generation of transgenic chickens expressing human interleukin 7 in egg white

Jiři Kalina
BIOPHARM, Research Institute of Biopharmacy and Veterinary Drugs, Czech Republic

10:30-10:45 General discussion

10:45-11:15 Coffee Break

11:15-12:30 PhD Award Session

Chairs: Krzysztof Kozłowski *(Poland)*, Kellie Watson *(United Kingdom)*

11:15-11:35 Genetic markers linked to bone properties in White Leghorn laying hens

Khrystyna Kurta
Swedish University of Agricultural Sciences, Uppsala, Sweden

11:35-11:55 Molecular diagnostics of *Campylobacter* in urban and domestic pigeons (*Columba livia*)

Szymon Mazgaj
Institute of Biology, University of Szczecin, Poland

11:55-12:15 Genetics underlying growth curve characteristics in German local chicken breeds

Chi Mei Sun
Friedrich-Loeffler-Institut, Institute of Farm Animal Genetics, Neustadt, Germany

12:15-12:30 General discussion

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13:30-15:15 Session 3: Epigenetics – genotype by environment interaction

Chairs: Yuval Cinnamon *(Israel)*, Rudolf Preisinger *(Germany)*

13:30-14:00 Deciphering GxE interactions with omics approaches: insights from the GEroNIMO EU project

Tatiana Zerjal
Université Paris-Saclay, INRAE, Jouy-en-Josas, France

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14:00-14:15 Leveraging local breeds and landscape genomics to detect adaptive genes

Gwendal Restoux
Université Paris-Saclay, INRAE, Jouy-en-Josas, France

14:15-14:30 Impact of genetics on behavioral variations in outdoor raised hens

Alice Racanati
Université Paris-Saclay, INRAE, Jouy-en-Josas, France

14:30-14:45 Using genome-wide association studies to identify novel genomic regions associated with laying hens’ behaviour within aviary housing systems

Kyle Hoeksema
University of Bern, Switzerland

14:45-15:00 Breeding chickens for the future: International competition versus European isolated solutions

Rudolf Preisinger
EW GROUP GmbH, Germany

15:00-15:15 General discussion

15:15-15:45 Coffee Break

15:45-17:45 Session 4: Use of advanced phenotyping and Artificial Intelligence for breeding

Chairs: Milan Tyller *(Czech Republic)*, Mailys Faure *(The Netherlands)*

15:45-16:15 Use of novel metagenomics phenotypic information to predict breeding values in Broilers

Andreas Kranis
Aviagen, Edinburgh, United Kingdom

16:15-16:45 Artificial Intelligence in poultry management and breeding

Anna Wolc
Iowa State University, Hy-Line International, USA

16:45-17:00 General discussion

Short oral presentations

17:00-17:15 AI-powered imaging of keel bone traits for genetic selection in laying hens

Moh Sallam
Swedish University of Agricultural Sciences, Uppsala, Sweden

17:15-17:30 Deep learning to automate chicken tibia-breaking strength annotation from X-ray images to improve animal welfare

Tanmay Debnath
Roslin Institute, University of Edinburgh, United Kingdom

17:30-17:45 General discussion

17:45-19:15 WG3 Business Meeting

Chair: Martino Cassandro *(Italy)*

20:00-22:00 Conference Dinner

FRIDAY, OCTOBER 10, 2025

9:00-11:00 Session 5: Manage of inbreeding in local and pure lines

Chairs: Anna Wolc *(USA)*, Andreas Kranis *(United Kingdom)*

9:00-9:30 Conservation of poultry genetic resources in Poland

Katarzyna Połtowicz
National Research Institute of Animal Production, Poland

9:30-10:00 The use of genetic resources in breeding programs: Why, what and how

Gwendal Restoux
Université Paris-Saclay, INRAE, Jouy-en-Josas, France

10:00-10:15 General discussion

Short oral presentations

10:15-10:30 Preservation of genetic diversity in poultry: The role of commercial breeding programs

Mailys Faure
Institut de Sélection Animale S.A.S., Hendrix Genetics

10:30-10:45 Investigating pedigree and genomic inbreeding in pure line of Pekin ducks

Florian Herry
Grimaud Frères, Sèvremoine, France

10:45-11:00 General discussion

11:00-11:15 Coffee Break

11:15-12:30 Session 6: Microbiome in poultry sector

Chairs: Maria Siwek *(Poland)*, Elisabeth Le Bihan-Duval *(France)*

11:15-11:45 Chickens represent an ideal model for host-microbiota studies

Ivan Rychlik
Veterinary Research Institute, Brno, Czech Republic

Short oral presentations

11:45-12:00 Impact of acute heat stress and body weight difference on Cecal Microbiota and survival in broilers

Yang Ho Choi
Division of Animal Science, Gyeongsang National University, Jinju, South Korea

12:00-12:15 Microbiome programming before hatch: *In Ovo* delivery of XOS and MOS in broiler chickens

Maria Siwek
Bydgoszcz University of Science and Technology, Poland

12:15-12:30 General discussion

12:30-12:45 Closing Ceremony

Martino Cassandro
Chair of WG3,University of Padova, Italy

Tomasz Szwaczkowski
Chair of Organising Committee, Poznań University of Life Sciences, Poland

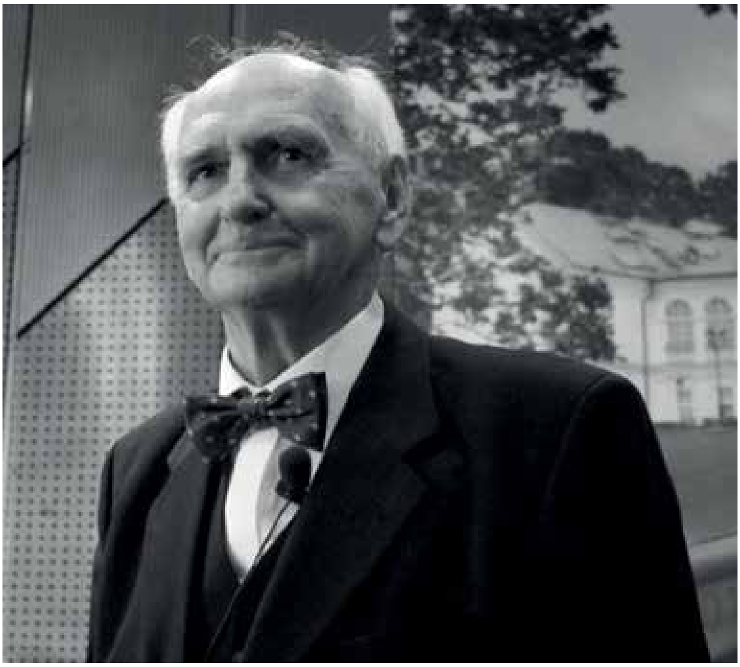
12:45-14:00 Lunch

14:15-16:15 Gdańsk City Sightseeing

In memory of Professor Stanisław Wężyk (1934-2024)

Tomasz Szwaczkowski

Poznań University of Life Sciences, Poland



Professor Stanisław Wężyk was a remarkably accomplished scholar whose contributions to genetics and poultry breeding had an extensive impact on both Polish and international research. He was a brilliant organizer, facilitating scientific discourse and offering his expertise wherever he could. Above all, he was a wonderful person, brimming with enthusiasm.

Stanislaw was a descendant of the noble Wężyk family, who settled in the Ostrzeszów region in the early 17th century. He was born in Ostrów Wielkopolski, where he also passed his matriculation exams. He completed his engineering studies at the Higher School of Agriculture (HAS) in Poznań and earned his master’s degree in animal science at the HAS in Kraków. As a student, he was employed as an assistant, initially at the Institute of Experimental Animal Breeding of the Polish Academy of Sciences (PAS), and later at the Department of Animal Breeding at the HAS in Kraków.

In 1963, he obtained his doctoral degree in animal science (on basis of thesis entitled “Comparison of different methods of estimation of heritability (h2) in hens”), followed by his habilitation („The effects of selection conducted over several generations in a closed population of hens” in 1970). And in 1977, he gained the academic title of professor of agricultural sciences. From 1966 to 2007, he worked at the National Research Institute of Animal Production in Kraków, serving as Deputy Director of Research for 12 years.

His contributions included preserving the biodiversity of native chicken populations and introducing innovative methods of genetically strengthening poultry populations. He also conducted research on poultry housing conditions, production systems, ethology, animal welfare, and nutrition. His work assessed the quality of poultry products and issues related to overarching agricultural policy in order to optimize the profitability and efficiency of production. This broad span of academic work resulted in an impressive record, amassing 1,233 publications. He also authored several patents and numerous expert opinions and reviews.

Professor Wężyk supervised 13 PhD students and conducted numerous specialized training courses for poultry farmers and breeders. Significantly, he was highly active in the WPSA. He was one of the founders of the Polish Branch of the Waterfowl Working Group of the European Federation of the WPSA, and served as a chairman there for 32 years. Moreover, he was Vice-President of the Polish Branch of the WPSA and organizer of the AVIAGEN conference (held in Eastern European countries preceding the European Symposium on Poultry Genetics). He co-organized and chaired sessions at European Poultry Conferences and World Poultry Congresses.

Professor also served as President of the National Chamber of Poultry and Feed Producers for 16 years. In addition, he was a member of numerous important groups, including the FAO, the Committee on Animal Sciences of PAS, and the Scientific Council of the Institute of Animal Genetics and Breeding of PAS in Jastrzębiec.

His extensive work and contributions are all well recognized and endorsed by the academic community. Prof. Stanislaw Wężyk was honored by the President of the Republic of Poland with the Silver Cross of Merit and the Knight's Cross of the Order of Polonia Restituta. It is worth noting that he received an honorary doctorate from the University of Warmia and Mazury in Olsztyn, and he also received honorary membership in the Polish Branch of the WPSA and in the Polish Society of Animal Production.

In addition to his research and teaching, Professor Wężyk had many other interests, such as skiing, military history, painting, and occasionally, poetry.

He loved singing around a fire at his mountain home in Bielanka, and merrily shared his summers with family; his beloved wife of 53 years Jolanta, his children, grandchildren, and countless friends.

A great scientist and a wonderful man, distinguished by his integrity, refinement, and profound knowledge; an overflowing source of joy in life, has passed away.

Session 1: Animal/poultry model and gene editing for animal health

GenoPHEnix: European research infrastructure for animal phenotyping and animal biobanking

Emily Clark[1], Klaus Wimmers[2], Michèle Tixier-Boichard[3], Tina Hartwig[2], Etienne Labussière[4], Catherine Larzul[5], René Baumont[6]

[1] *EMBL-EBI, Wellcome Genome Campus, Hinxton, United Kingdom*
[2] *Research Institute for Farm Animal Biology (FBN), Dummerstorf, University of Rostock, Faculty of Agricultural and Environmental Sciences, Germany*
[3] *INRAE, GABI, Jouy-en-Josas, France*
[4] *INRAE, PEGASE, Saint-Gilles, France*
[5] *INRAE, GenPhySE, Castanet-Tolosan, France*
[6] *INRAE, UMR Herbivores, Theix, Saint-Genès-Champanelle, France*

Background

The Agri-Food sector in Europe needs to adapt quickly to increase production capacity whilst flexibly meeting the goals of the European Green Deal and Farm to Fork strategy (https://food.ec.europa.eu/horizontal-topics/farm-fork-strategy_en). Sustainable improvements in animal production are required and high on the list of priorities is improving our ability to link an animals characteristics with its genetics to link genotype and phenotype (G2P) and predict performance in specific environments. To address this priority the farmed animal phenotyping and genotyping communities need to work together to provide both increased capacity and access for in vivo phenotyping studies on farm, laboratory studies with in vitro models, and genetic and genomic studies, providing a holistic approach to developing more sustainable farming systems.

Over the last 10 years several large collaborative projects have focused on farmed animal science including the H2020-funded Research and Innovation Action EuroFAANG projects GEroNIMO, AQUA-FAANG, BovReg, GENE-SWitCH, Rumigen, and HoloRuminant, as well as specific infrastructure projects such as the INFRA-DEV EuroFAANG RI project and the INFRAIA projects AQUAEXCEL3.0, PIGWEB and SmartCow. Two COST Actions focused on animal agriculture (FAANG-Europe and EU-LI-PHE) have also facilitated significant networking opportunities and interconnectivity between researchers and countries. As such the European farm animal and aquaculture genomics and phenotyping research community has more than a decade of investment and experience working together to address research questions focused on developing more sustainable farming systems. These projects have provided many services to the animal science community including a coordinated and managed data infrastructure, which is coordinated through the FAANG Data Portal (https://data.faang.org/home). Further consolidation and investment is required to maintain and expand the services beyond the lifetime of the projects and to build further capacity and increase across Europe, a formalised research infrastructure is one way to approach this.

What are Research Infrastructures?

Research infrastructures are facilities, resources and services that enable research and innovation. They are not only large physical structures, such as experimental farms, but also services and collections of resources such as biobanks. Infrastructures can take a long time to plan and build and often have a life cycle of more than 20 years, from concept development through to the implementation, operational and finally termination phases. There are many large infrastructures in Europe including, for example, ELIXIR (https://elixir-europe.org) which builds and maintains life sciences informatics capacity and Euro-BioImaging which offers open access to European biological and biomedical imaging technologies (https://www.eurobioimaging.eu).

Addressing the need for a European consolidated infrastructure for farmed animal science

The need for a European consolidated infrastructure for farmed animal science was mentioned in the European Strategy Forum for Research Infrastructures (ESFRI) "Landscape Analysis 2021 and 2024" documents (Fig. 1).

> *"Concerted effort to continue bringing together national facilities at the pan-European level in the field of animal genetic resources, phenotyping and breeding and animal health is needed to contribute to address the challenge to produce safe, healthy and sustainable food."*
>
> ESFRI Landscape Analysis 2021
>
> *"In addition, an important gap identified is related to the phenotyping of biotechnological improvements for animal farming systems (livestock and fish), whose characterisation is not included within the EMPHASIS portfolio. EMPHASIS does not have the required infrastructure to develop phenotyping studies in animals. So, there is a need to further develop and enhance EMPHASIS capabilities for animal phenotyping studies, including fish species used in aquaculture. Alternatively, this need may be covered by a new RI dedicated to animal farming studies".*
>
> ESFRI Landscape Analysis 2024

Fig. 1: Quotations from the ESFRI Landscape Analyses for 2021 and 2024 relating to the gaps in farmed animal science.

