Research Institute for Farm Animal Biology

Transcriptional and metabolic responses in chickens infected with mixed parasite species

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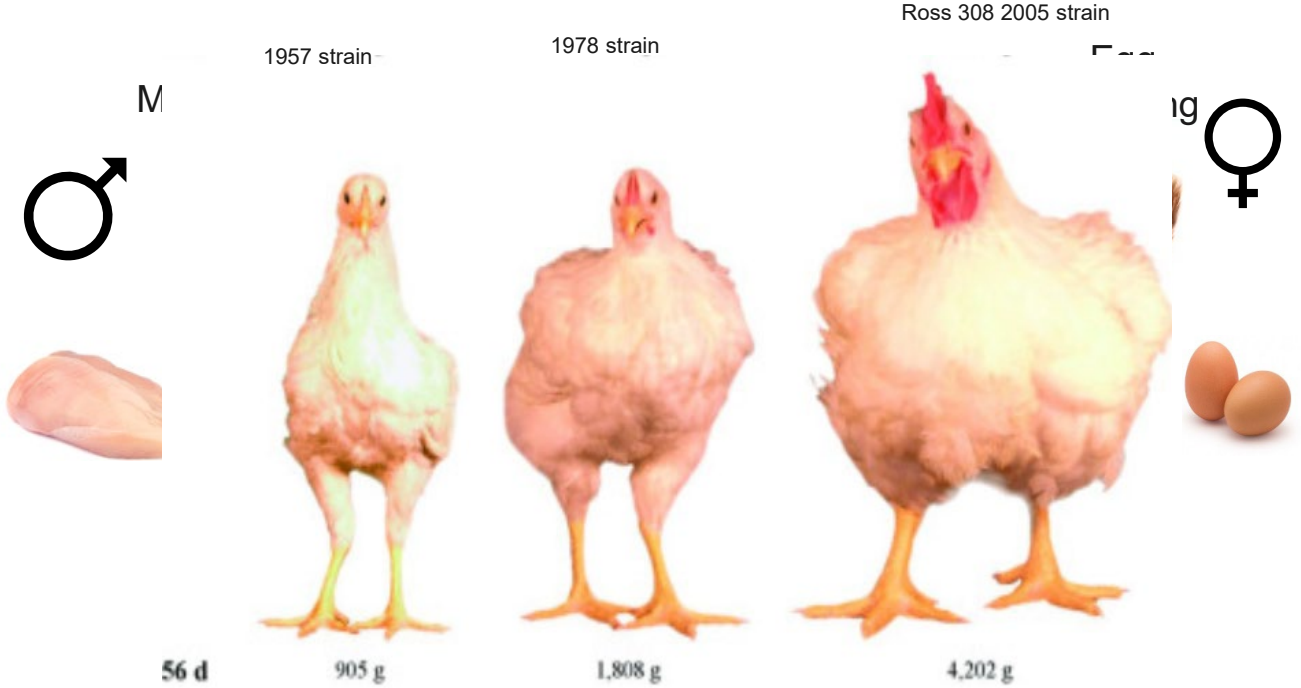
The 75th EAAP Annual Meeting
Florence -Italy

03.09.2024

Background

- Decades of genetic selection has substantially improved chicken productivity[1]

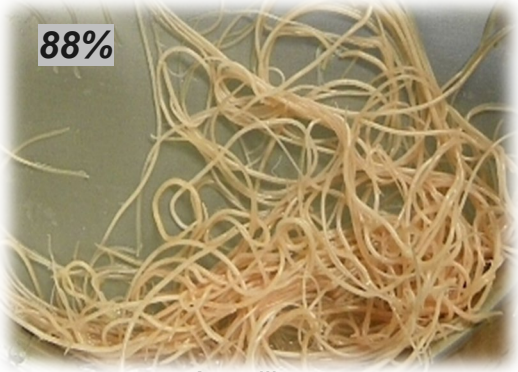


This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 955374.

(1) Zuidhof et al., 2014, *Poultry Science*

Background

- *Ascaridia galli* and *Heterakis gallinarum* impair chicken productivity[1]



A. galli

H. gallinarum

MSD Vet Manual

- They cause pathogenic effects associated with
  - Damage to intestinal tissue[2]
  - Reduced nutrient absorption and utilization[3]
  - Impaired growth and laying performance[4]

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Optimal gut function in monogastric livestock

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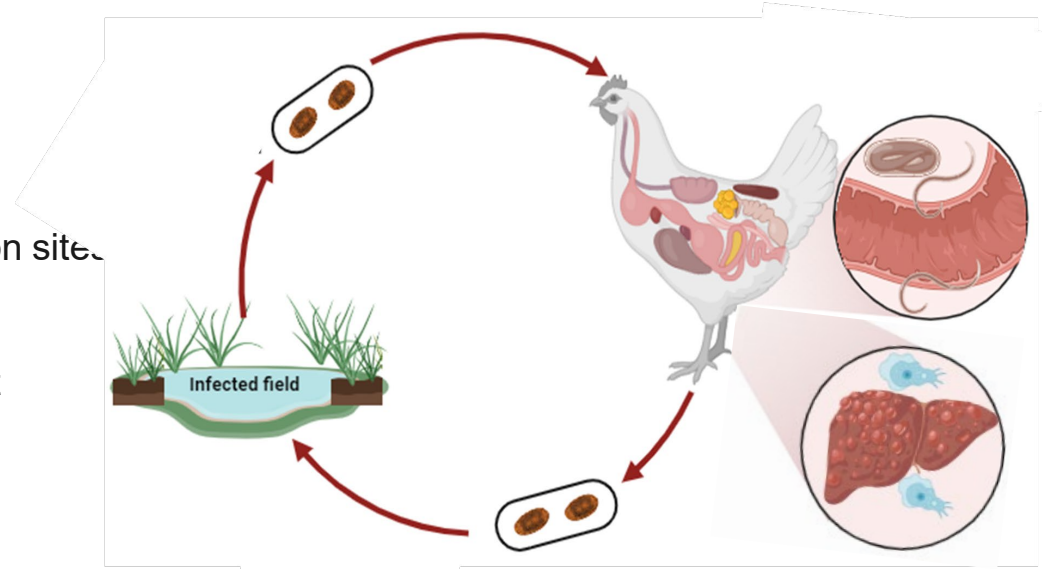
[1]Kaufmman et al., 2011, Livestock Science
[2]Dahl et al., 2002, Veterinary Microbiology
[3]Daş et al., 2011, Veterinary Parasitology
[4]Stehr et al., 2019, Veterinary Parasitology

Background

- Life cycle is direct
- Chickens ingest embryonated eggs from contaminated environment
- Ascarids grow and reproduce in predilection site
- Eggs are released into the environment
- Pasture, water, feed from poultry areas get contaminated with eggs



Eggs of *H. gallinarum* harbour histomonads

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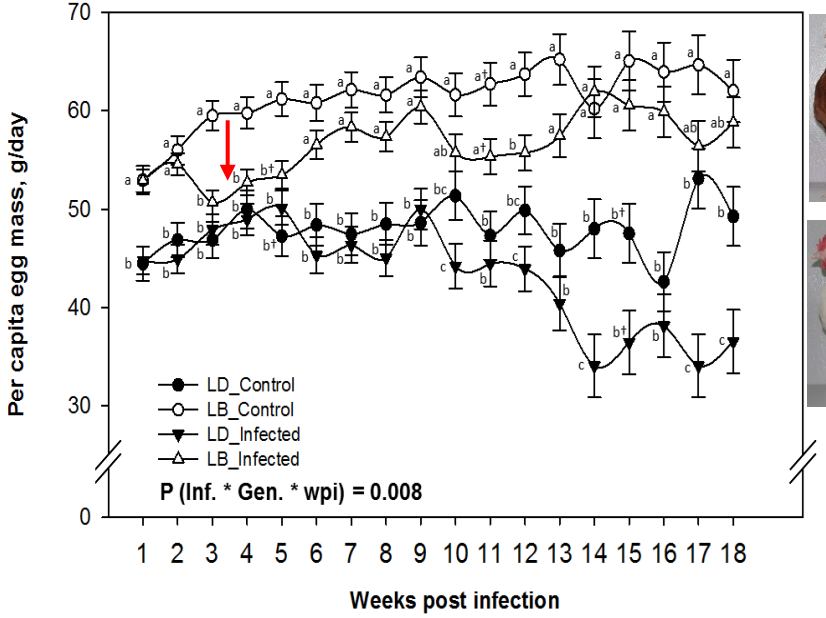
Background

