

# WIAS

## Annual Conference

# 2025

## **Unravelling the genetic and epigenetic bases of lipid related trait variability in laying hens aged 90 weeks**

Alexandre HUBERT<sup>1,3\*</sup>, Laëtizia LAGOUTTE<sup>1</sup>, Bénédicte LEBEZ<sup>1</sup>, Marta GÒDIA<sup>3</sup>, Ole MADSEN<sup>3</sup>, Mathieu EMILY<sup>2</sup>, Sophie ALLAIS<sup>1</sup>, Sandrine LAGARRIGUE<sup>1</sup>

<sup>1</sup> PEGASE, INRAE, Institut Agro, 35590 Saint-Gilles, France

<sup>2</sup> Institut Agro, CNRS, - Université de Rennes, IRMAR -UMR6625, Rennes, France

<sup>3</sup> Animal Breeding and Genomics, Wageningen University & Research, Wageningen, The Netherlands

\* Corresponding author. E-mail: [alexandre.hubert@institut-agro.fr](mailto:alexandre.hubert@institut-agro.fr)

The present project is being conducted to elucidate the genetic and epigenetic bases of lipid related trait variability in laying hens aged 90 weeks, aligning with the objectives of the European project GERO NIMO in the context of productive life extension of laying hens from 60-70 weeks to over 90 weeks. Such a productive longevity increase enables a reduction of hens required for production while addressing societal, economic, and environmental challenges.

The liver has been chosen as the study subject due to its central role in energy metabolism, particularly lipid metabolism, which is crucial for maintaining production longevity and coping with unpredictable events, which are more frequent in long-lived animals such as viral infections, or heat stress that lead to a reduction in feed intake, or feed shortages.

The genetic bases of variations in the liver transcriptome and methylome are being investigated, as well as their impact on phenotypic variations associated with this organ. Various hepatic omics data, including SNPs from the genome, the epigenome (methylome), and the transcriptome, are being analyzed in relation to phenotypes of interest (egg and body reserves, laying rate ...)

The first objectives are the identification of differential methylated regions between 70 and 90 weeks of age, followed by the identification by GWAS of genomic regions responsible for methylation variations. Secondly, potential co-locations between meQTL, QTL, and eQTL will be investigated, and EWAS analyses will be performed to identify CpG sites that may explain a part of the variability of a trait.