To provide a long-term, fully collaborative and coordinated institutional framework, the European farmed animal genomics and phenotyping research community submitted for consideration to the 2026 update of the ESFRI RoadMap a proposal for the GenoPHEnix Research Infrastructure (RI) (https://genophenix-ri.eu), a pan-European, multi-species, multidisciplinary platform for animal genetic resources, phenotyping, genome analyses, and sustainable breeding.

GenoPHEnix addresses the needs of a wide range of stakeholders including, farm animal breeding and husbandry companies, academic researchers, welfare and ethics experts among many others. The farmework for GenoPHEnix is focused on key areas including for example, data infrastructure and biobanking as well as developing links with other research infrastructures in the ESFRI landscape.

Scientific goals and technological innovation focused on data infrastructure include:

- Development of consolidated data portals and data repositories to access genome and phenome data, as well as samples, cell models and cell lines.
- Encouragement of multilateral scientific cooperation to tackle the challenges of varying technological capacities across EU countries, inequality, building AI readiness and improved knowledge transfer.
- Opening new areas of expertise and innovation, in the areas of robotics, high-throughput phenotyping, sensors, big data and analytical tools, in-vitro models including organoids and cell lines, as well as improvement of machine learning models with high resolution phenotyping for model training.
- Leveraging omics data in breeding programmes including through pangenomes for highly phenotyped breeding populations and genome enabled management.

Building a consolidated infrastructure for data integration and sharing to support the above scientific and innovation goals is a key component of the concept for GenoPHEnix. This would involve:

- Rebranding the FAANG Data Portal (https://data.faang.org/home) as the GenoPHEnix Data Portal to support a highly standardised submission and management system for animal agriculture data.
- Developing the data management plan and associated data access policies with inputs from the GenoPHEnix consortium, ensuring appropriate levels of data access for academic and industrial contributors.
- Expanding the GenoPHEnix portal, to include new data types, including qualitative data in the form of, for example, phenotypic measurements and image data. This would involve bringing new EMBL data archives into the portal infrastructure.

Connections with other European initiatives e.g. ELIXIR:

The GenoPHEnix RI is strategically linked and working closely with ELIXIR towards developing shared goals and objectives for animal agriculture data management. There is an emerging Domestic and Animal Genomes and Phenomes Community within ELIXIR with a white paper and road map.

C**onsolidating biobanks across Europe:**

Building on the foundation provided by projects such as CRB-Anim GenoPHEnix aims to: i) provide a framework of connecting biobanked material from different species, breeds and populations, inclusive of cryobanked organoids for different organs and of genome edited animal cell lines, that will be accessible to stakeholders from academia and industry across Europe, ii) establish a durable network enabling scientists to perform as many research steps as possible using in vitro cellular models to link G2P in farmed animals, and iii) popularise the use of such models as a case for pre-competitive research on G2P.

Summary and next steps

The GenoPHEnix-proposal unites scientific partners from eleven countries, one intergovernmental and one professional organisation. If successful in becoming an ESFRI project GenoPHEnix would provide a catalogue of more than 350 services including laboratory analyses, experimentation, data analysis, biobanking and training and education, provided either online, or in one of several of the around 50 analytical and experimental facilities. Access to GenoPHEnix services will underpin European research and innovation in farmed animal science across the main and emerging farmed animal species both terrestrial and aquatic. The GenoPHEnix proposal is currently awaiting a decision from the ESFRI evaluation panel which is expected in early 2026.

Bridging the gap between genomics and phenomics: Advancing sustainable and welfare-oriented animal breeding

Klaus Wimmers

Research Institute for Farm Animal Biology (FBN), Dummerstorf; University of Rostock, Faculty of Agricultural and Environmental Sciences, Germany

The increasing scarcity of natural resources driven by global population growth and climate change demands the development of sustainable and efficient agricultural and food systems. Farm animals play a central role in these systems by contributing to nutrient cycling and resource efficiency. In Europe, livestock production generates more than 40% of agricultural value, and over 90% of the population consumes animal-derived products on a regular basis. Livestock are indispensable for closing nutrient cycles, as they provide not only high-quality animal-source foods but also essential by-products such as leather, wool, and organic fertilizers. They contribute by valorizing co-products and residues unsuitable for human consumption and by ensuring the sustainable use of grasslands. In doing so, livestock systems deliver crucial ecosystem services, including soil health improvement, production of recyclable resources, and the preservation or even enhancement of biodiversity.

At the same time, a societal trend toward reduced meat consumption, combined with rising expectations for product quality, is highly likely. Nevertheless, poultry production in particular is currently experiencing considerable growth worldwide, highlighting the complexity of evolving dietary demands. The European Union's Farm-to-Fork Strategy aims to establish sustainable food systems, which inherently requires the integration of livestock production.

Why Genotype-to-Phenotype (G2P) Matters

In order to meet human nutritional needs and the demand for animal-derived foods while ensuring high standards of animal health and welfare, it is essential to improve the prediction of phenotypic expression and trait inheritance. Advanced functional annotation of genome sequences and transcripts, together with the dissection of complex traits into genetically tractable features, will enable more reliable estimations of breeding value than current genomic selection approaches and allow the prediction of individual responses to specific environments (Pan et al. 2023). Genotype-to-phenotype (G2P) research plays a pivotal role in this transformation by deciphering the molecular, physiological, and environmental interactions that shape economically and ecologically relevant traits. Multi-omics approaches integrating genomics, epigenomics, transcriptomics, proteomics, and metabolomics are providing insights into the mechanisms underlying disease resistance, climate resilience, feed efficiency, and reproductive performance (Clark et al. 2020).

Case Study 1: Phosphorus Use Efficiency in Chicken

Analyses along the G2P map in chickens illustrate the power of such approaches. One example addresses the efficient use of phosphorus (P) in poultry. Considering the global limitations of rock phosphate resources and the environmental burden of P emissions from livestock production, strategies are needed to improve the bioavailability, digestibility, and endogenous utilization of P. This is particularly relevant for plant-derived phosphorus, of which up to 80% is present in the form of inositol phosphates (InsPx) that cannot be efficiently utilized by monogastric animals due to their low endogenous phytase activity. Dietary variation in P supply across the full production cycle of laying hens was used to illuminate effects on both molecular and organismal levels. Comparing two commercial strains revealed distinct breed-specific responses to variable P supplementation, indicating genotype-by-environment (G×E) interactions. Holistic analyses integrating transcriptomic, epigenomic, metabolic, immune, and gut microbiome data were performed using both hypothesis-driven and machine-learning approaches. These multi-omics integrations revealed biosignatures associated with strain and production stage that were linked to phosphorus-use efficiency. This case study, recently reported in detail (Ponsuksili et al. 2022), demonstrates how G2P research can disentangle complex host–environment–microbiome interactions. The findings highlight how integrative approaches can identify biomarkers and molecular pathways underpinning nutrient efficiency, providing insights for genetic improvement and sustainable management in poultry production.

Case Study 2: Prenatal Programming and Postnatal Phenotype

Another line of research aims to decipher the molecular mechanisms by which prenatal events shape postnatal phenotypes in poultry. The concept of prenatal programming suggests that environmental conditions during early development can have long-lasting effects, often negative, but targeted modulation may also prepare animals for future challenges. Using the avian *in-ovo* model, altered incubation temperatures at specific embryonic stages (ED 7–10 and ED 10–13) were investigated with respect to growth, energy metabolism, and gene expression (Krischek et al. 2016). Transcriptome analyses of leg and breast muscles revealed developmental stage- and tissue-specific shifts in mRNA expression. Elevated incubation temperature programmed faster growth and higher body weight at day 35, reflecting activation of phenotypic plasticity pathways, while lower incubation temperature induced molecular changes without overt phenotypic effects, suggesting resilience-promoting mechanisms (Naraballohb et al., 2016a,b, 2018). To further address the molecular nature of this "developmental memory," histological, biochemical, and metabolic characterizations (e.g., glycogen and lactate metabolism, muscle fiber typing, mitochondrial activity, and yolk lipid utilization) are being combined with transcriptomics and metabolomics to identify affected molecular pathways. Bulk and single-cell ATAC-seq analyses are employed to uncover epigenetic mechanisms underlying these changes. Data are integrated across levels of the genotype-phenotype map using established statistical pipelines as well as supervised and unsupervised machine learning approaches. This work demonstrates how environmental modulation during prenatal development can leave lasting molecular and physiological signatures, providing opportunities to study G2P relationships and to explore strategies for improving growth performance and thermotolerance in poultry.

Together, these examples demonstrate the potential of G2P research to link molecular mechanisms with complex traits, thereby supporting genetic improvement and management strategies that enhance resilience, efficiency, and sustainability in modern poultry production.

References

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Genetic engineering in poultry

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Keywords: poultry, primordial germ cells, genome editing, avian influenza

Introduction

Sustainability in poultry farming would be increased if genetic resistance for the major chicken pathogens could be identified and introduced into poultry populations. Genome editing offers a tool to test specific genetic alleles for their value in both production and disease resistance. Poultry species pose a particular difficulty for genetic manipulation in comparison to other terrestrial livestock species as the avian zygote (laid egg) is difficult to access and manipulate and also cannot be cryopreserved due to the large amount of yolk present in the egg.

We and other research groups use the primitive germ cells of the embryo for both genome editing and for poultry cryopreservation. The primitive, or primordial germ cells, are a type of diploid stem cell found in the very early vertebrate embryo. These cells migrate through the early embryo and colonise the gonad where they produce semen in male and eggs in the females. The PGCs are present in low numbers in the early embryo and multiple in the embryonic gonad. Our laboratory developed a cell culture medium to propagate chicken germ cells in vitro. This provides a useable 'stem cell' that can be genetically manipulated in vitro. The cells are returned to a surrogate host embryo where they will form functional gamete in the adult host embryo and produce offspring that derive from the donor germ cells (Fig. 1). We are using these cells to investigate the genes that could increase genetic resistance to avian influenza in poultry or other traits such as heat tolerance.

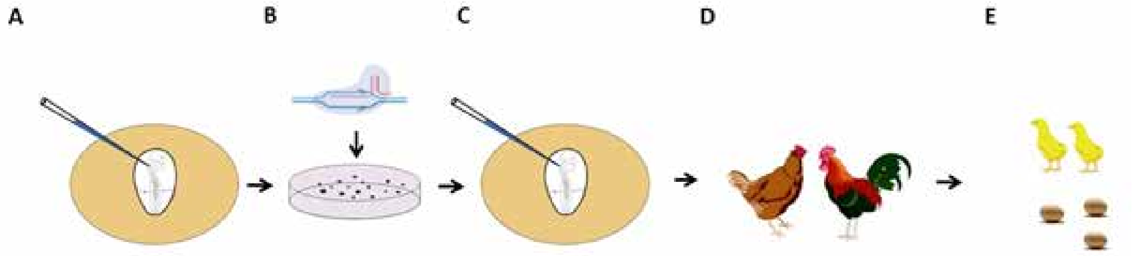

Fig. 1. Generation of Genome edited chickens from PGCs

A. Isolate embryonic blood from any breed of chicken eggs.
B. Genome edit cultured PGCs and screen cells for correct genetic change.
C. Microinject donor PGCs into surrogate host embryos.
D. Breed Surrogate host chickens
E. Produce gene edited offspring

Material and Methods

For primordial germ cell culture:

1 μl of blood was isolated from single Hy-line brown layer day 2.5 embryos (stage 16HH) and cultured in serum free medium (Whyte et al, 2015). PGC medium was called FAOT medium and contained the following reagents:

Avian KO-DMEM basal medium DMEM (250 mosmol/kg, 12.0 mM glucose, 0.15 mM calcium chloride)

1x B-27 supplement, 1.0 mM GlutaMax, 1.0 mM Glutamine, 1× NEAA, 0.1 mM β-mercaptoethanol, 1× nucleosides, 1.2 mM pyruvate, 0.2% ovalbumin (Sigma), 0.02% sodium heparin.

The following growth factors were added to the medium: 25 ng/ml Human Activin A, 25 ng/ml, 4 ng/ml human FGF2, 10 μg/ml ovotransferrin. Cells were counted at three weeks and then frozen for subsequent genome editing.

For genome editing: 2ug of CRISPR Cas9 guide RNAs in Px458 were transfected into 100,000 PGCs. Cells were sorted for GFP fluorescence after 48hours. PGCs were grown clonally and then analysed for the genetic edit at the selected locus. Edited cells were cryopreserved at concentrations of 50,000 PGCs per vial.

For breeding genome edited offspring:

3,000-5,000 PGCs were injected into single surrogate host eggs at day 2.5 (stage 16 HH). Eggs were sealed with Leukosilk tape and incubated to hatch. Hatchlings were raised to sexual maturity and then bred to produce offspring that were genetically screened for the intended edit and then analysed for a phenotypic change.

Results and Discussion

We genome edited PGCs at the ANP32A locus to test for reduce susceptibility to avian influenza infection (Long et al, 2019). We challenged chickens with a low dose of avian influenza and found that the GE chickens were resistant to both infection and subsequent shedding of the virus (Fig. 2A). However, when chickens were challenged with a high dose, we found that the virus was able to replicate in the directly infected chicken (Fig. 2B).