- *Histomonas meleagridis c*auses liver and caeca damage and trigger patho-physiological responses[1]
- A robust immune response is required to tackle nematode infections[2]
- Infection particularly penalizes high performing genotypes[2]



Lohmann Brown (LB)

Lohmann Dual (LD)

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(1) Shifaw et al., 2021, *Poultry Science*
(2) Stehr et al., 2019, *Veterinary Parasitology*

Hypotheses

- Parasite infections can alter the chicken metabolome
- The liver switches from metabolism to immune-related functions in parasite infected chickens
- The extent of the impacts of parasites depends on the performance level of genotypes

Objectives

- To investigate the metabolomic alterations in plasma associated with worm development **(Exp -1)**
- To assess the hepatic pathways activated due to mixed parasite infections in three chicken genotypes with distinct growth rates **(Exp -2)**

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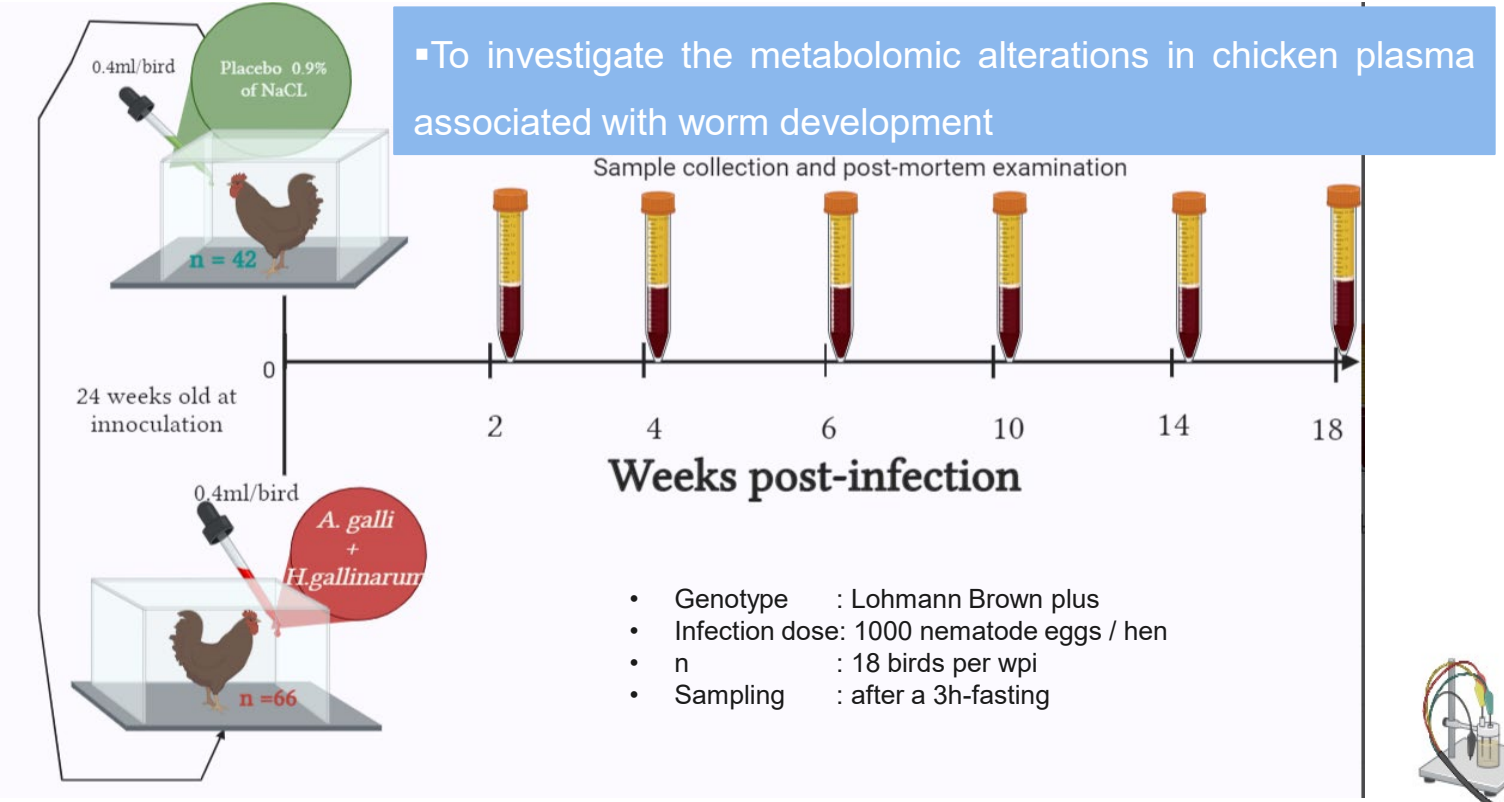
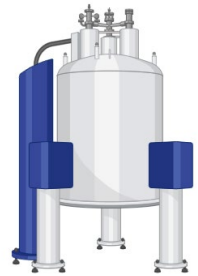
Experimental design - Objective 1 (laying hens)



- To investigate the metabolomic alterations in chicken plasma associated with worm development

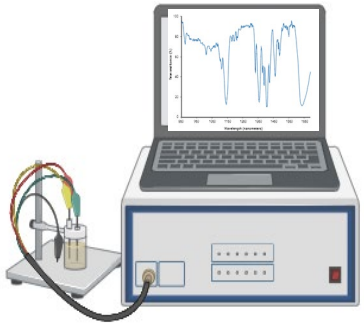
- Genotype : Lohmann Brown plus
- Infection dose: 1000 nematode eggs / hen
- n : 18 birds per wpi
- Sampling : after a 3h-fasting



NMR Spectroscopy

+

Bioinformatics



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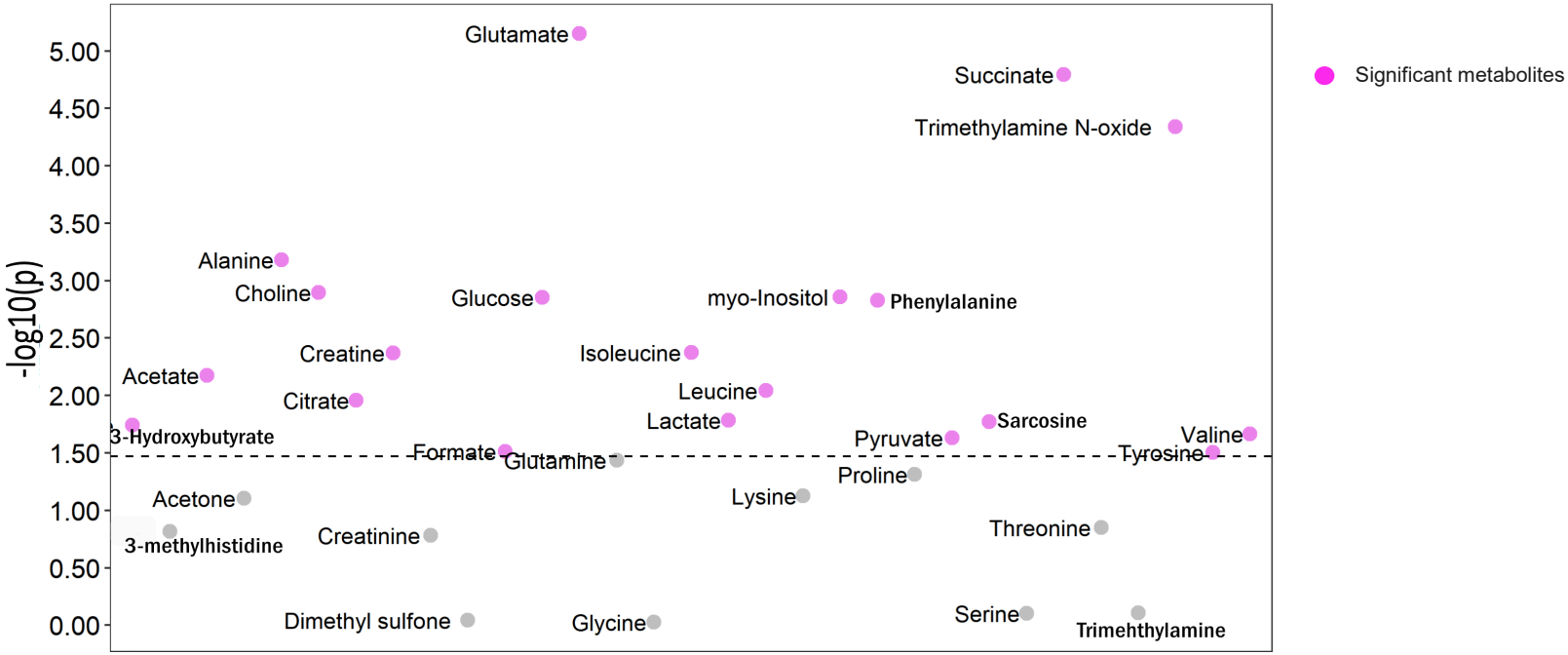
Parasite-induced alterations in plasma metabolites of laying hens

- Twenty plasma metabolites were significantly different between infected and non-infected hens



Oladosu et al., 2023 *Gut Pathogens*

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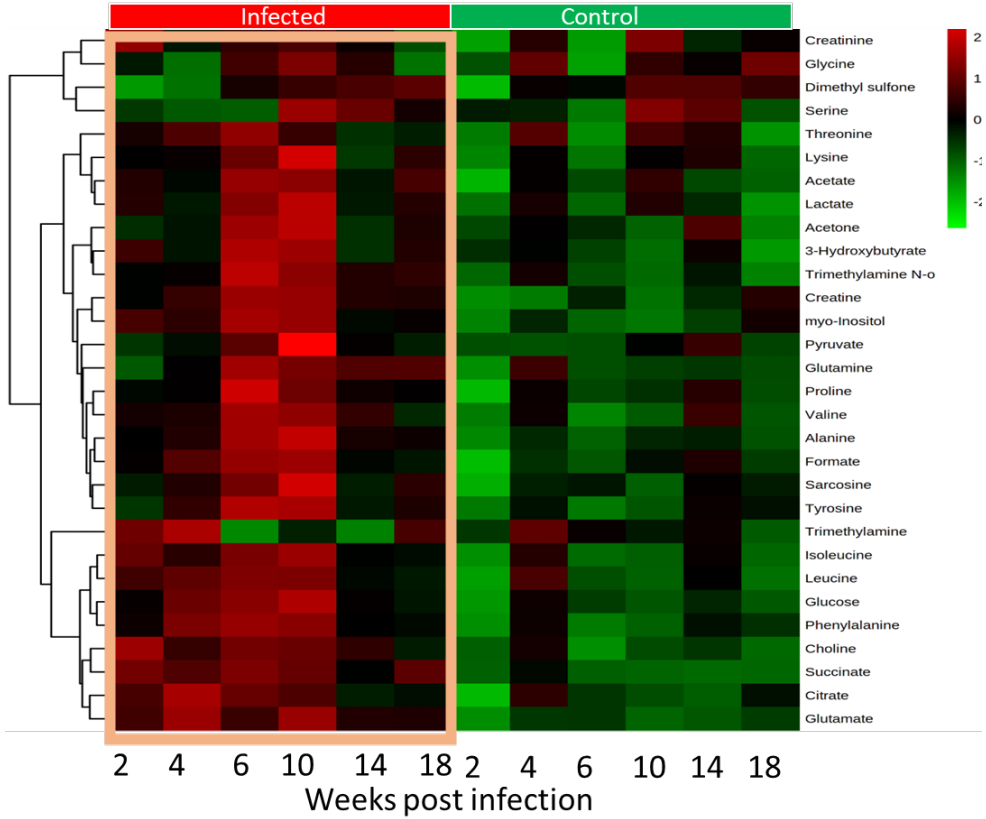
Plasma metabolites in layers at different time of infection



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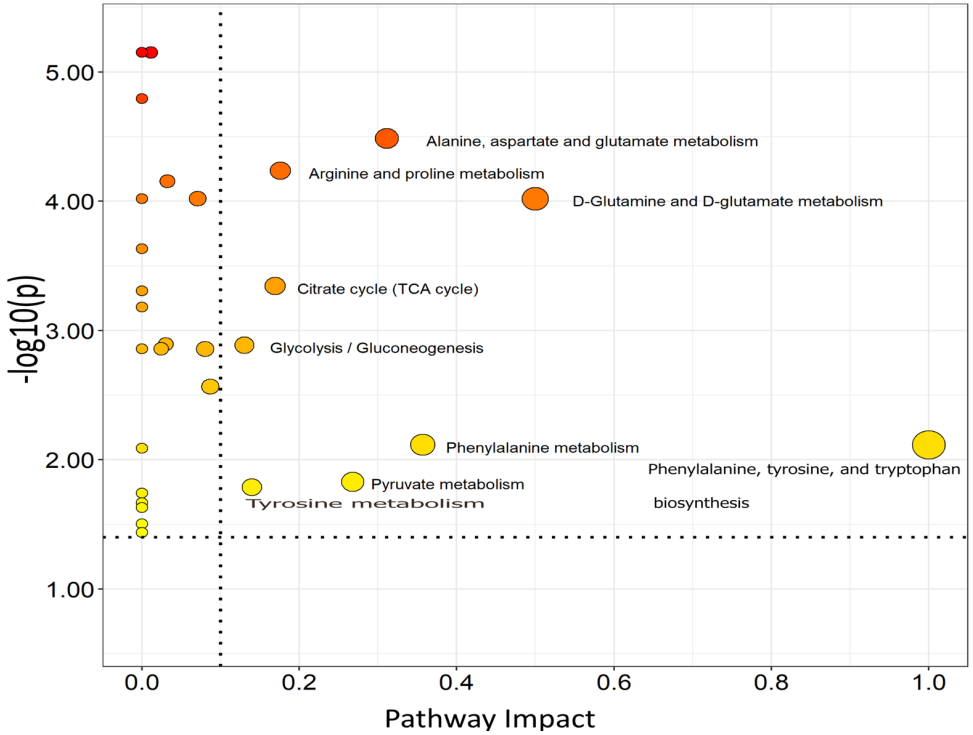
Infection-induced upregulation of metabolic pathways in layers



Oladosu et al., 2023 *Gut Pathogens*

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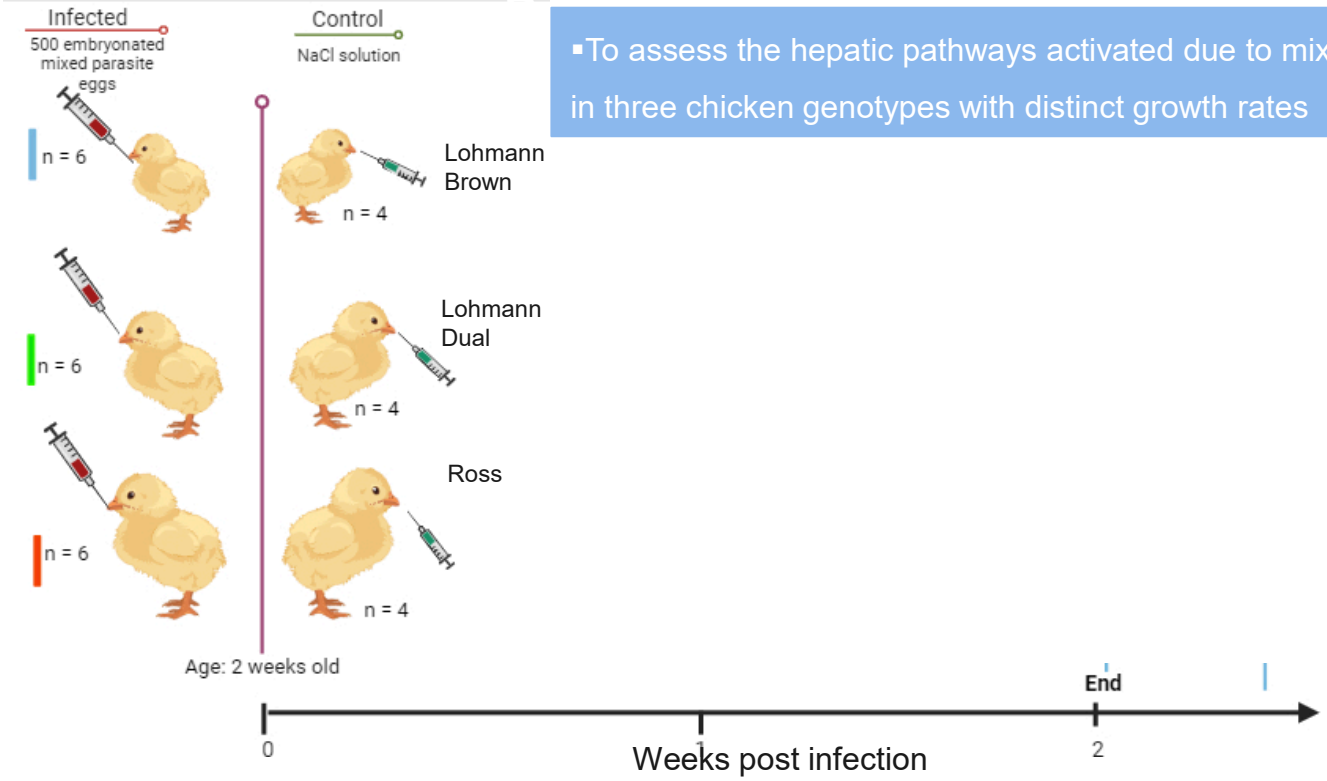
Experimental design – Objective 2 (male birds)