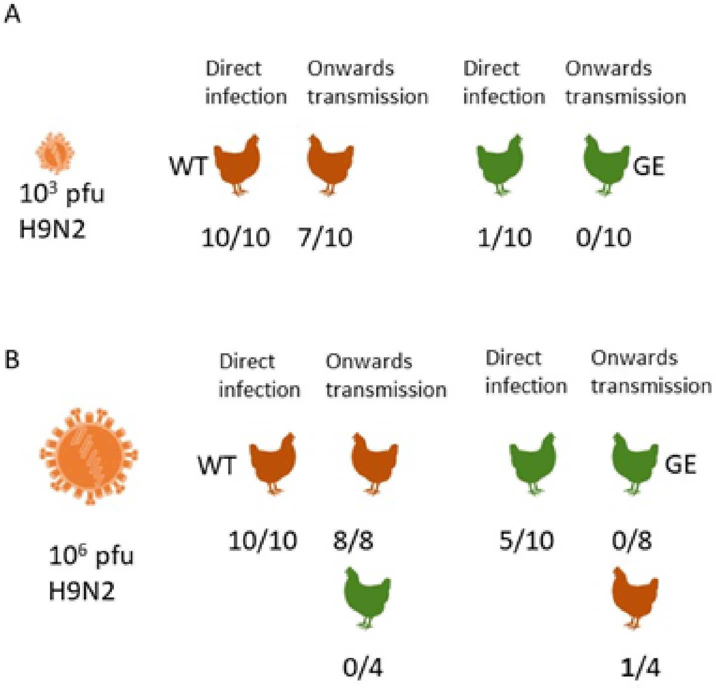

Fig. 2. Chickens genome edited at the ANP32A locus and challenged with Avian Influenza

A. Chicken were challenge with a low 'physiological' dose of avian influenza.

B. Chickens were challenged with a high dose of avian influenza.

From Idoko-Akoh et al (2023).

These results show that chickens can be genome edited for reduced susceptibility to avian influenza but complete genetic resistance will be needed to stop the spread and mutation of the virus. It is probably that a chicken will need multiple genome edits to produce a product that will be useful to chicken breeders and consumers.

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Genetic analysis of keel bone fractures in laying hens housed in a commercial aviary

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Keywords: keel bone fractures, laying hens, genetics, heritability, association

Keel bone fractures (KBF) are a widespread welfare problem in laying hens, with a prevalence of up to 97% in aviary systems. While environmental factors such as collisions with housing features contribute to KBF, genetics may play an important role too. This study estimated the heritability of KBF and identified genomic regions associated with KBF in laying hens. We used data from 1,065 white laying hens from a two-way cross of parental lines (Hendrix Genetics). The hens were housed in five groups of approximately 213 animals within a quasi-commercial aviary system with three stacked tiers and a winter garden. KBF severity was scored as a continuous variable (0.0-10.0) using radiograph images taken at 27 weeks of age. All animals were genotyped with a 60K SNP panel. The heritability of KBF on the logarithmic scale was moderately high, with an estimate of 0.21 (SE=0.06). We identified three genomic regions (on chromosomes 2, 3, and 20) that were suggestively associated with KBF. The top SNPs in these regions had moderate to high minor allele frequencies (0.21-0.43). Together, the 35 SNPs in these regions explained about 29% of the genetic variance (6% of phenotypic variance). The identified regions were near genes previously associated with bone (mineral) density and blood concentrations of vitamin D or calcium in humans. In addition, the region on chromosome 20 was near a locus associated with age at first egg in laying hens, supporting the hypothesis that KBF susceptibility may be related to early sexual maturity. These results demonstrate substantial genetic variation for KBF that could be exploited through genetic selection. Future work will focus on estimating genetic correlations between KBF and egg production traits.

Genomic selection on live radiographic phenotypes to improve laying hen bone health

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Keywords: keel bone, bone health, genomics, selection

Keel bone health is a concern for laying health welfare. Moderate to high heritability for bone traits suggest that selective breeding can be part of a solution. Tibial density, which can now be measured on live birds, can be used as a proxy to improve the health of the keel. We implemented a genomic prediction workflow for multi- and single-trait models. The first selection was based on training data from a single purebred population. Crossbred hens were produced, one group (n = 500) selected for higher and one (n = 500) for lower tibia density based on genomic estimated breeding values of the parents. Crossbreds were measured for bone density using live radiography at 22 and 40 weeks of age. There was a significant difference ($p < 0.001$) between the high and low bone density group for live bird tibia density at both ages and for post mortem tibia breaking strength ($p = 0.007$) which was 288±3 v 277±3 N for the high and low group respectively. Forthcoming selections will use multi-population models and data from crossbred selected hens and purebred lines. We tested genomic prediction with these different data sources. The best accuracy was achieved by bivariate models that use crossbred data in combination with one parental line. The genetic correlations between tibia density in the different populations were estimated to be 0.77 and 0.80 between the crossbred first cohort and the parental lines, but 0.33 between parental lines. In summary, genomic selection improved tibia density measured on live radiography and post mortem breaking strength, and multi-trait genomic prediction models allows sharing of information between crossbred offspring housed in different environments and the parental lines.

The work was funded by the Foundation for Food and Agricultural Research.

Metagenomic survey on the influence of humus additives to bedding during broiler chicken rearing

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Keywords: microbiome, antibiotic resistance genes, litter

Poultry litter environment creates excellent conditions for the spread of antibiotic-resistant bacteria (ARBs). Their presence often leads to the transmission of the antibiotic resistance genes (ARGs) via horizontal gene transfer (HGT). Our study aimed to evaluate the effects of humic substances (biochar and peat) on the poultry litter microbiota and to analyse their effectiveness in reducing the spread of ARBs and ARGs in faeces. Pens were lined with standard sawdust litter (control) and supplemented with a 15% admixture of charcoal (GrC) and peat (GrP) in duplicates. Each pen was planted with 10 1-day broilers of the Ross-308 breed and raised for 35 days under optimal conditions. Litter samples from the experimental and control groups were collected every 7 days to estimate the number of selected ARGs (*blaTEM, ermB, qnrS, sul1, sul2, tetW, tetG*) among E. coli and Enterococcus spp., by qPCR. Additionally, the microbiome of litter was assessed by 16s rRNA sequencing using NGS.

The most abundant phylum in the starting material were bacteria belonging to the Actinobacteria (93%) and Proteobacteria (5%) following marked increase of Firmicutes (23-95%) and Cyanobacteria (30-65%). In the first three weeks of the experiment, bacterial communities were significantly diverse at both the qualitative and quantitative levels between control and GrC and GrP groups ($p<0.01$). The addition of peat was effective in promoting the removal of mulch-borne ARGs. Network analysis showed that Actinobacteria and Firmicutes were potential bacterial hosts for ARGs. Redundancy analysis showed that bacterial community succession played a key role in ARG changes. Overall, this study provides evidence that peat and carbon additives promoted the ARG removal from litter during broiler chicken rearing.

Update on the chicken genome diversity consortium

Laurent Frantz[1], Steven Fiddaman[2], Mathieu Charles[3], Christophe Klopp[4], Michèle Tixier-Boichard[3] and the CGDC consortium

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Following the 11th European Symposium of Poultry Genetics in Prague, the Chicken Genome Diversity Consortium was established under the leadership of Prof. L Frantz with the funding obtained in 2021 from the SuperMUC computing cluster of the Leibniz-Rechenzentrum near Münich in Germany. The CGDC gathers around 30 members from 10 institutions in Europe and North America. Partners provided raw sequencing data they obtained in the frame of various national or international projects. The SuperMUC funding covered the costs of data storage and bioinformatics analysis.

This data set currently includes samples from wild junglefowl (Gallus varius, n=19; Gallus sonneratii, n=12; Gallus lafayettii, n=10 – the Green, Gray and Ceylon junglefowl, respectively) and the five subspecies of Red junglefowl (Gallus gallus), G. g. bankiva, n=5; G. g. gallus, n=93; G. g. jabouillei, n=23; G. g. murghi, n=85; G. g. spadiceus, n=81. Within the domestic chickens, samples represent a large range of breeds and geographic locations covering a significant portion of the global chicken distribution (North America, n=1023; South America, n=12; Europe, n=409; Middle East, n=259; Africa, n=1044; East Asia, n=836; South Asia, n=135; Southeast Asia, n=442; Oceania, n=25; Commercial breeds, n=475). In addition, the dataset is supplemented with ancient chicken genomes, largely derived from Europe and the Middle East from the last 2000 years. More than one hundred ancient samples have already been sequenced, imputed where necessary, and added to the dataset. Altogether, this yields a dataset size of more than 5100 genomes. Variant calling was performed after alignment of these sequence data to the current broiler reference genome (GRCg7b). A total of 80 million SNP and 1.1 million INDELs have been identified, which yielded, after recalibration, 46 million SNP of high quality.

This constitutes a unique data set to unravel domestication and adaptation processes in chicken as well as a reference data set to facilitate the identification of causal mutations of rare genetic defects. For example, the candidate mutation for a dwarf phenotype was identified at INRAE thanks to filtering out the polymorphisms of the affected birds that could be found in the CGDC data set, where this phenotype was not present. This step highly facilitated the finding of the causal mutation, by reducing the number of candidate variants from 11000 to 6.

Central to the consortium are the concepts of inclusivity and openness - all data are to be made available to all members of the consortium, as well as to the wider community, and collaborations between groups are fostered and actively encouraged. The dataset and metadata are in the final stages of curation prior to deposition in a publicly accessible repository. Requests for early access to the data from members of the community are encouraged, and the consortium welcomes any offer of collaboration. Enquiries can be sent to steven.fiddaman@biology.ox.ac.uk in the first instance. It is hoped this state-of-the-art resource, curated in-house by bioinformaticians, will enable the community to answer previously intractable questions in chicken evolution.

New developments in biotechnology applied to farm animals: EFSA 2025 assessment

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Keywords: NGTs, policy, EU

In 2021, the European Commission – DG SANTE published a study regarding the status of New Genomic Techniques under Union law. It concluded that the existing legislation, or so-called GMO directive in the EU, is not fit for purpose for some NGTs. It also concluded that "safety data are mainly available for genome editing in plants, making it difficult to draw relevant conclusions on other techniques and applications in animals and micro-organisms."

Following this publication, the Commission initiated several follow-up actions, including the publication of a proposal for regulation for some NGTs in plants, in June 2023. Given the conclusions for animals and the increasing interest in using NGTs to improve disease resistance and enhance the welfare of animals, the European Commission asked EFSA to evaluate whether its current risk-assessment guidance for genetically modified (GM) animals is adequate and sufficient when applied to NGT-derived animals. This official request reflects both the need for policymakers to have an updated evidence base for future regulatory and legislative discussions and for researchers and breeders to understand the regulatory framework for these techniques and its animal products in the EU.

In June 2025, EFSA adopted the assessment of the adequacy and sufficiency of current guidance for risk assessment for farm animals. The publication includes a horizon-scanning exercise identifying potential applications of NGT-derived animals expected to reach EU markets in the short to medium term.

No new hazards were identified when comparing NGT-derived animals with those developed using established genomic techniques (EGTs) or conventional breeding. Off-target mutations were also considered, and they were judged similar to mutations occurring spontaneously or through conventional methods, and therefore not representing novel risks.

The presentation will explore further the recommendations made by EFSA and the potential implications for researchers and breeders in Europe in the European and Global context.

Optogenetic spatiotemporal control of gene expression in avian embryos using the magnet-cre system

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Keywords: optogenetics, avian embryo, gene expression, magnet-cre

Chickens serve as an excellent model organism for developmental biology, offering unique opportunities for precise spatiotemporal access to embryos within eggs. Optogenes are light-activated proteins that regulate gene expression, offering a non-invasive method to activate genes at specific locations and developmental stages, advancing developmental biology research.

This study employed the Magnet-Cre optogenetic system to control gene expression in developing chicken embryos. Magnet-Cre consists of two light-sensitive protein domains that dimerize upon light activation, each attached to an inactive half of the Cre recombinase enzyme, which becomes active upon dimerization.

We developed an all-in-one plasmid containing a green fluorescent protein marker, the Magnet-Cre system, and a light-activated red fluorescent protein gene. This plasmid was electroporated into the neural tube of Hamburger and Hamilton (H&H) stage 14 chicken embryos. Embryo samples were cleared using the CUBIC protocol and imaged with a light sheet microscope to analyze optogenetic activity via red-fluorescent cells.

We established a pipeline for Magnet-Cre activation in chicken embryos, demonstrating that a single 3-min exposure to blue light following incubation at 28 °C was sufficient to trigger gene activity within the neural tube, with increased activity upon additional light exposure. Finally, we showed a spatiotemporal control of gene activity using a localized laser light induction.

This research lays the groundwork for further advancements in avian developmental biology and poultry research. The Magnet-Cre system enables precise, light-controlled gene activation and is adaptable to other effectors. It offers a scalable platform for spatiotemporal functional genomics in embryology and biotechnology.

Current performance of *in-ovo* sexing through PCR analysis: the Seleggt process

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Keywords: *in-ovo* sexing, PCR

Over the last few years *in-ovo* sexing has matured from being a novelty in the layer industry to becoming common practice in several European countries. One method that is currently commercially available is analyzing the sex through PCR on allantoic fluid (AF), as is done in the Seleggt procedure. Over time numerous techniques and automation (e.g. blood vessel detection and PCR data analysis) were developed to optimize the complete process. In-ovo sexing through PCR was examined from set till hatch to gain more insight into the current status and performance of the Seleggt process.

Dekalb White eggs (n=4,400) originating from one breeder flock (34 weeks old) were incubated at an eggshell temperature of 37.8°C. On incubation day 10 all eggs containing a living embryo were automatically processed by the Seleggt sampling Circuit to obtain an AF sample. AF was then analyzed with a singleplex endpoint PCR to determine the sex of the embryo. All eggs labeled as female were sorted and incubated further until pull. At pull, all hatched chicks were feather sexed, and hatchability was determined.

Results show that 48.7% of tested eggs were categorized as female by the PCR analysis, with a positive predictive value of 99.0% and negative predictive value of 97.4%. Transferred female eggs had a hatchability of 93.5%. Overall, the Seleggt *in-ovo* sexing process resulted in a 39.8% hatch of set of first grade female chicks, and 0.4% of set eggs hatched as male. These findings show that a high efficiency, accuracy and hatchability can be achieved by *in-ovo* sexing trough PCR analysis of allantoic fluid. Future research efforts will focus on further decreasing the percentage of males at hatch and working towards cost prices comparable to the costs of incubating and hatching male chicks.