- To assess the hepatic pathways activated due to mixed parasite infections in three chicken genotypes with distinct growth rates

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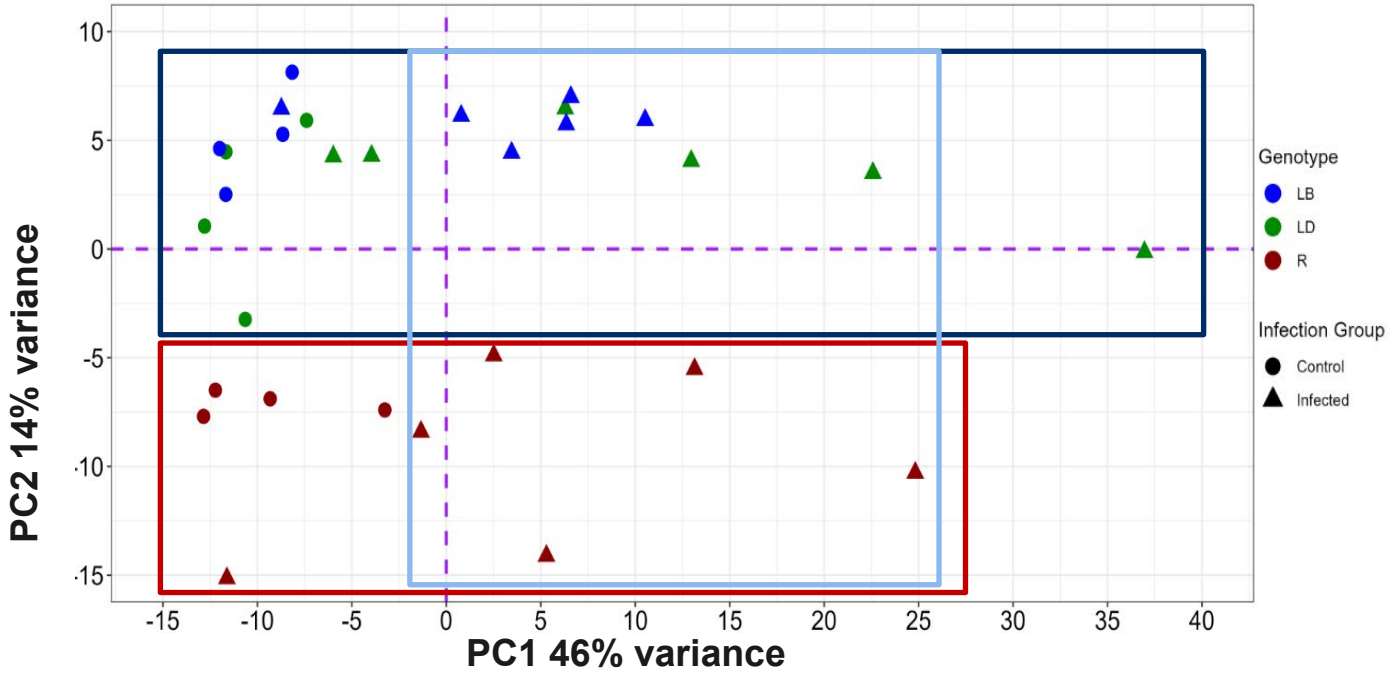
Infection influenced the expression of hepatic genes in male birds

- Both genotypes and infection have effects on the liver transcriptome
- 1927 genes were significantly differentially expressed due to infection



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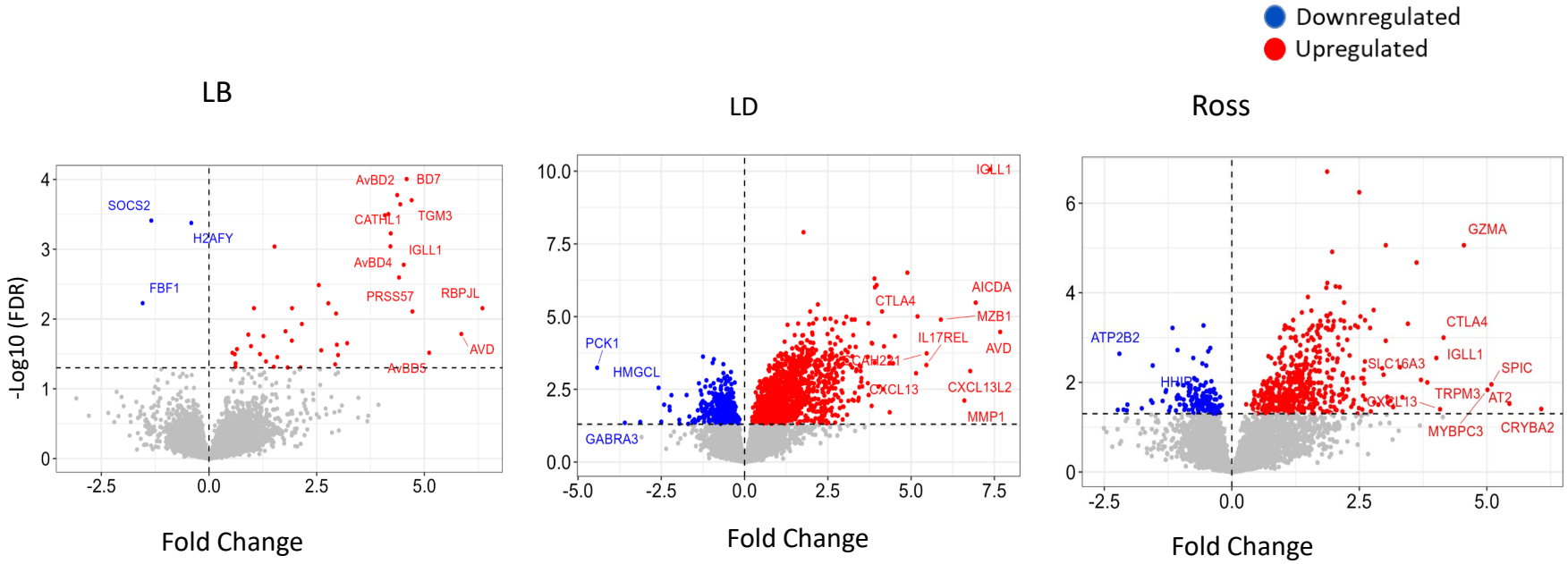
Differentially expressed genes across genotypes



- More upregulated genes than downregulated genes across all genotypes due to infection

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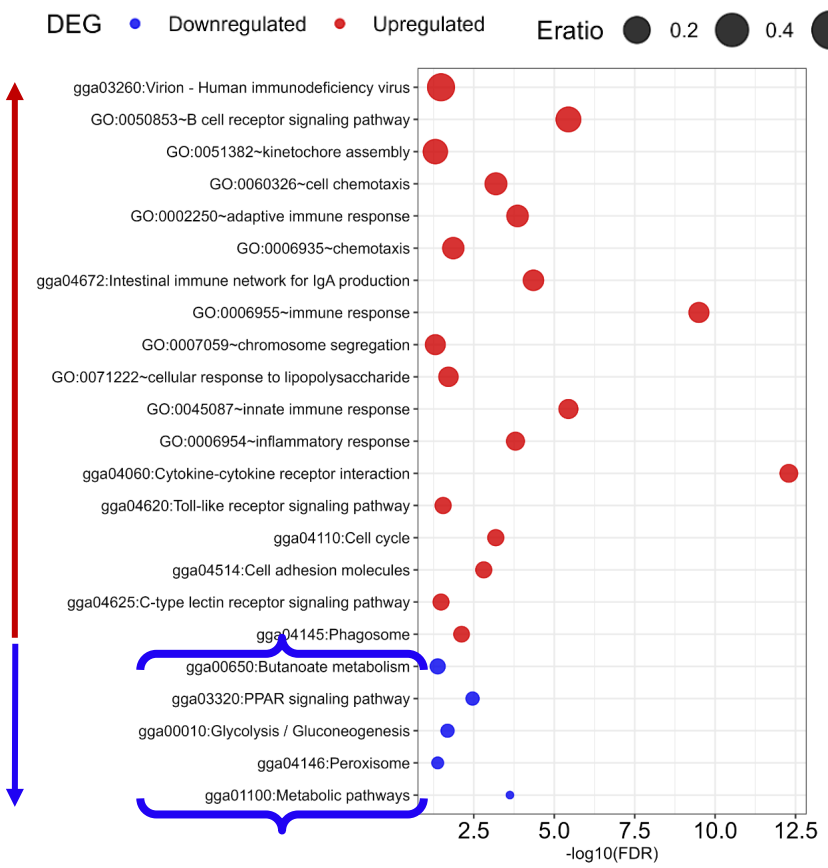
Pathways enriched in LD

Immune-associated pathways are enriched by upregulated genes

Metabolic pathways are enriched by downregulated genes



Oladosu et al., 2024 *Veterinary Research*

*Eratio = Enrichment Ratio

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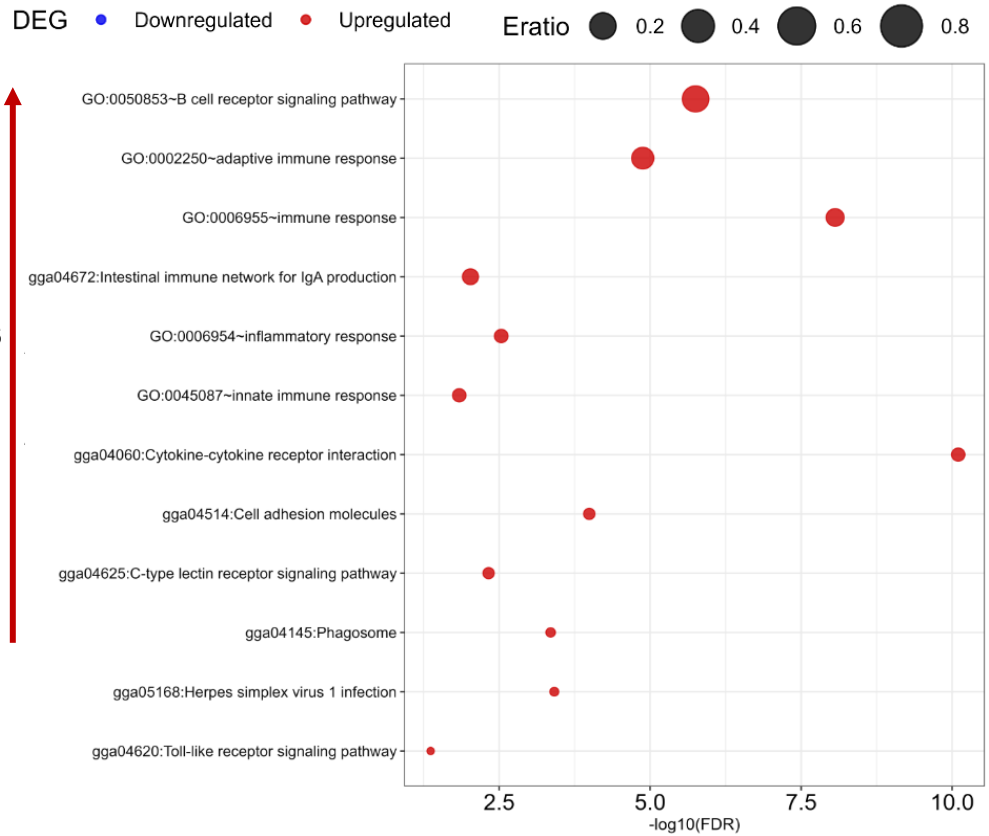
Pathways enriched in Ross

Immune-associated pathways are enriched by upregulated genes



No significant pathways are enriched in the LB genotype

*Eratio = Enrichment Ratio

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Take home messages

- Parasite infections significantly altered the plasma metabolome of high performing layers
- There exists an infection-induced hepatic switch from metabolic to immune functions in male birds as evident in the transcriptional pathways
- **Higher performance = higher sensitivity to environmental challenges**

monogut health
Optimal gut function in monogastric livestock

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Acknowledgements

Dr. Solvig Görs,

Birgit Mielenz,

Susanne Dwars, & Co in Nutritional Physiology-AG

Research Institute for Farm Animal Biology

Aarhus University

The NMR data were generated through accessing research infrastructure at AU, including FOODHAY (Food and Health Open Innovation Laboratory, Danish Roadmap for Research Infrastructure).

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This work is an outcome of the MONOGUTHEALTH project which has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 955374

Scan to read publications

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8th EAAP International Symposium on Energy and Protein Metabolism and Nutrition (ISEP 2025)

15 – 18 September 2025

Rostock-Warnemünde, Germany

Research Institute for Farm Animal Biology

Freie Universität Berlin

Universität Rostock Traditio et Innovatio

Christian-Albrechts-Universität zu Kiel

THANK YOU

Do you have any questions?

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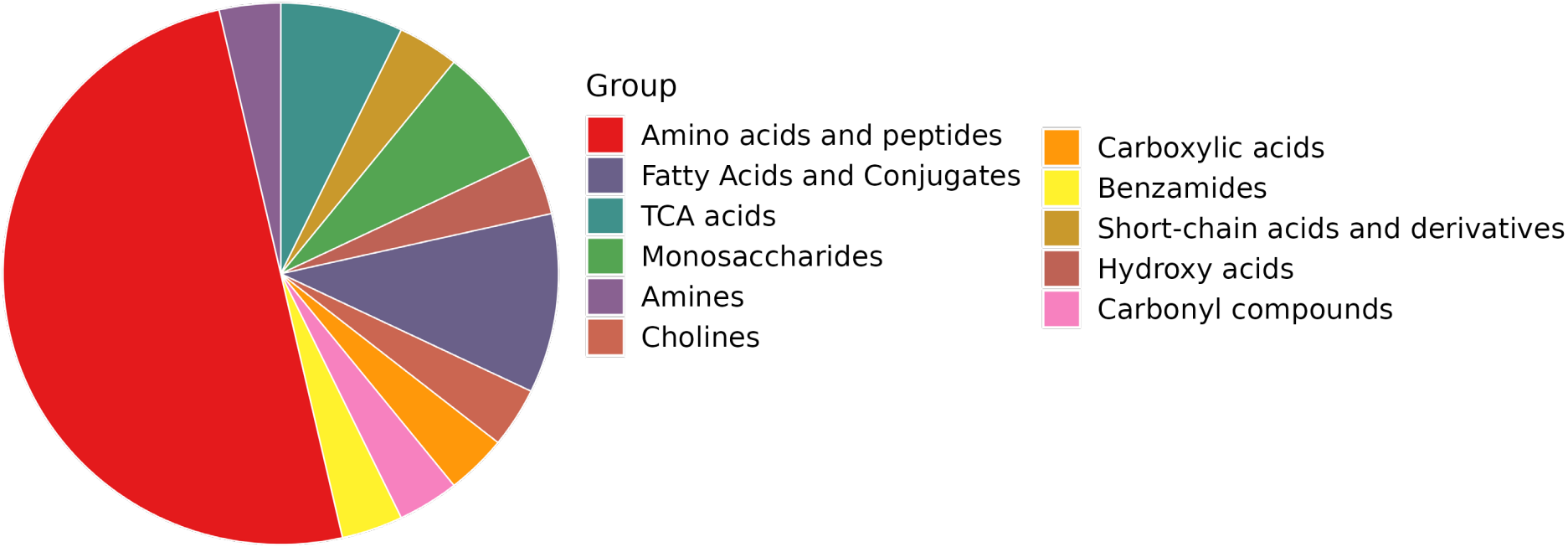
Compounds from the NMR spectroscopy



- A total of 31 and 54 compounds were identified in the plasma and liver respectively
- Amino acids were the most abundant compounds