Exploring allelic variants in pHu divergent lines of chicken by RNA-sequencing in *Pectoralis Major* and *Jejunum* tissues

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Keywords: pHu, allelic variants, RNA-seq

Poultry has become the most consumed and produced meat worldwide, driven by low production costs and the absence of religious restrictions. To meet demand, breeding programs and farming practices have intensified growth and yield, but also led to muscle defects that compromise meat quality, such as abnormal post-mortem pH declines and structural issues (e.g., white striping, wooden breast). In chickens, meat quality is largely determined by ultimate pH (pHu), which reflects glycogen reserves at slaughter. Glycogen content in the pectoralis major (PM) is highly heritable ($h^2 = 0.3–0.5$) and strongly negatively correlated with pHu ($r_g = –0.97$).

To study the genetic and physiological bases of glycogen variation, two broiler lines, pHu− (low pHu) and pHu+ (high pHu), were divergently selected based on breeding value for pHu at 6 weeks of age. These lines form a robust model: pHu− birds show a carbohydrate-based metabolism, while pHu+ individuals rely more on amino acid catabolism and lipid oxidation. RNA-seq was performed on the jejunum (nutrient absorption) and PM (glycogen storage) to dissect tissue-specific contributions.

Recent advances now enable RNA-seq data to be used not only for differential gene expression but also for identifying expressed genetic variants, thanks to tools such as GATK adapted for transcriptomic variant calling. A GWAS revealed 1,813 and 760 variants in the jejunum and PM, respectively, differentially represented between 15 pHu+ and 15 pHu− individuals. Several QTL regions, novel or known, harbored genes potentially involved in energy metabolism, muscle function and cellular signaling pathways (e.g., *PPP1R3A*, *IRAK2*, *MIA2*). These variants, whether coding or regulatory, may help explain the phenotypic divergence between the two lines.

Generation of transgenic chickens expressing human Interleukin 7 in egg white

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Keywords: transgenic chicken, CRISPR/Cas9, IL-7 production

Interleukin 7 (IL-7) is a key cytokine involved in lymphocyte development and homeostasis, with clinical potential in immunotherapy and regenerative medicine. Traditional production platforms for recombinant IL-7 are costly and limited in scalability. In this study, we aimed to establish a transgenic chicken model for efficient and stable production of human IL-7 (hIL-7) in egg white.

We used CRISPR/Cas9-mediated homology-directed repair to insert the hIL-7 coding sequence into the final exon of the ovalbumin gene, an oviduct-specific gene. For bicistronic expression, a self-cleaving 2A peptide was placed between the albumin and hIL-7 sequences. Chicken primordial germ cells (PGCs) were modified via nucleofection and selected *in vitro*. Genetically modified PGCs were then orthotopically transplanted into testes of sterilized recipient roosters, in which spermatogenesis was successfully reconstituted.

Transgenic hens laid eggs containing human IL-7 in the egg white, confirmed by ProQuantum immunoassay and Western blot. The recombinant cytokine displayed biological activity *in vitro*, indicating correct folding and processing. Expression was stable over time and had no observable effect on animal welfare or egg-laying capacity.

Our results demonstrate a robust and scalable method for cytokine production using genome-edited chickens, supported by efficient germline transmission via transplantation into sterilized surrogate hosts.

Genetic markers linked to bone properties in White Leghorn laying hens

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Keywords: White Leghorn laying hens, bone quality, genetic markers

Bone fractures in modern commercial poultry have significant welfare and economic impacts and is recognized as one of the primary challenges faced by the poultry industry. The present study aimed to investigate genetic markers that contribute to genetic variance in 44 bone strength and composition traits in White Leghorn laying hens (n=987) using a genome-wide association study. Bone quality was assessed on live birds and postmortem using physical methods such as X-ray radiography, thermogravimetry (TGA), and infrared spectroscopy (FTIR).

This study detected a set of markers in strong LD with each other ($r^2 > 0.8$) significantly associated with bone breaking strength, stiffness, and cortical thickness, located within the previously reported QTL on chromosome 20 for bone biomechanical strength and body weight. Furthermore, this region contains the bone morphogenetic protein 7 (BMP7) gene, which plays a well-established role in skeletogenesis and growth in chickens. We detected genetic markers with the strongest suggestive association with bone organic and mineral contents and the total amount of carbonate in bone mineral in the tibia medullary bone within the QTL region on chromosome 1: 173.5-173.6 Mb. Heritabilities with higher accuracy were estimated for thermogravimetry measurements of bone compositional traits compared to infrared spectroscopy. Out of all studied traits, the most heritable (h^2~0.26) and highly correlated with tibia density were medullary organic (r_g= -0.71) and mineral (r_g=0.72) contents. In conclusion, the genetic markers associated with bone quality traits were identified in this study. These can support future functional genomic research and aid in breeding value predictions for improving bone strength in White Leghorn laying hens.

Molecular diagnostics of *Campylobacter* in urban and domestic pigeons *(Columba livia)*

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Keywords: *Campylobacter jejuni,* real-time PCR

Bacteria of the genus *Campylobacter* are widely distributed in warm-blooded animals, including poultry, which is the main reservoir of infections in humans. The most frequently isolated pathogenic species are *C.jejuni* and *C. coli*. Due to the frequent occurrence of pigeons in urbanized and breeding environments, these birds may be a significant source of zoonotic transmission, especially *C. jejuni*, which is a potential threat to public health. Human infection can occur through the alimentary or aerogenous route; therefore, it is important to determine the scale of *Campylobacter* occurrence in these birds.

The study aimed to develop and evaluate the effectiveness of a two-stage molecular test for the detection of *C.jejuni* in pigeon feces - a classic PCR test and a real-time PCR test for verification of results.

A total of 131 pigeon fecal samples (fresh and dry) were collected from two locations: an urban park in Szczecin (n=75) and a rural pigeon loft in West Pomerania (n=56), collected from April to December 2023. DNA isolation was performed using the GeneMATRIX Stool DNA Purification Kit. Then, a classic PCR test was performed using primers for amplifying the *hipO* gene, characteristic of *C. jejuni*. PCR products (130 bp) were visualized electrophoretically in a 2% agarose gel. Positive results were verified by real-time PCR, using melting curve analysis. DNA of reference strains of *C. jejuni* ATCC 33560 and poultry isolates was used as positive controls.

In the classic PCR test, 10 positive results (7.6%) were obtained: 5/75 samples from the park (6.7%) and 5/56 from the dovecote (8.9%). The real-time PCR test confirmed 8 of them, which means the actual frequency of *C. jejuni* occurrence at the level of 6.1%. Detection of bacteria concerned only fresh fecal, mainly from the summer and autumn months.

The developed two-stage molecular test (PCR and real-time PCR) effectively identifies *C. jejuni* in pigeon fecal samples. Real-time PCR allows for the elimination of false-positive results and offers a faster, more sensitive, and quantitative analysis. The role of pigeons as potential carriers of zoonotic strains of *C. jejuni* was confirmed. Due to the presence of inhibitors in fecal samples, further optimization of DNA purification procedures is recommended in order to eliminate factors interfering with the test.

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Genetics underlying growth curve characteristics in German local chicken breeds

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Keywords: growth curve, local chicken breeds, genetics

Biodiversity has long been global concern, especially in light of increasing environmental dynamics. Although the high efficiency of commercial chicken breeds plays a crucial role in poultry production, there has been a change towards understanding and integrating local breeds that are rich in genetic diversity and offer flexibility for future breeding. The RegioHuhn project, which aims to preserve and revitalise local chicken breeds by creating crossbreeds for agricultural use, is intended to support this concept. RegioHuhn relies on a crossbreeding program in which local breeds from nucleus flocks are mated with high-performance commercial parent lines that can be used in regional farms. In this study, we analysed one of the important economic traits, the growth performance, in three local chicken breeds: the Altsteirer ($n = 104$), Bielefelder ($n = 93$), and Ramelsloher ($n = 105$), based on longitudinal body weight measurements from hatch to 71 weeks of age and SNP data genotyped using a 53k array. Individual growth curves were fitted using the Gompertz model to derive growth parameters: the asymptotic weight (A), growth rate parameter (k), and age at inflection (ti). Principal component analysis of these parameters showed partial separation between the three breeds. To explore the genetic architecture underlying these parameters, we conducted both single-trait GWAS and multi-trait metaGWAS, identifying significant variants on several chromosomes. Genomic best linear unbiased prediction (GBLUP) models were applied to estimate parameters heritability using a linear mixed model, that included an intercept and treated pen as a fixed effect. Although standard errors were relatively high due to the limited sample size, heritability estimates varied across breeds and parameters, ranging from 0.31 to 0.79, 0 to 0.64, and 0.1 to 0.6 for A, k, and ti, respectively. These findings suggest that within-breed selection based on growth parameters as one of the indicators is potentially feasible. However, further optimization of model structures is necessary to ensure the robustness of these parameters.

Deciphering GxE interactions with omics approaches: insights from the GEroNIMO EU project

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Keywords: chicken, DNA methylation, environment effects

GEroNIMO (Genome and Epigenome eNabled breedIng in MOnogastrics) is a Horizon 2020-funded multi-actor project involving 22 partners from 11 European countries (June 2021–May 2026). The consortium includes academic institutions, breeding companies, professional associations, and experts in project management and innovation. GEroNIMO aims to provide knowledge and tools to promote innovative genome and epigenome-enabled selection methods in chickens, quails, and pigs.

With a strong focus on sustainability, robustness, and welfare, GEroNIMO investigates the environmental impact on animal performance and resilience, as well as the epigenetic memory of environmental stimuli.

GEroNIMO's multi-omics approach includes genome wide genotyping, epigenotyping (RRBS or GBS-MeDIP) and transcriptomics (RNA seq) on many individuals from commercial and local chicken lines and breeds, exposed to diverse environments.

Animals in livestock systems face stressful events during life and must adapt to changing environments such as housing systems, feed transitions, climate fluctuations, and diseases. These events can significantly affect production, health and welfare, with the magnitude of impact varying among individuals, according to their genotype, but also to the age of the animal.

Genotype × environment (G×E) interactions, long recognized as a key mechanism underlying trait variation, occur when the genetic effect on a trait varies depending on the environment. In GEroNIMO, G×E interactions are studied through multi-genotype × multi-environment designs. However, as the study of environmental factors is central to the project's approach, GEroNIMO also explores non-traditional interaction layers shaped by complex environmental influences. These include tissue × environment (T×E) interactions, which examine how the same genotype exhibits tissue-specific epigenetic responses to environmental stimuli, revealing tissue-specific plasticity and stability. They also include age × environment (AxE) interactions, which investigate how early-life rearing conditions affect gene expression in an age-dependent manner providing insight into molecular signatures of past environmental conditions.

For analysing GxE interaction, we used an experimental design funded in a previous project, and composed of three experimental chicken lines (Naked Neck, Fayoumi, and Rm selected for high feed efficiency) and one commercial line (Novogen) exposed to 4 weeks of chronic heat stress (32°C) in adulthood. GxE interactions emerged across traits related to feed efficiency, egg production, and metabolic parameters, revealing contrasting adaptive capacities among genotypes. In GEroNIMO, the same lines were analysed for CpG methylation patterns in the liver under heat stress. A clear stress-induced shift in methylation profiles was observed, with distinct separation between control and stressed groups in the experimental lines, but less so in the commercial line (Fig. 1A). Considering the number of differentially methylated CpG (DMC) sites as an indicator of the degree of response, we observed genotype specific methylation profiles among the four genotypes (Fig 1B), with the majority of DMCs being genotype-specific.

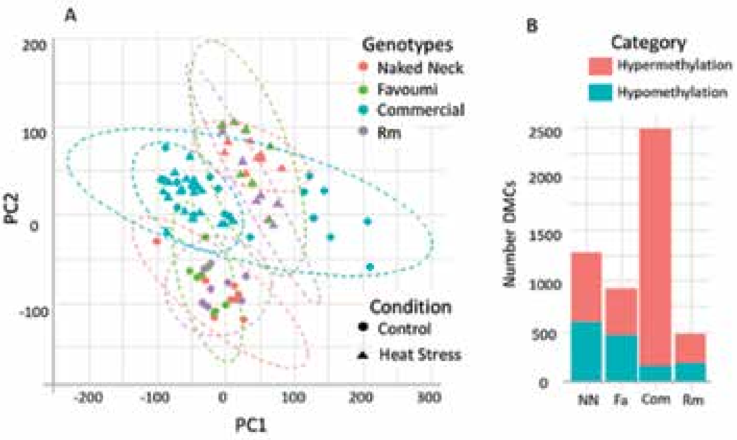

Figure 1. Principal Component Analysis of liver RRBS data (A) and number of DMCs for each genotype (B). NN = Naked Neck, Fa = Fayoumi, Com = Commercial, Rm = High efficiency).

Transcriptomic analysis of the same liver samples revealed a similar pattern: the commercial line had the highest number of heat-induced differentially expressed genes (DEGs, ~4000), 230 of which harboured DMCs in at least one of their gene features (e.g., promoter, intron, exon). Functional analysis of these DMC/DMG genes revealed enrichment for regulation of transcription, RNA metabolic process, and DNA-binding processes and functions.

GEroNIMO explored also the existence of tissues x environmental epigenetic effects of one-day-old transportation stress (T) versus on-farm hatched (O) across 11 life stages, in chicks from a Dekalb White line.