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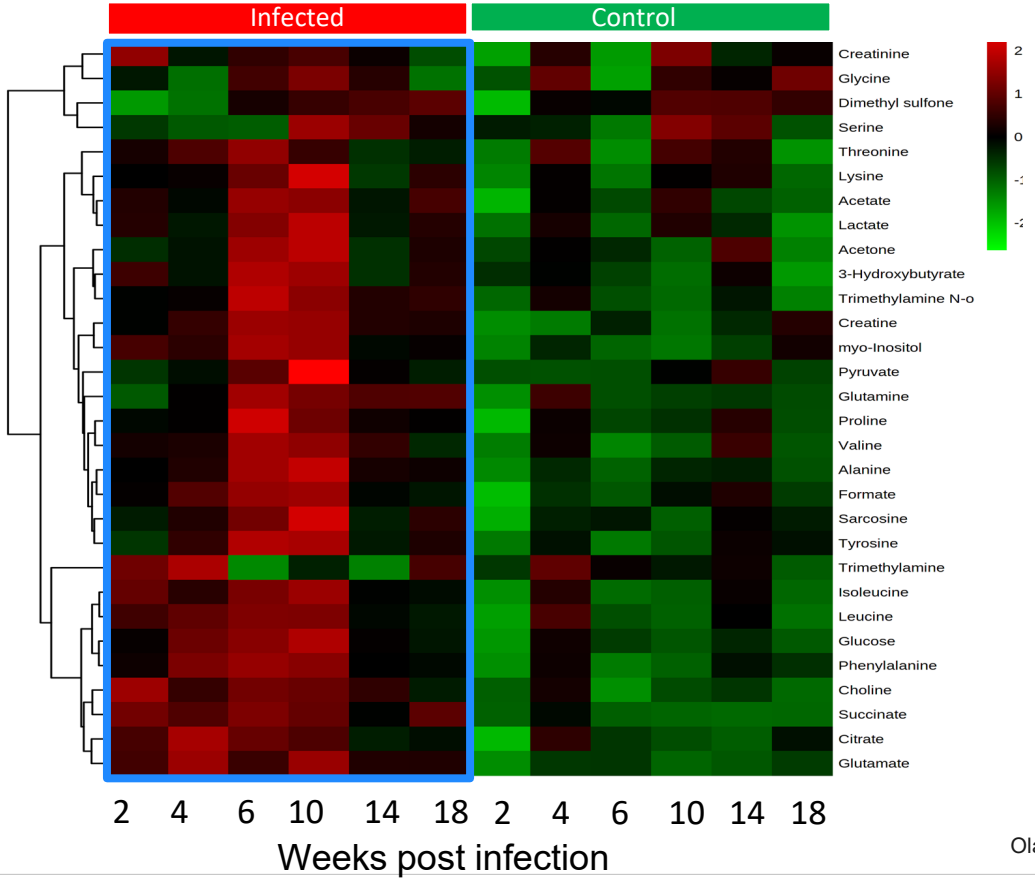
Plasma metabolites at different times of infection



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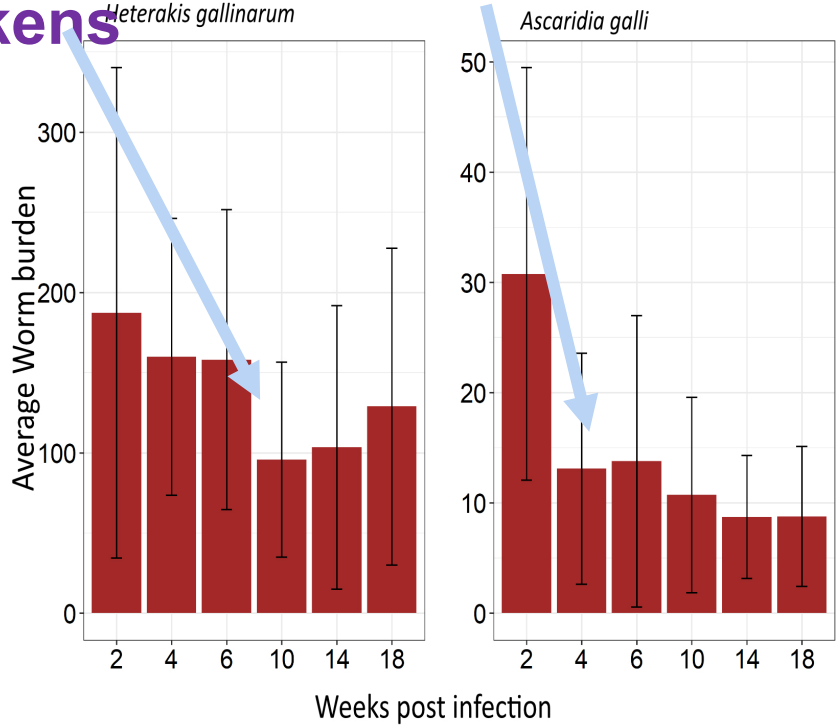
Worm recovery from infected chickens



Heterakis gallinarum

Ascaridia galli

- All infected hens harbored worms throughout the experimental period
- Worm expulsion was highest during early phase of infection

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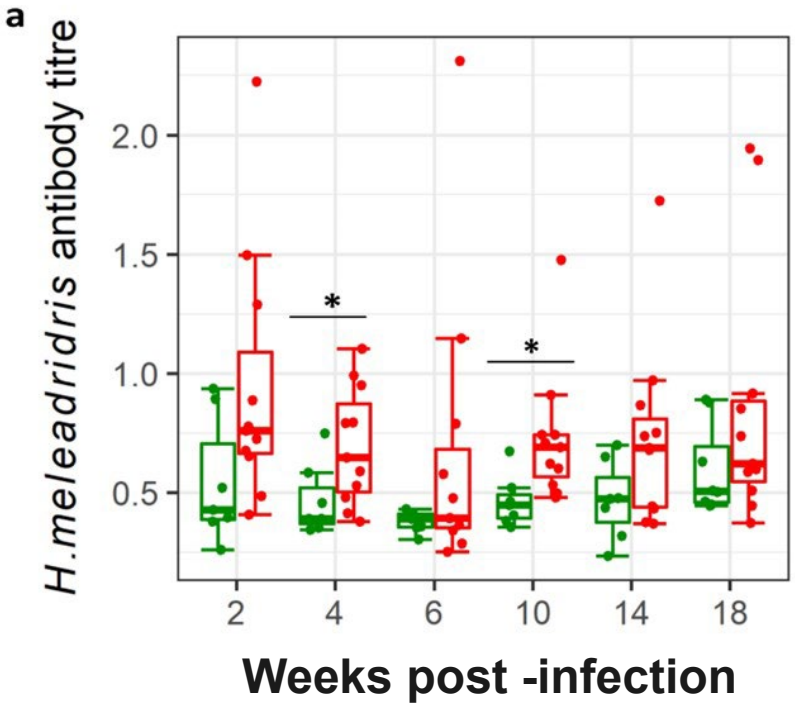
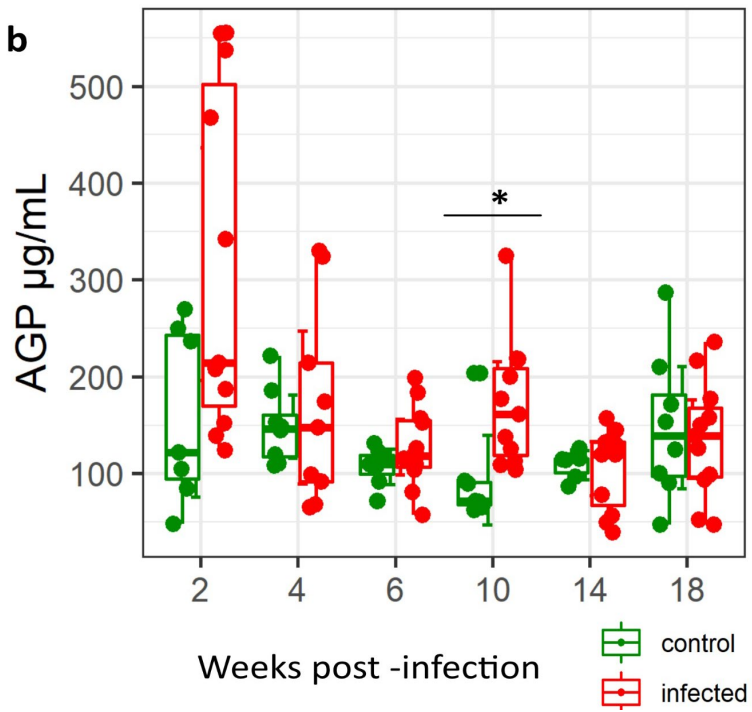
Involvement of histomonosis in the infections





- About 65% of experimentally ascarid-infected birds were positive histomonas infection
- The increased AGP in plasma suggests tissue inflammation

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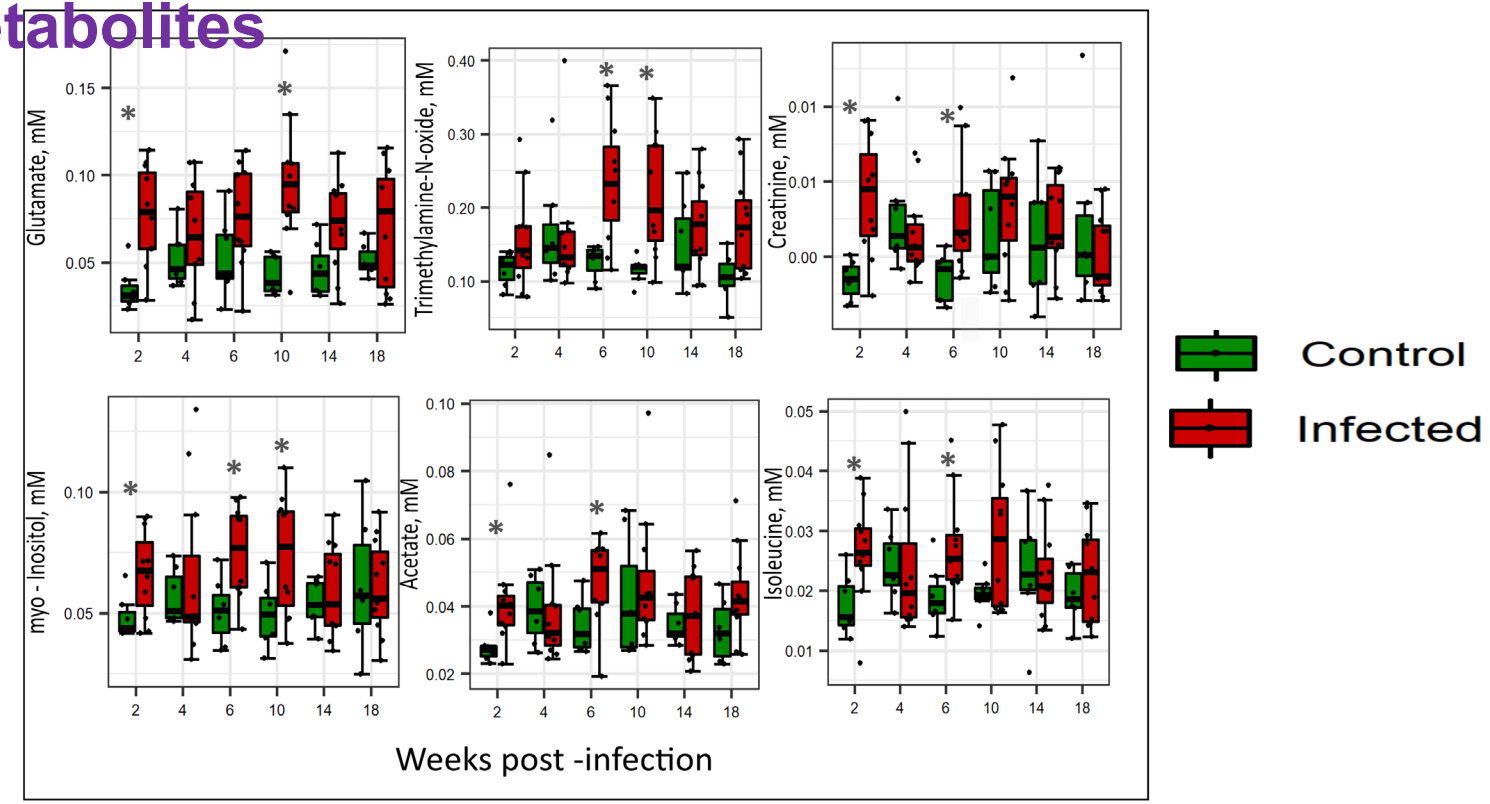
AGP *– Alpha-1-acid glycoprotein*

Time-dependent changes in selected plasma metabolites



- Most changes in wpi 2, 6 and 10
- Overlapping with the pre-patent period of worms

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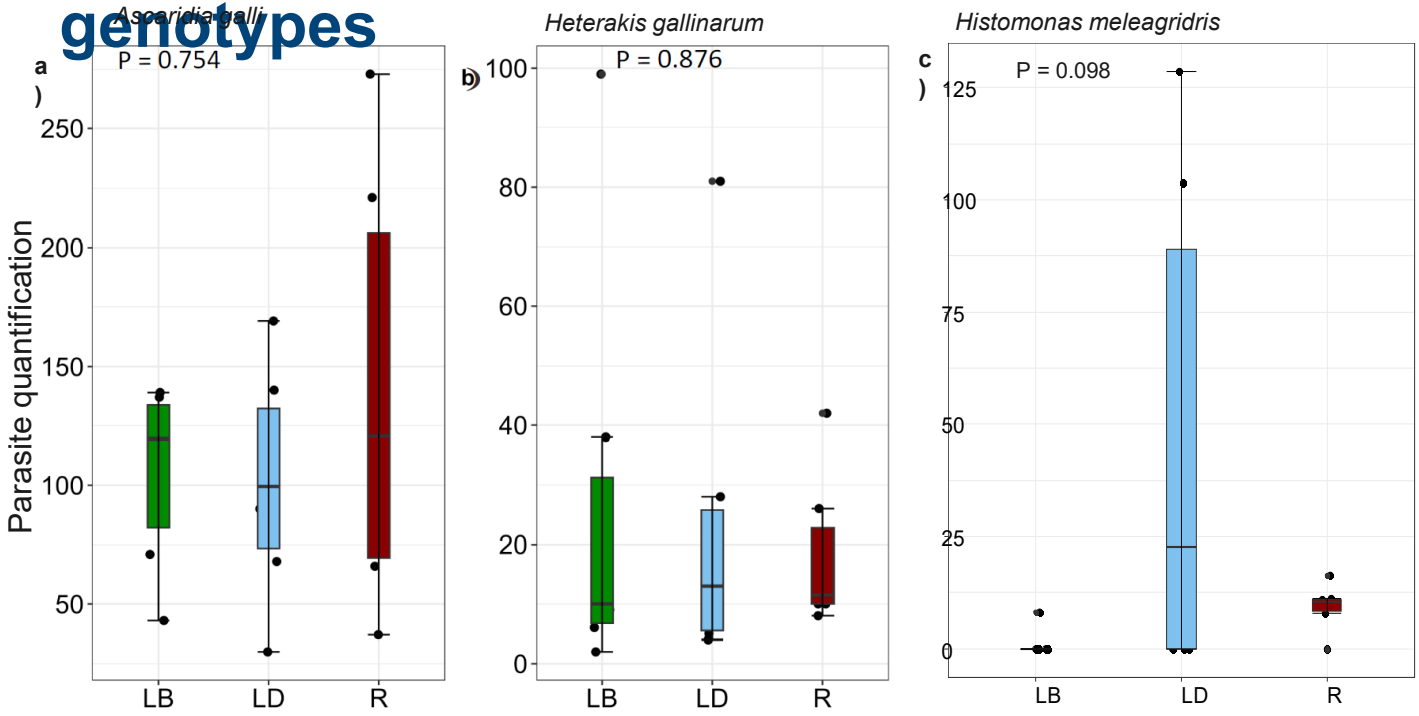
Infection intensity with respect to genotypes



- All infected birds harbored worms
- Parasite burden was not significantly different between genotypes

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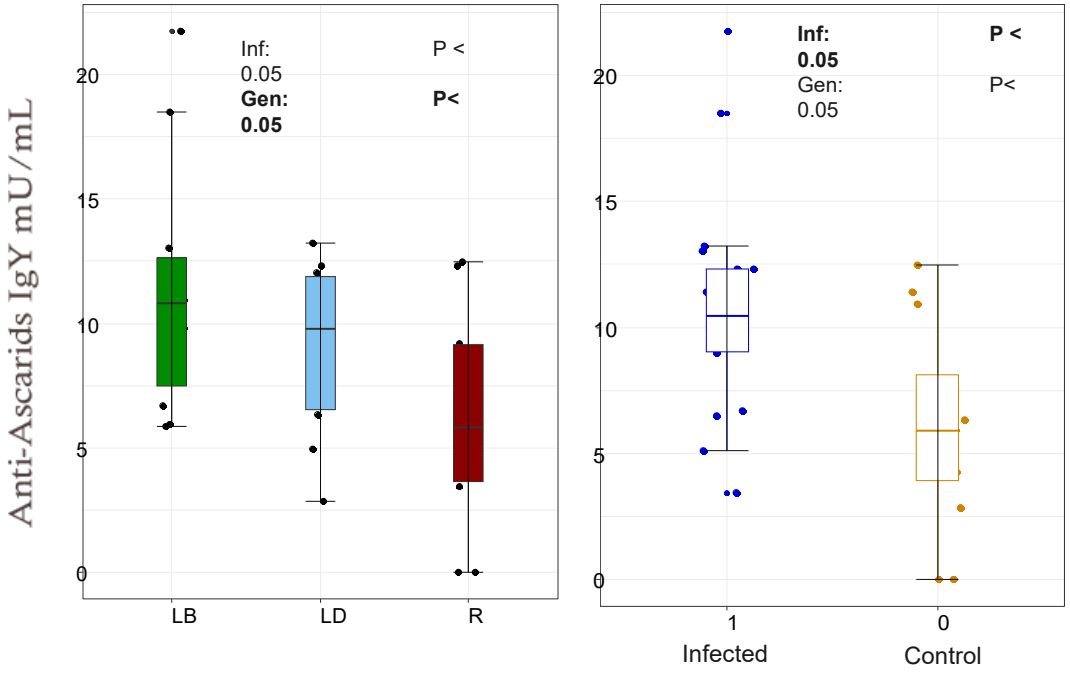
Anti-ascarids antibody levels