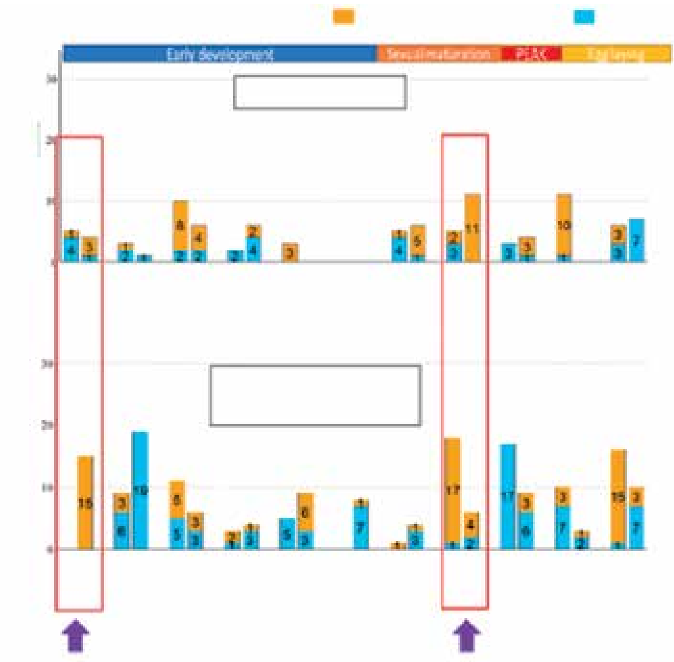

Figure 2
DMRs counts across life stages (p≤0.01) from amygdala and rostral hippocampus identified in transported (T) versus on-farm hatched chicks (O). Red boxes indicate stress events as the one-day transportation and the change of barn just before lay. Embryo plus 11 life stages were compared two by two (1-> 0 = stage 1 vs embryo; 2->1 = stage 2 vs 1 etc.)

Different brain regions involved in stress and emotion responses were analysed. The analysis revealed that different tissues have different methylation dynamics across life, responding differently to transportation stress. For example, in the rostral hippocampus, hyper-methylated DMRs are observed upon transportation, while hardly any change is observed in the amygdala (Fig 2).

Finally, GEroNIMO investigated age × environment (AxE) interactions by comparing transcriptomes from liver samples collected at 70 vs. 90 wk of age in hens of a Novogen parental line reared previously either in collective cages or in floor pens. Among the 13,929 expressed gene models, 215, with a FC >= 2-fold for at least one factors, showed significant AxE interaction. These included several genes involved in cholesterol synthesis, which showed a more pronounced expression decrease from 70 to 90 weeks in cage-reared hens compared to floor-reared hens. A notable number of other genes showed scale variation interactions, highlighting that early-life environment may modulate the extent of age-related gene expression changes.

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Leveraging local breeds and landscape genomics to detect adaptive genes

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Keywords: adaptation; climate; landscape genomics

Since the introduction of *Gallus gallus domesticus* to Europem the species has differentiated into numerous local breeds specific to regions. Local chicken breeds exhibit a large morphological diversity as a result of human driven selection, it is hypothesized that these breeds have adapted to the environments of their origin. This study aimed to identify genes involved in such local adaptation. Blood samples from 27 breeds (1337 individuals) spanning 6 countries were genotyped on a 57K SNP Chip. All statistical analyses were performed within R studio. Two landscape genomics approaches were performed to assess Genomic-Environment Associations (GEAs): redundancy analysis (RDA) in the *vegan* package and latent factor mixed models (LFMM) in the *LEA* package. Twenty climate variables were extracted from the WorldClim database for each breeds origin. Admixture proportions, calculated within the *LEA* package, was included as a covariate in the models to account for genetic structure. A total of 422 (p-value < 0.05) and 65 significant SNPs (q-value < 0.1) were identified with RDA and LFMM, respectively, with 27 SNPs common to both tests. In total, 287 and 46 genes were found associated with the significant SNPs identified by RDA and LFMM, respectively. The Database for Annotation, Visualization, and Integrated Discovery (DAVID) was used on the RDA significant genes to perform gene ontology and enrichment analysis, which highlighted a significant increase (p-value < 0.05) in genes related to gene expression, UV response and sensory perception to sound. These results emphasize the value of local breeds and landscape genomics for identifying genomic regions associated to climate adaptation that can be used to inform future breeding efforts.

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Impact of genetics on behavioral variations in outdoor raised hens

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Keywords: laying hens, ranging behavior, genetics

Introduction

Poultry welfare is an increasing concern among consumers. Outdoor access enhances natural behaviors, but the use of outdoor space varies greatly among laying hens. Our study investigated genetic factors influencing outdoor access in White Leghorn hens and associations between range use and immune response traits to explore the impact of range use on immune competence.

Methods

Range use was recorded in 397 hens using radio frequency identification technology over a 26-day period. All hens were vaccinated against Infectious Bronchitis Virus (IBV), Newcastle Disease Virus (NDV), Avian Pneumovirus (APV), Avian Encephalomyelitis Virus (AEV), genotyped, and assessed for vaccine-specific antibody responses and heterophil-to-lymphocyte (H/L) ratio. Animals were genotyped using a 57k SNP chip. Association of ranging with weather conditions and immune traits were examined and genetic parameters were estimated.

Results

We found a consistent negative association between duration and frequency based ranging metrics, suggesting ranging behavior as multidimensional. Temperature slightly reduced, while humidity, rainfall, and wind increased number of outdoor hens. Weak and inconsistent correlation was observed between outdoor access and NDV vaccine response, while no significant links for other vaccines. Moderate heritability estimates for all measured ranging traits ($h^2 = 0.24 – 0.33$), suggest a genetic component; however, genome-wide association analyses revealed no significant variants, supporting a polygenic architecture.

Conclusion

Outdoor access in laying hens is partly influenced by weather and genetics, but shows weak association with the immunity and stress. Further studies should examine ranging behavior with these parameters in larger populations over longer periods.

Using genome-wide association studies to identify novel genomic regions associated with laying hens' behaviour within aviary housing systems

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Keywords: laying hen, aviary, behaviour

Understanding how a bird interacts with their environment, particularly their housing system, can be an asset for commercial egg production. Previous research investigating duration spent in different areas of an aviary barn has indicated moderate heritabilities, however the underlying mechanisms for these behaviour traits remain unknown. The objective of this study was to identify potential genes associated with the duration spent in the different areas of an aviary barn using a genome wide association study (GWAS) and to provide insight into the biological processes of the traits. For this study 1,098 white pure line crosses were tracked using a radio frequency identification system that determined the hens' duration spent in each of the five designated zones of a semi-commercial aviary (wintergarden, litter, lower tier, nestbox tier, and upper tier) across days 4 to 290 of production. All hens were genotyped using a proprietary 60K SNP array. After data filtering, 252,154 days of records were used for phenotypes, where average duration spent in a specific zone over the entire period of study, as well as in segments of approximately 50 days were investigated. Association analysis using a mixed linear model was carried out for each zone, with number of visits to the zone and pen number fitted as fixed effects, the top two principal components fitted as covariates, and the polygenic effects as random. Across the different zones and time periods, 13 unique SNPs were identified using chromosome-wise Bonferroni corrections. Significant SNPs were mapped to within 100,000 base pairs of 22 annotated genes, where the genes' function provides insight into the physiological mechanisms relating to how hens use their housing system, but further validation is needed.

Breeding chickens for the future: International competition versus European isolated solutions

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The global poultry industry stands at a crossroads. On one hand, international markets demand highly efficient hybrids, optimized for rapid growth, feed conversion, and maximum egg output. On the other hand, European stakeholders—facing stricter environmental regulations, increasing animal welfare demands, and consumer pressure—are exploring more localized and alternative breeding strategies. A bio-based economy requires the sustainable and efficient use of limited resources to reduce the carbon footprint while maintaining biosecurity. However, politicians, NGOs, and some retailers often prefer simple, easily communicated solutions. Since animal welfare indicators are often too technical for public debate, they instead focus on limiting performance levels, reducing stocking densities. Some critics argue for new genetics that focus exclusively on resilience and robustness. Climate neutrality can only be realized through excellent feed conversion and efficient resource utilization. High performance, combined with the use of synthetic amino acids and enzymes, reduces nitrogen excretion. Likewise, closed housing systems and soybean-based diets produce lower emissions compared to organic systems, which face numerous limitations. These conflicting goals highlight the gap between biological realities and idealized worldviews. In contrast, EU initiatives place greater emphasis on animal welfare, biodiversity, and resilience. However, simple solutions come with significant trade-offs. Performance restrictions and reduced stocking densities decrease feed efficiency and require the construction of more poultry houses. Developing different genetics for every market increases breeding costs and reduces population size, which negatively impacts genetic progress across traits. Likewise, lower breast meat yield in dual purpose chicken do not meet consumer expectations, even in organic markets. The future of poultry breeding will likely be shaped by sustainable intensification when selecting for increased lifetime efficiency and scientifically measurable animal welfare traits. A hybrid model could emerge—where global genetic progress provides the backbone of productivity, while European initiatives develop complementary lines tailored to local conditions and societal expectations. This approach could balance competitiveness with sustainability and Europe could set ethical and ecological standards for the global poultry industry applying transparent breeding goals, grounded in biological and economic realities. Developing different line combinations for different markets—cost-efficient and market-driven—may be the key to addressing current and future challenges.

Use of metagenomics phenotypes to predict breeding values in broilers

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Keywords: microbiability, microbiome, genomic evaluations

Introduction

The significance of the gut microbiome in health and productivity of farm animals has been highlighted by a large body of studies in the last decade. The intricate interplay between microbiota and the host has been shown to have a genetic basis (Camarinha-Silva *et al.*, 2017). This relationship is quantified as the proportion of phenotypic variance for a trait explained by the microbiome diversity among individuals, also known as microbiability (m2). In chickens, the estimates of m^2 exhibit variability across traits and populations (Wen et al, 2021; Borda-Monlina, 2021, Zhou et al, 2022).

From a breeding perspective accounting for m^2 presents opportunities to investigate the potential of incorporating metagenomics information into genetic evaluations. The objective of this paper is to quantify the m^2 in a broiler population for body weight (BWT) and feed intake (FI), and assess the impact of including metagenomics information for genomic prediction.

Materials and Methods

The study included 2,963 animals from an Aviagen broiler pure line with records (pre-adjusted for fixed effects) for BWT and FI and genotyped with a 50K SNP array. The cloacal samples collected from all the animals were sequenced for the whole 16S rRNA gene using long-reads with Oxford Nanopore. This approach offers a higher resolution for taxonomic assignment of microbial species to obtain more precise diversity insights. The 16S reads were mapped to a MetaSquare database and 1535 microbial species were identified using Centrifuge to construct relative abundance tables.

To estimate m^2 four models were investigated that included (i) only the $\boldsymbol{m}$ random effect of the microbiome; (ii) only the $\boldsymbol{g}$ random effect of 50K genotypes; (iii) both $\boldsymbol{m}$ and $\boldsymbol{g}$ effects; and (iv) the common environment effect due to the dam ($\boldsymbol{c^2}$) added an extra random effect. A log-likelihood ratio test was used to assess which model fitted best the data.

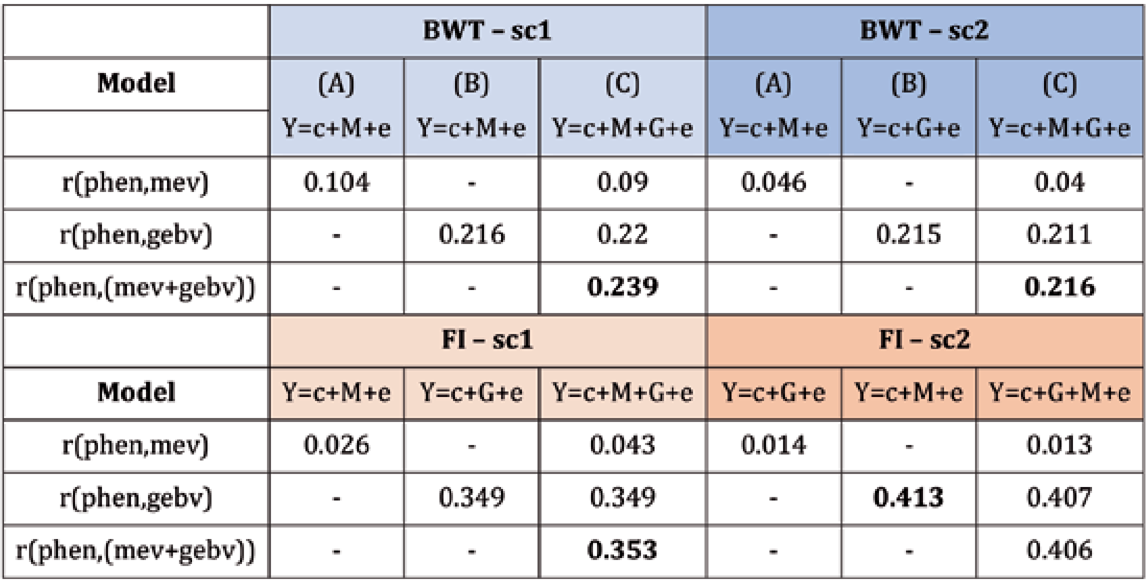
For genomic prediction, models including c^2 and (**A**) *m* that yields metagenomic estimated values (MEV); (**B**) *g* that yields genomically estimated breeding values (GEBV); and (**C**) *g* and *m* were considered. A forward in time prediction was conducted, where older animals were assigned to a training set (TRN) while the phenotypes of the most recent animals were masked as a testing set (TST). Two scenarios were investigated: **sc1** with 2135 and 828, and **sc2** with 2512 and 451 animals in TRN and TST respectively. The accuracy of genomic prediction was defined as the correlation between pre-adjusted phenotypes with predicted GEBV (B&C), MEV (A&C), or the sum of the GEBV and MEV (C only).

Results and Discussion

The m^2 estimates for model (i) with only the *m* effect were higher for both BWT and FI compared to the other models (7% and 3% respectively). Including the g effect in model (iii) reduced the m^2 estimates to 5% for BWT and 2% for FI. The proportion of variance explained by genotypes (h^2) didn't differ between model (ii) and (iii) suggesting no detectable interplay between microbiome and host genetics. The full model (iv) that included the c^2, fitted better the data (statistically significant for BWT and marginally for FI). Including all three random effects did not change the m^2 estimates for both traits, indicating that microbiome effects appear not to be dependent on the common dam environment.

The accuracies of genomic predictions using the three models under the two scenarios are presented in Table 1.

Table 1: Accuracy of prediction (in rows, as correlation r between adjusted phenotype and breeding values) for BWT and FI for the two training and test set scenarios and the three models (in columns).



	BWT – sc1			**BWT – sc2**		
Model	(A)	(B)	(C)	(A)	(B)	(C)
	Y=c+M+e	Y=c+M+e	Y=c+M+G+e	Y=c+M+e	Y=c+G+e	Y=c+M+G+e
r(phen,mev)	0.104	-	0.09	0.046	-	0.04
r(phen,gebv)	-	0.216	0.22	-	0.215	0.211
r(phen,(mev+gebv))	-	-	**0.239**	-	-	**0.216**
	FI – sc1			**FI – sc2**		
Model	Y=c+M+e	Y=c+G+e	Y=c+M+G+e	Y=c+G+e	Y=c+M+e	Y=c+G+M+e
r(phen,mev)	0.026	-	0.043	0.014	-	0.013
r(phen,gebv)	-	0.349	0.349	-	**0.413**	0.407
r(phen,(mev+gebv))	-	-	**0.353**	-	-	0.406

Model A, which incorporates only the microbiome effect m, exhibits lower accuracies. Conversely, model B, which solely considers the genotype effect (g), achieves higher accuracies. Summing *m* and *g* effects in model C achieves slightly higher accuracies in three out of the four combinations of scenarios and traits investigated. Notably, the accuracy of GEBV in model C was unchanged compared to model B, indicating that the inclusion of metagenomic information does not significantly enhance the accuracy of genomic predictions. Consequently, the re-ranking of GEBVs produced by models A and C is minimal, with only a single animal difference between the top 15 candidates.

One reason for the low increases in GEBV prediction accuracy could be that both traits were recorded in a homogeneous high-hygiene environment in which microbiome diversity can be lower. Even though to our knowledge this study is the largest of its kind in broilers, the dataset could still be limited to capture the complex interplay between the microbiome and the host. Many factors can influence the composition of the microbiome through the life of a bird and these may need to be better understood and accounted for in future analyses. Future work will expand the dataset by combining metagenomics samples from different environments.

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Artificial Intelligence in poultry management and breeding

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Keywords: Artificial Inteligence,poultry management, poultry breeding

Applications of artificial intelligence (AI) have been rapidly expanding over the last decade with the increase in computational capacity, new algorithms and high-resolution monitoring technologies. These developments have also affected agriculture including the animal production sector and poultry industry. While opening new opportunities these tools are also not free of challenges. The objective of this report is to review some of the technologies and algorithms with potential applications for poultry management and breeding.

To cover a range of applications within a limited scope several examples in the following categories will be discussed:

- sound analysis for stress detection and disease detection and identification;
- image analysis for *in-ovo* sex determination, automatic sexing, automatic egg grading and sorting, disease diagnosis, development of new traits t based on CT scans mostly related to meat production, health and welfare, development of digital twins and 3D models to better understand anatomy, physiology and behavior of birds;
- video recording and processing for welfare assessment (for example leg health and mobility scoring), monitoring of behaviors (such as standing, laying, eating, drinking, resting, dust bathing, perching, pecking, egg laying), automatic egg production and egg quality recording, piling and smothering prevention;
- wearable monitors for activity and space utilization monitoring and egg production recording in cage free systems; changes in activity levels may also suggest potential stressors or welfare concerns;
- smart nutrition to optimize individual growth trajectory and flock uniformity;
- robots for floor egg collection, bird activity stimulation, increasing nest utilization, improving litter quality, barn cleaning and disinfection, monitoring environment on the bird level and removal of sick or dead birds;
- genomic selection models incorporating non-additive or non-linear SNP effects (Convolutional Neural Networks, Support Vector Machines, Random Forest, Gradient Boosting Decision Trees, Extra Tree, CatBoost, Light Gradient Boosting Machine, Extreme Gradient Boosting, Multilayer Perceptron, Kernel Ridge Regression, K-nearest neighbors, and Deep Neural Networks with different architectures) or adding an additional layer of information with intermediate phenotypes such as gene expression, genome annotation, proteomics or microbiome.

The major barriers for implementations included the following limitations of current technologies: algorithms developed in controlled setting of a small pen in a laboratory do not scale well to large numbers of birds in the real world production facilities, addition of sensors or wearables was potentially affecting bird behavior, technology and high tech equipment was performing poorly in a challenging farm environment (for instance high level of dust, ammonia, bird interactions), high costs of system installation and maintenance, requirement for highly skilled labor for system monitoring and maintenance, costs of data storage, model interpretation, difficulty with transferring and processing of the unending stream of data, and the lack of accurate individual bird tracking and phenotyping especially in large groups. Despite current limitations, rapid development of AI and high-resolution monitoring technology brings hopes for large scale individual tracking, automatic data collection on individual level, development of new traits related to performance, behavior, bird interactions, resilience and welfare.

AI-powered imaging of keel bone traits for genetic selection in laying hens

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Keywords: AI, keel bone, breeding

Introduction

Keel bone fractures and deviations are common in laying hens, and can lead to pain, reduced mobility and decreased egg production. Genetic selection offers a solution, but progress is limited by the lack of efficient phenotyping methods. This study aimed to develop AI-powered imaging to measure keel bone traits and estimate their heritability and genetic correlations with post-mortem bone scores.

Methods

A total of 1,051 commercial laying hens (Bovans Brown and Lohmann Brown) were X-rayed, followed by keel bone dissection and scoring. Deep learning and computer vision were used to extract automated measurements of keel bone geometry and radiopacity. Genotyping was performed using 50K SNP chips, and genetic parameters were estimated via genome-based restricted maximum likelihood.

Results

Post-mortem keel bone deviations and fractures showed heritability estimates of 0.28–0.30. Image-based traits of keel bone had heritability estimates of 0.09–0.39 for geometry and 0.10–0.12 for radiopacity. Genetic correlations between image-based and dissection traits ranged from 0.52 to 0.81.

Conclusion

The image-based traits of keel bones are easy to measure and relevant to bone fractures and deviations. On-farm X-ray imaging with automated analysis offers a scalable tool, which breeding companies can use to advance welfare and productivity of laying hens.

Deep learning to automate chicken tibia-breaking strength annotation from X-ray images to improve animal welfare

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Keywords: deep learning, chicken, bone health, X-ray, tibia

Egg laying increases the risk of bone damage, leading to welfare issues. Tibiotarsal bone strength is an important indicator of chicken health. Measurement of bone quality parameters could enable breeding for improved bone strength, but measures like breaking strength are traditionally measured post-mortem. This makes implementation of a breeding programme for bone strength difficult. Recently, manual, non-invasive methods on live bird X-rays have been developed as proxies to characterise bone strength. However, manually identifying regions of interest and determining bone quality metrics from X-rays is time-consuming and prone to human error and biases, making it challenging to implement at scale.

In this project, we have developed an AI approach to identify the tibia and predict its breaking strength from X-ray images. Our system can annotate each bone in ~0.13 seconds, making it extremely efficient for breeding purposes. We have used a segmentation model that can extract the bones from the images with high accuracy. These extracted bone regions are then passed to a regression-based model that can predict the tibia-breaking strength from pixel features. For the regression model, we achieved a Pearson correlation of 0.74 between the empirically measured and predicted breaking strengths, demonstrating a high ability to predict the required features. Furthermore, we conducted a genetic correlation analysis to understand if our results had any biological significance. We achieved a genetic correlation >0.9 between tibia-breaking strength and our predictions. Such a system could consequently be effective for enabling the breeding for welfare traits, such as reducing bone damage, and provide a framework to extend the approach to other image-derived phenotypes.

Conservation of poultry genetic resources in Poland

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Globalisation and the intensification of livestock production, particularly poultry farming, have contributed to the extinction of many indigenous poultry breeds. According to Szwaczkowski (2022), the percentage of endangered poultry breeds worldwide is very high, i.e. turkeys –34%, chickens – 33%, geese – 31% and ducks – 21%. Meanwhile, the conservation of indigenous poultry breeds is of great importance both in highly developed countries and in developing countries, where indigenous poultry breeding predominates. The issue of conservation and the effective use of genetic resources was under discussion as early as the late 1940s, and the first guidelines for FAO plans in the field of animal and plant genetics were presented in 1946 at the International Congress of Genetics in Stockholm. Subsequently, a series of recommendations were drawn to conserve the poultry population including, among others, the recognition of the need to develop a catalogue of poultry genetic resources covering information from around the world. Conservation efforts were intensively pursued in France, the Netherlands, Spain and Bulgaria. Also in Poland, in the 1970s, a team of researchers from the National Research Institute of Animal Production led by Prof. Stanisław Wężyk and Prof. Adam Mazanowski, in cooperation with other research centres, undertook the initiative to develop guidelines for programmes to protect indigenous poultry breeds. To this end, an inventory of hen flocks was carried throughout the country, and their genetic and production characteristics were determined. Subsequently, the concepts of conservation and reserve flocks were defined, and conservation methods, breed standards and an appropriate mating system were developed (Wężyk, 1975; Mazanowski, 1984). In 1995, Poland ratified the Convention on Biological Diversity, which imposed on each of its signatories the obligation to preserve the diversity of plants and animals within their own countries. It was also decided at that time to establish the Domestic Animal Diversity Information System (DAD-IS) and then, based on the information contained in DAD-IS, a catalogue of genetic resources, known as the World Watch List for Domestic Animal Diversity 2000, was developed.

As a result, Poland has one of the most extensive and valuable collections of local breeds/lineages of chickens, geese and ducks, which are perfectly adapted to difficult environmental conditions and closely linked to the agricultural landscape, traditions and culture of local communities. Currently, 13 breeds of laying hens, 14 breeds of geese and 10 breeds of ducks are covered by genetic resource conservation programmes for poultry populations.

Detailed characteristics of poultry breeds/lineages covered by conservation programmes are presented in the Album of livestock covered by genetic resources conservation programmes in Poland (Krawczyk et al., 2025) and on the website www.bioroznorodnosc.izoo.krakow.pl/drob.

Breeders of protected flocks of chickens, geese and ducks participate in the implementation of protection programmes, as do entities that maintain livestock registers for these populations, i.e. the National Research Institute of Animal Production and the National Poultry Council – Chamber of Commerce in Warsaw (KRD – IG), which is also responsible for assessing the utility value of all poultry species in Poland. Pursuant to Article 34(3) of the Act on the organisation of livestock breeding and reproduction (Polish Journal of Laws of 2021, item 36), the coordination of activities related to the protection of livestock genetic resources is carried out by the National Research Institute of Animal Production. In its work on the protection of indigenous/local chicken breeds, the Institute cooperates with the FAO, the Ministry of Agriculture and Rural Development, universities, the National Animal Breeding Centre, the National Poultry Council – Chamber of Commerce, agricultural advisory centres and non-governmental organisations.

Endangered poultry populations are protected using the in situ method, which involves protecting live animals in their natural habitat. The main objective of programmes for the conservation of genetic resources of chickens, geese and ducks is to protect individual populations from extinction by maintaining genetic balance at a constant level in each protected flock, while preserving the characteristics specific to each population. In poultry flocks covered by conservation programmes, the effective protection of endangered poultry breeds is ensured by their constant monitoring, enabling a rapid response to unfavourable changes in the structure and size of the protected population, as well as in production results. In accordance with applicable regulations, in conservation poultry flocks, a utility value assessment is carried out and the data is published annually in the „Results of the utility and breeding value assessment of poultry populations covered by the genetic resource conservation programme". In recent years, as a result of observations and researches, as well as global solutions adopted, and based on data from the implementation of conservation programmes, a model for assessing the threat status of native breeds, adapted to Polish conditions, has been developed at the National Research Institute of Animal Production (Polak et al. 2021). Based on the number of males and females entered in the registers and the value of the endangered status index in all the above-mentioned poultry populations, it was concluded that these breeds currently require further protection.

The research conducted do date shows that indigenous or locally adapted poultry breeds are phenotypically and productively diverse. They constitute valuable material for research in immunogenetics, cytogenetics, embryology, serum protein polymorphism and molecular genetics methods (Wolc et al, 2024).

Local poultry populations play an important role in preserving biodiversity and, when kept in backyard farming are a valuable part of the rural landscape. They make good use of the local feed base, meadows and pastures, and provide products with high taste and dietary values (Calik et al, 2015; Lewko et al, 2022).

Current scientific research on poultry genetic resources focuses on the application of biotechnological methods in ex situ conservation and on molecular analyses aimed at determining the genetic basis of phenotypic plasticity in indigenous chicken breeds.

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The use of genetic resources in breeding programs: Why, what and how

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Keywords: diversity, breeding goals, agroecology

The climate is changing at an unprecedented rate and this is affecting both the mean and the range of temperature and humidity (Calvin et al., 2023). This is in turn affecting the animal production sector directly by modifying the raising conditions of animals, sometimes to the limits of their metabolic tolerance capacities, or indirectly by changing feed and water supply in terms of quantity, quality and stability (Cheng et al., 2022). Moreover, the distribution of diseases and of their vectors is also widely changing, exposing animal populations to new threats. The picture is even more complex since animal production is amongst the main drivers of climate warming. Finally, the perception of conventional livestock by the society is changing and a growing part of the consumers is worried about raising conditions and animal welfare, aiming at alternative systems like free-range or organic farming (Harper & Makatouni, 2002).

This raises the need for a change in the animal production systems and genetic improvement can be a key to adapt to these new challenges. Indeed, the new breeding systems should make it possible to initiate the necessary agroecological transition by providing the animals meeting the breeding goals to cope with this changing world and to mitigate their impact (Phocas et al., 2016). This is relying on the ability to get access to a sufficiently large reservoir of genetic diversity. In this context animal genetic resources offers a good opportunity for breeders to obtain the necessary material when lacking it into current breeding nucleus.

The first step is to identify and characterize the available material, in terms of breeds, population sizes and genetic or functional diversity (Jacques et al., 2024; Nigussie, 2011; Restoux et al., 2022). Second, if resources have been identified as at risk, conservation actions must be taken by i) adopting appropriate management programs (Bortoluzzi et al., 2024), ii) storing reproductive material into cryobanks, or iii) reintroducing genetic diversity (Jacques et al., 2023). Indeed, animal genetic resources can be available and conserved ex situ (e.g. cryobanks…) or in situ (i.e. on farms), both having advantages and drawbacks depending on the targeted goals.

However, the conservation of genetic resources should not be the ultimate goal, and their use is also crucial. In particular, in animal breeding they can be used i) to restore an extinct breed, or ii) to support a breeding program. The modalities, both in terms of materials and methods, for using animal genetic resources are context dependent. In particular, the diversity of the material available, its link to the current germplasm and its performance level make it more or less prone to be used in a given breeding program. In particular, the strength of selection and the stability of the breeding goals over time is crucial (Jacques et al., 2024).

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Preservation of genetic diversity in poultry: The role of commercial breeding programs

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The consolidation of poultry breeding around a limited number of high-performance lines for meat and egg production has led to a significant reduction in genetic diversity within commercial populations. In this context, Hendrix Genetics contributes to the preservation of biodiversity by maintaining and supplying a broader range of pure lines, including those not commonly used in mainstream production. These lines represent valuable genetic resources that may hold traits relevant for future breeding needs, such as robustness, disease resistance, and adaptability to changing environmental conditions. By keeping these lines available, Hendrix Genetics supports research, conservation efforts, and the potential diversification of production systems. This approach helps mitigate the risks associated with genetic uniformity and supports the long-term resilience of poultry breeding. While primarily a commercial entity, Hendrix Genetics' maintenance of alternative genetic lines plays a role in balancing production efficiency with the need to preserve genetic variation.

Investigating pedigree and genomic inbreeding in pure line of Pekin ducks

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Keywords: pedigree inbreeding, genomic inbreeding, genomic selection, duck

The main principle of selection involves choosing a limited number of individuals to produce the next generation. However, this restricted use of breeders can lead to an increase in inbreeding over generations. To date, various recommendations exist to limit inbreeding, but they mostly focus on pedigree-based coefficients. Meanwhile, many genomic inbreeding coefficients exist, with no real consensus on the most appropriate indicator to use.

Therefore, from a pure line of Pekin ducks selected and genotyped with a custom 50K SNP chip, pedigree (F_{PED}) and genomic inbreeding coefficients were estimated and compared. Six genomic inbreeding coefficients were studied depending on the information they rely on: correlation between uniting gametes (F_{UNI}), genomic relationship matrix (F_{GRM}), variance-standardised relationship minus 1 (F_{VR2}), excess of homozygosity (F_{HOM}), runs of homozygosity (F_{ROH}) and heterozygosity by descent (F_{HBD}).

Two groups of genomic inbreeding coefficients emerged based on their correlations: a first group with $F_{UNI,}$ F_{GRM} and F_{VR2} (correlations between 0.78 and 0.97), and a second group with F_{HOM}, F_{ROH} and F_{HBD} (correlations between 0.88 and 0.93). Interestingly, F_{PED} showed no correlation with F_{GRM} (-0.08) and only a low correlation with F_{HOM} (0.25), suggesting that pedigree information available is finally relatively recent compared to the genetic history of the line.

All these results highlight the relevance of genomic indicators in capturing historical inbreeding. Depending on the depth and quality of pedigree and availability of genomic information, genomic inbreeding coefficients may be more relevant than pedigree inbreeding for selection.

Chickens represent an ideal model for host-microbiota studies

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Chickens are hatched in a clean environment of hatcheries, free of any contact with adult birds which would otherwise act as natural donors of chicken-specific gut microbiota. This fact represents real threads if performing experiments with chicks from hatcheries and ignoring all consequences. On the other hand, this fact, together with a number of chicks hatched worldwide daily, represents a specific opportunity and makes chickens as fantastic model for studies of host – gut microbiota interactions. It is impossible to find another model in which offspring are separated from their parents and are available for any type of experimental inoculation. But if ignored, many mistaken conclusions can be drawn since chicks from hatcheries do not represent a control group. Instead, due to the absence of contact with parents, these chicks represent a highly experimental group that cannot be considered as reference, if real biological processes are to be studied.

One of the mistaken conclusions is dogma on age-dependent development of chicken gut microbiota, sometimes reported to require weeks, sometimes months, and stating necessity for anaerobisation of gut environment by facultative anaerobes to enable its colonisation by strict anaerobes. This is completely wrong conclusion caused by non-critical handling with chicks from hatcheries, without contact with their parents. If newly hatched chicks were orally colonised by faecal material from adult birds, or were even kept in the same environment with adult birds, correct conclusion would be obtained and this is that newly hatched chicks can be colonised by adult type of microbiota from the very first moments of life and gut colonisation is accomplished within 48 hours of their life, where this time represents only a time needed for plain multiplication of anaerobic bacteria from tens of cells to 10EXP10 CFU/g of digesta. This is possible also due to the fact that newly hatched chicks forage on nearly the same feed formula as adult hens. This does not argue against subsequent modification of gut microbiota composition by feed formula or delayed appearance of some microbiota members that are slowly growing, *e.g. Bacteroides gallinaceum*.

Once correctly understood, chickens indeed offer an extra space for experiments that are nearly impossible to set up with other animal models. One can colonise newly hatched chicks with pure cultures of individual gut microbiota members and check for their ability to colonise. Experiments of this type show that not all chicken gut microbiota members permanently colonise after a single dose administration. Bacterial species capable of prolonged survival under aerobic conditions, *i.e.* aerotolerant bacteria like Lactobacilli, facultative anaerobes or all spore-forming bacteria poorly colonise intestinal tract after a single dose administration. Their presence in intestinal tract represents an equilibrium between their continuous income from environment, their ability to multiply anaerobically and gut peristalsis. If provided experimentally only once, these bacteria quickly, in a few days, disappear from the gut. On the other hand, strict anaerobes without any form of survival in aerobic environment efficiently colonise chicken intestinal tract after a single dose administration. Why it is so is not known but this is a clear consequence of natural selection since if poorly surviving outside the host and also poorly colonising, such bacteria would be outcompeted by the others and lost in evolution. These bacteria include nearly all Bacteroidetes (*e.g.* genera *Bacteroides*, *Parabacteroides*, *Barnesiella*, *Alistipes* etc), but also class Negativicutes from phylum Firmicutes (genera *Megamonas*, *Megasphaera*, *Phascolarctobacterium* or *Veillonella*) or strictly anaerobic Proteobacteria such as *Succinatimonas*, *Sutterella* or *Parasutterella*.

Chickens also posses highly developed mucosal microbiota in their caeca. Mistaken conclusions are obtained if mucosal microbiota is studied in broilers from commercial production for reasons mentioned above. However, if caeca from adult hens are analysed, genera *Helicobacter*, *Mucispirillum*, *Desulfovibrio*, *Anaerobiospirillum*, *Brachyspira* and a few other Spirochaeta which are commonly reported as minority chicken gut microbiota members become a majority if caecal mucus is collected.

Available genetic lines, two extreme lines represented by egg layers and broilers, and cost of newly hatched chicks has no competitors among other animal species. Moreover, if the main focus is given to gut microbiota, nearly any experiment can lead to practical outputs in a form new types of probiotics. All these small pieces of information collectively make chickens an exciting and accessible model for host-microbiota interactions.

Impact of acute heat stress and body weight difference on *Cecal Microbiota* and survival in broilers

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Keywords: heat stress, microbiota, body weight

This study tested the effects of acute extreme heat stress (EHS) on the cecal bacterial community in broilers relative to body weight (BW). Ninety 36-day-old birds were grouped by BW into low (L) (2373.9 ± 32.1 g), medium (M) (2681.1 ± 11.2 g), and high (H) (3009.5 ± 36.0 g) BW, and subsequently exposed either to EHS (35°C, 8h) or kept under thermoneutral conditions (CON) (21°C, 8h). At the end, six birds per treatment were slaughtered their cecal microbiota was subjected to 16s metataxonomic sequencing analysis. EHS increased evenness indices in EHS-L group compared with CON-L. EHS-L had also significantly higher evenness than EHS-H. Conversely, beta diversity analyses revealed no significant impacts of EHS or BW. Bacterial communities were dominated by phyla *Bacillota* and *Bacteroidota*, with *Bacteroides fragilis*, *Blautia hominis*, and *Enterococcus cecorum* as the most abundant species. More microbial taxa were enriched in EHS compared with CON groups. Identified biomarkers included twelve for EHS-L, five for EHS-M, and three for EHS-H, with *Mediterraneibacter glycyrrhizinilyticus*, *Pseudoflavonifractor capillosus*, and *Clostridium phoceensis* being most significant for each group, respectively. Relative abundance of *Erysipelotrichia, Erysipelotrichales*, and *Erysipelotrichaceae* exhibited a linear decrease with higher BW changes during the trial. Microbial co-occurrence networks were resilient to acute EHS, with no significant structural differences between CON and EHS groups. Overall, these findings suggest minimal impact of short-term acute EHS on the cecal microbiota. The greater EHS resistance observed in lighter birds may be associated with rapid changes in microbial evenness during exposure. *Erysipelotrichaceae* could potentially be a microbial indicator of HS resistance in broilers.

Microbiome programming before hatch: *In Ovo* delivery of XOS and MOS in broiler chickens

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Keywords: prebiotic, gut, microbiota

This study explores how in ovo administration of oligosaccharides affects broiler chicken gut microbiota. 360 Ross 308 eggs were divided into 3 groups: one received 0.2 ml saline (control), the second 1.2 mg xylotetrose (XOS4), and the third 1.2 mg mannotriose (MOS3) on the 12th day of incubation. Post-hatching, birds were raised for 42 days, after which cecal contents were collected for DNA analysis using a 16S rRNA barcoding kit (SQK-16S114.24, Oxford Nanopore Technologies).

Data processing involved Dorado (v0.9.1), Cutadapt (v5.0), and Nanofilt (v2.8.0) for demultiplexing, trimming, and quality filtering. Alpha diversity differences among groups were assessed using the Kruskal-Wallis test with post-hoc pairwise Wilcoxon testing. Microbial community shifts were analysed via Bray-Curtis dissimilarity matrices and visualized with Principal Coordinate Analysis (PCoA). Linear discriminant analysis (LDA) effect size (LEfSe) identified significant microbial changes (LDA threshold ≥ 2.0).

Significant variations in gut microbiota composition and diversity were observed across the groups. The MOS3 group showed the highest alpha diversity followed by XOS4 and the control. Beta diversity showed significant difference in microbiota composition among groups. LDA analysis identified differentially abundant taxa between groups. *Ligilactobacillus* was enriched in the control group, *Blautia* and *Faecalibacterium* were more abundant in the MOS3 group, while *Helicobacter* was enriched in the XOS4 group. The study demonstrates that in ovo modulation with XOS4 or MOS3 impacts early gut microbiome development, potentially affecting host physiology.

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Towards genetic selection against chicken coccidiosis: a genetic-epidemiological approach

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Keywords: *Coccidiosis*, genetic-epidemiological modelling, host genetic resistance

Coccidiosis, caused by Eimeria parasites, remains a major economic challenge for the poultry industry. As resistance to anti-parasitic drugs increases and vaccines prove costly, genetic selection for disease resilience offers a promising alternative. Genetic-epidemiological prediction models are crucial as it considers both direct effects on individual performance and indirect effects on parasite transmission—aspects not captured by classical genetic models. This integrated perspective is essential for developing effective genetic improvement programs against coccidiosis.

In this study, we developed an epidemiological model of coccidiosis in chickens to evaluate the relative impact of five key host response phenotypes to infection: susceptibility, infectivity, recoverability, tolerance, and compensatory growth. Parameters were estimated using published experimental data from controlled infection studies involving Eimeria acervulina. We implemented an individual-based model that captures both the epidemiological dynamics and growth impacts of infection.

Our findings suggest that recoverability may be a particularly valuable target for genetic improvement in poultry, potentially offering great population-level benefits. Our model framework can guide breeding strategies by identifying the traits that most effectively improve flock-level resilience to coccidiosis, accounting for both direct and indirect effects. This approach represents an important step toward developing more effective genetic selection programs for coccidiosis resistance in poultry, potentially reducing reliance on antimicrobials and improving production efficiency in commercial flocks.

Combined effect of genetics & microbiota on vaccine responses in laying hens

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Keywords: microbiota, vaccine response, heritability

Understanding the combined impact of host genetics and microbiota and their interaction on vaccine responses is essential for improving poultry health. This study aimed to investigate the role of host genetics in shaping gut microbiota composition and vaccine responses to vaccination in White Leghorn laying hens.

To assess the genetic basis of microbiota and immune traits, 552 hens from the same line were raised over 22 weeks and genotyped using a 57k SNP chip for heritability estimation and genome-wide association studies (GWAS). Humoral and cellular immune responses to vaccines against Newcastle disease virus, infectious bronchitis virus, avian encephalomyelitis virus, and avian pneumovirus were measured at multiple time points. In parallel, caecal microbiota was characterized at the end of the experiment using 16S rRNA gene sequencing.

Heritability estimates for vaccine response traits reached up to 0.39, and GWAS identified quantitative trait loci (QTL) on several chromosomes with candidate genes involved in immune regulation indicating a vaccine-specific genetic contribution to vaccine response variability.

Heritability estimates for microbiota diversity indices (0.20–0.25) and phylum-level relative abundances (0.01–0.08) suggest modest genetic influence. Preliminary analysis identified a QTL on chromosome 4 linked to Campylobacterota relative abundance. Ongoing work includes heritability and GWAS analyses at lower taxonomic ranks.

These results highlight the genetic basis of microbiota composition and vaccine response, supporting integration of host genomics and microbiome data into breeding strategies. Follow-up studies will explore microbiota's direct role in vaccine response to better understand microbiota-genetics interactions on vaccine responses.

Examining the genetic relationship between beak shape traits, egg production, and egg quality in a White Leghorn pure line population

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Keywords: severe feather pecking, geometric morphometrics, welfare

It has been suggested that selection for blunter beak phenotypes may help prevent feather pecking damage to benefit hen welfare. However, this may have consequences for production traits. Previous work in pure line hens suggests that certain beak shape traits (e.g., curvature) may negatively impact egg production, but the reason for this relationship is unclear. This study examined the influence of beak shape and size on production traits. The maxillary and mandibular beak shapes of 2973 White Leghorn pure line hens and 203 roosters were analysed using geometric morphometrics. Beak overhang length (BOL; difference between maxillary and mandibular beaks) was also measured. Heritability and genetic correlations were estimated using ASReml (hens only). Most beak shape variation was attributable to length, curvature, and depth. Surprisingly, sexual dimorphism in the beak shape traits was not apparent; however, the sexes were separated by beak size, with males having larger beaks. Heritability for hen beak shape and size traits ranged from 0.17-0.48. Maxillary beak curvature negatively correlated to egg weight (EW), maxillary beak size, and mandibular beak curvature. BOL positively correlated to maxillary beak size, mandibular beak size, and body weight (BW), but negatively correlated to maxillary beak length and EW. Maxillary and mandibular beak size were highly positively correlated. Maxillary and mandibular beak size positively correlated with EW and BW. The results of this study suggest that genetic selection of naturally blunter beaks is feasible without negatively impacting egg production or quality. However, considering previous work, the effect of beak shape traits on production in pure lines is inconsistent and may become insignificant in commercial crossed lines.

Targeted long-read sequencing of the *EDNRB2* gene in local chickens using nanopore technology

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Keywords: nanopore sequencing, long-range PCR, SNP, structural variant detection, local chicken genetic diversity, melanocyte-associated gene

In this study, we applied nanopore sequencing using the MinION platform to analyze the full-length endothelin receptor type B2 (*EDNRB2*) gene in domestic chickens (*Gallus gallus domesticus*). The target region was amplified via long-range PCR, yielding amplicons ranging from 11,910 to 12,094 base pairs, fully covering the *EDNRB2* gene. Sequencing was performed on individuals representing local traditional chicken populations. Individuals were selected to represent a range of feather pigmentation phenotypes, particularly with respect to the presence of white to the plumage. *EDNRB2* was selected as a target gene due to its key role in melanocyte development and neural crest-derived processes. Understanding its variation may help clarify receptor function in vertebrates.

Across sequencing runs, we obtained between 118 and 2,200 reads per individual (n = 13), with an average of approximately 615 reads per sample and a median of 305. High read coverage enabled reliable variant detection and haplotype phasing. The resulting assemblies revealed both single nucleotide polymorphisms (SNPs) and structural variants within and between individuals. One of the key advantages of using long-read sequencing in this context is the ability to resolve full-length haplotypes, allowing for precise phasing of variants across entire gene loci. This approach demonstrates the utility of nanopore-based long-read sequencing for capturing allelic diversity and structural variation in functionally relevant candidate genes, enabling the genetic characterization of endangered local chickens and supporting their conservation.

Pedigree recording and parental contribution in cage-free breeding of Pekin and Muscovy ducks

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Keywords: duck, cage-free system, parentage assignment

Currently, individual cages are used in Pekin and Muscovy duck pure lines to ensure accurate pedigree recording and balanced parental contributions to progeny. To address potential restrictions on cage use in breeding programs, this study pursued two objectives: develop molecular tools for parentage assignment, and evaluate parental contributions in cage-free systems.

Four panels of 96 SNPs were designed (one per species for each breeding company). Ducks were bred in cage-free systems varying sex-ratios and densities, with 3 replicates for each condition. Densities compared were 12 or 18 females for Muscovy ducks and 15 or 20 females for Pekin ducks, while sex ratios tested were 1:3 and 1:3.6 for Muscovy ducks, and 1:5 and 1:6.6 for Pekin ducks. Genotyping of 528 parents and 1,775 offspring was conducted using SNP panels, and parentage was determined via exclusion. Pedigrees were used to measure parental contribution.

The SNP panels reached a 97% assignment rate when all parents were correctly genotyped. Assignment rates dropped to 81% and 83% when some parents were excluded due to poor genotype quality. Density had no effect on contribution of parents to progeny. In Muscovy ducks, one male failed to contribute to progeny in all replicates at a 1:3.6 sex ratio, while all males could potentially sire offspring at a 1:3 ratio. In Pekin ducks, at a 1:6.6 ratio, two of three males sired over 85% of ducklings in all replicates, whereas at a 1:5 ratio, all four males contributed 20%–35% of progeny in two of three replicates.

In conclusion, parentage assignment is feasible for both duck species in cage-free systems. Lower sex ratios may promote more balanced sire contributions. Further research should explore the impact of free-mating on genetic diversity and genetic gain.

Genetic diversity of Italian local chicken breeds: a worldwide comparative analysis

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Keywords: SNP, conservation, poultry, genomic

Domesticated approximately 3,500 years ago, chickens play a fundamental role in global agriculture, resulting in the development of hundreds of distinct breeds. In Europe, intensive selection has shaped highly specialized commercial lines, often at the expense of local breeds. Advances in genotyping and bioinformatics have enabled comprehensive genetic analyses. This study provides an in-depth assessment of the genetic diversity of Italian chicken breeds in a global context, highlighting the need to safeguard local genetic resources. A total of 192 chicken breeds genotyped from multiple countries were analyzed, with a strong representation of Italian breeds. Genetic clustering showed that Italian chickens grouped with several European, African, and Asian breeds. Admixture analysis identified 25 genetically distinct populations, revealing close genetic affinities between certain Italian breeds and breeds from Germany, France, and Switzerland. Genetic diversity was the highest in African and some Asian and European breeds, while Italian chickens exhibited moderate variability. Italian chicken breeds had strong genetic connections with European, Asian, and African populations, reflecting historical trade routes and breeding exchanges. Southern Italian breeds formed a distinct genetic cluster, underscoring regional uniqueness. These findings reinforce the importance of conservation strategies to preserve genetic diversity while ensuring the long-term resilience of Italian poultry biodiversity in response to environmental and agricultural challenges.

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Monitoring the inbreeding coefficient and egg production in conserved chicken breeds

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Keywords: inbreeding coefficient, pedigree, laying performance

Maintaining genetic diversity is crucial for conservation, to provide essential resources for livestock improvement. The inbreeding coefficient (F) is a key indicator, estimated from pedigree data. However, poor management or changes in mating schemes can lead to data loss, making F estimation biased or impossible. Local chicken breeds face extinction due to lower production efficiency than commercial breeds. While conservation is essential, small populations risk inbreeding depression and genetic diversity loss. This study has two parts. Part 1 analyzed six conserved breeds: Hua-Tung, Hsin-Yi, Ju-Chi, Quemoy, Nagoya, and Shek-Ki. A regression imputation method estimated missing parental data using other generations. The simulated F value underestimated the real value by only 0.16% on average. This method was then used to calculate cumulative F values from the base population. The highest F value was in Hsin-Yi (56.7%), followed by Ju-Chi (52.0%), Quemoy (37.0%), Shek-Ki (36.7%), Hua-Tung (36.0%), and Nagoya (26.3%). Part 2 examined pedigree and egg production data from Generation 13 to 23, comparing F and estimated breeding values (EBV) with L2, a strain selected for egg production. Quemoy had the earliest age at first egg and the highest total egg number among conserved breeds. Strain L2 showed a longer clutch length but not shorter pauses than conserved breeds. For genetic analysis, L2 showed substantial improvement, while among conserved breeds, all except Quemoy and Nagoya exhibited a positive trend. Assessing changes in EBV per 10% F, a total egg number showed overall improvement. In conclusion, no inbreeding depression was detected, suggesting natural selection may have indirectly enhanced egg production traits.

Keel bone health in low-performing chicken genotypes and a high-performing hybrid layer

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Keywords: keel bone damage, laying hens, animal welfare

Keel bone damage is a widespread welfare issue in laying hens. Investigations of keel bone health in low-performing chicken genotypes are rare and often lack a systematic approach. Thus, our study aimed at systematically investigating and comparing keel bone health and development in low-performing genotypes (Red Jungle Fowl and Sumatra) and hybrid layers (Lohmann Selected Leghorn (LSL)) during rearing and laying period.

The experimental animals were kept in small groups of 11 to 20 hens accompanied by at least one rooster. For the examination of the keel bone, laterolateral X-ray images were taken at five time points: 16, 25, 33, 50–52, and 70–72 weeks of age (woa). The images were evaluated for fractures, percentage of deviated keel bone area (POD), radiographic density, and ossification of the keel bone. Laying activity was monitored at flock level.

Keel bone fractures were only detected in LSL hens. Deviations were present in all three genotypes from 25 woa onwards. The overall POD was low, but significantly higher in Red Jungle Fowl than in Sumatra ($p<0.05$) with LSL in between. At 16 woa, radiographic density of the keel bone was significantly lower in LSL compared to Sumatra hens ($p<0.05$) with Red Jungle Fowl in between. Keel bone ossification was completed significantly later in Sumatra than in the other two genotypes ($p<0.05$). The age at first egg differed significantly between LSL (18th woa), Sumatra (31th woa) and Red Jungle Fowl (24th woa).

Our study gives a deeper insight into the bone health of low-performing chicken genotypes in comparison with a high-performing hybrid. The results suggest that besides laying performance, age at full ossification of the keel bone in relation to onset of lay may influence a genotype's susceptibility to fractures.

Improving sustainability in broiler production through selection for water efficiency

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Keywords: broiler, water conversion ratio, selection

As global temperatures rise, and access to reliable sources of freshwater dwindle, finding ways to improve water usage in agricultural production is imperative. When it comes to broiler selection, water efficiency related traits have often been underutilized in selection indices due to a lack of knowledge on how selection for those traits may impact other economically important traits such as body weight of feed conversion ratio (FCR). In 2019, a divergent selection program was implemented at the University of Arkansas from a randombred population (MRB). Through a two-phase approach, focusing on both family (0-4 weeks) and individual (4-6 weeks) water conversion ratio (WCR=water intake/body weight gain), the low- (LWCR) and high- (HWCR) water conversion ratio lines were established. The goals of the divergent selection program were to 1. divergently select broiler lines for WCR, and 2. determine the response to selection. The LWCR and HWCR lines have been divergently selected for 6 generations with the LWCR proving to be an established model for improved water efficiency in broilers. Water intake for the LWCR during a 4-week test period was 3572.5g, nearly 475g of water less than the MRB line. The LWCR also exhibited a 21-point improvement in WCR (2.68) compared to the MRB line (2.89) while the HWCR had a WCR of 3.63, 74 points worse. Promisingly, body weight gain, feed intake, and FCR have not been negatively impacted by selection for WCR with the LWCR showing comparative values to the MRB line. After 6 generations, selection for improved WCR in broilers shows potential to decrease freshwater usage and improve sustainability in the broiler industry.

Mathematical modeling of eggshell thickness in the populations of laying hens under a selection

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Keywords: eggshell quality, genetic improvement program, longitudinal data

Eggshell quality is an important trait from an economic point of view. This trait shows both genetic and environmental fluctuations. The aim of the study was to evaluate the variability of eggshell thickness (ET) over time in the context of the implemented genetic improvement program of laying hens. The study included 1130 laying hens of two strains (Barried Rock – P55) and Sussex – S55) in 2022-2024 years. ET was measured in two periods: January-February and May. Statistical analysis included ET measurements, which recorded in each period: 5-6 days/bird for P55, while for S55 strain 5-7 days/bird. The functional data analysis (FDA) approach was applied, where observations over time are treated as realizations of some smooth functions. FDA allows for comparing the changes in ET over time. In this method, a continuous function is assigned to each treatment, where the B-spline base approach was used. This allows for modeling changes in the observed trait occurring over time through functions approximated between individual interpolation nodes, and not, as in the classical approach, through interpolation with one curve over the entire range of data variability. The significance of differences between the curves for the winter and spring periods was determined using functional analysis of variance. For both strains, the differences in the shapes of the curves between the winter and spring periods in 2023 and 2024 turned out to be statistically significant (measurements of started in 2022). Differences in the trajectory of averaged curves were observed both between strains and years (generations). In conclusion, applied method seems to be useful for modeling of ET.

Modulation of cecal microbiota dynamics in broiler chickens via in ovo administration of postbiotic and prebiotic

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Keywords: in ovo technology, galactooligosaccharides, sodium butyrate, microbiome

The gut microbiota is a key factor influencing poultry growth, immunity, and overall performance. Its development is shaped by both environmental factors and host genetics. Early-life microbial modulation may interact with genetic potential, affecting phenotypic traits relevant to breeding programs. This study examined the effects of embryonic stimulation with galactooligosaccharides (GOS) and sodium butyrate (SB) on gut microbiota composition in ROSS 308 broilers. In ovo injections were administered into the egg air chamber on day 12 of incubation. ROSS 308 eggs were divided into the following groups: non-injected control (C), saline-injected control (CI), prebiotic (GOS), and postbiotic (SB). Post-hatching, birds were raised for 42 days, after which cecal contents were collected for DNA analysis using a 16S rRNA barcoding kit (Oxford Nanopore Technologies). Data processing involved Dorado (v0.9.1), Cutadapt (v5.0), and Nanofilt (v2.8.0) for demultiplexing, trimming, and quality filtering. Alpha diversity differences among experimental groups were assessed using the Kruskal-Wallis test with post-hoc pairwise Wilcoxon testing. Microbial community shifts were evaluated using Bray-Curtis dissimilarity matrices and visualized through Principal Coordinate Analysis (PCoA). Significant microbial differences were identified using LEfSe (LDA score ≥ 2.0) and PERMANOVA. The results revealed significant variations in gut microbiota composition and diversity among the groups. LDA analysis identified differentially abundant taxa, with Lactobacillus enriched in the C group, Merdicola in the CI group, Sporobacter and Barnesiella in the GOS group, and Acutalibacteraceae and Clostridia in the SB group. These results indicate that targeted in ovo modulation shapes early gut microbial communities, which may influence expression of genetically determined traits such as feed conversion efficiency and disease resistance. The approach could complement genetic selection strategies to enhance productivity and resilience in commercial poultry lines.

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