- Anti-ascarid antibody was significantly different across genotypes and between infection groups

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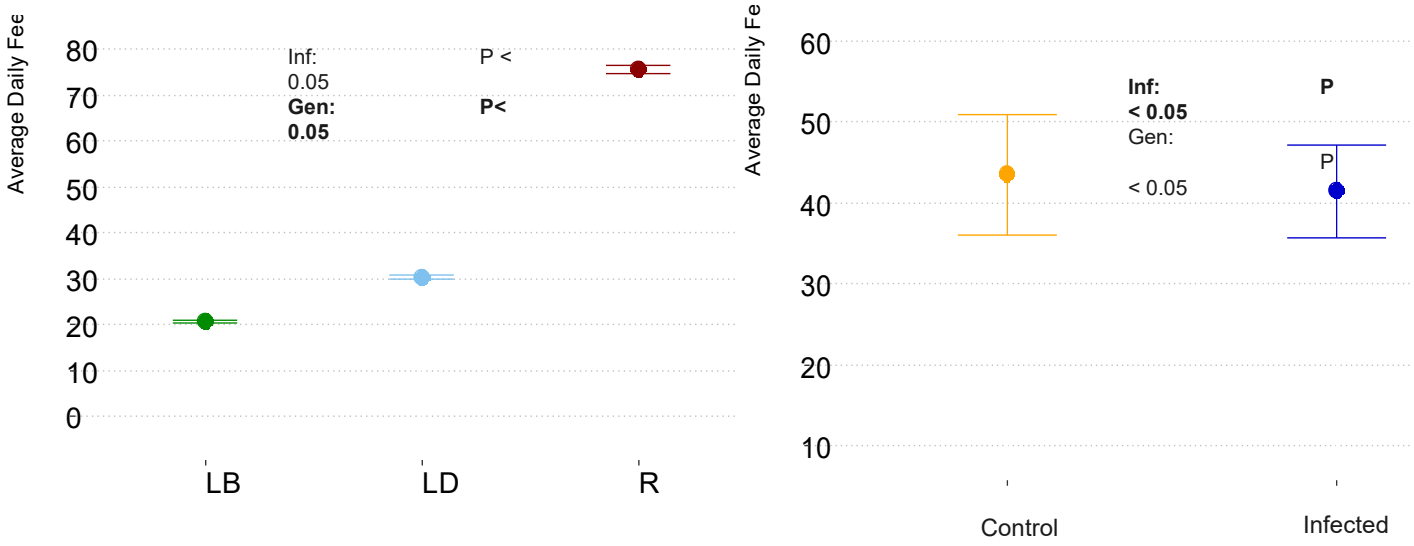
Performance of chickens



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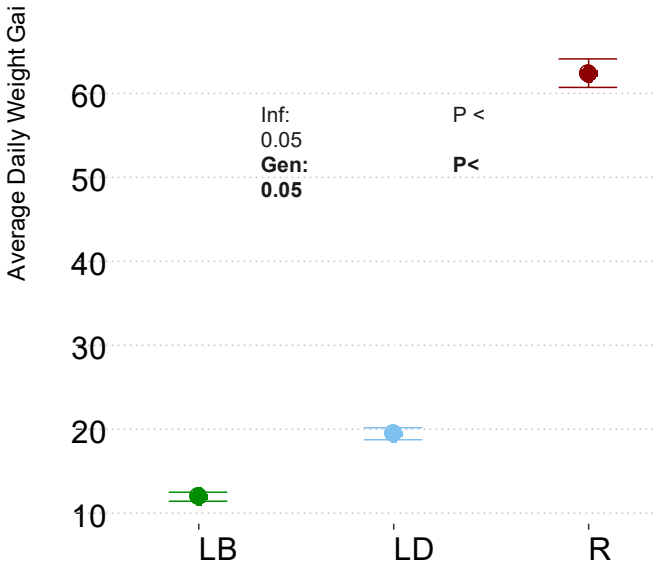

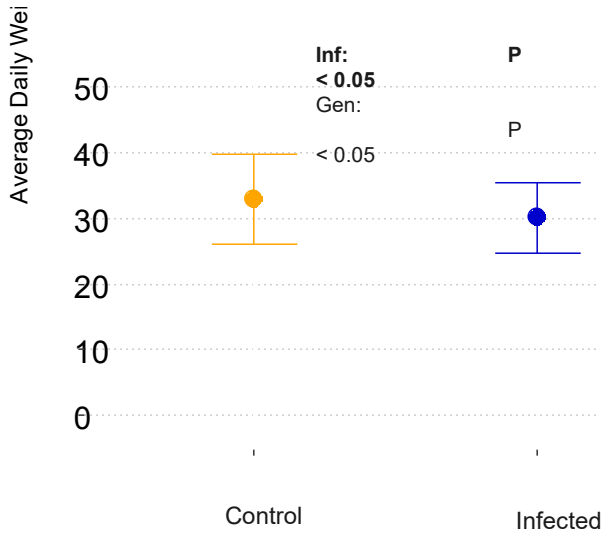

- Infections impaired the performance of the birds

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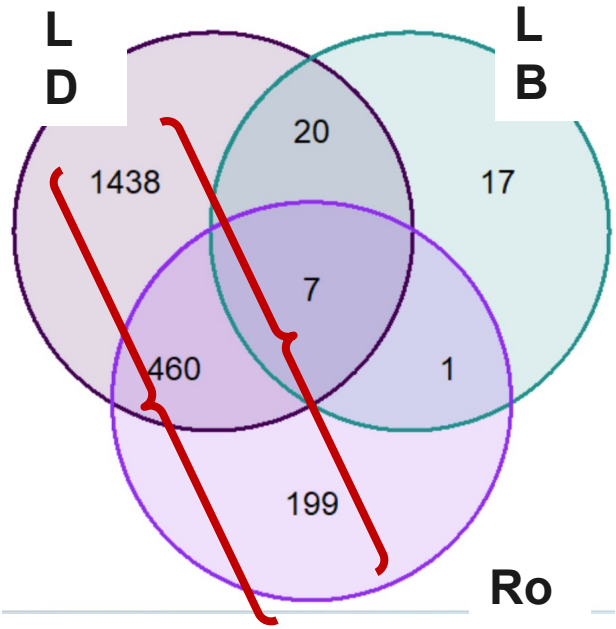
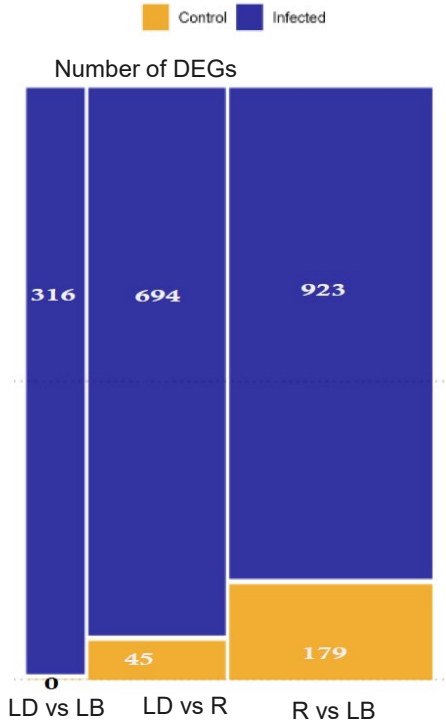
Pairwise comparisons of DEGs



Infection effects within genotype i.e Infected vs Control

- DEGs were profound in LD and Ross



Differences between genotypes

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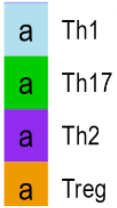
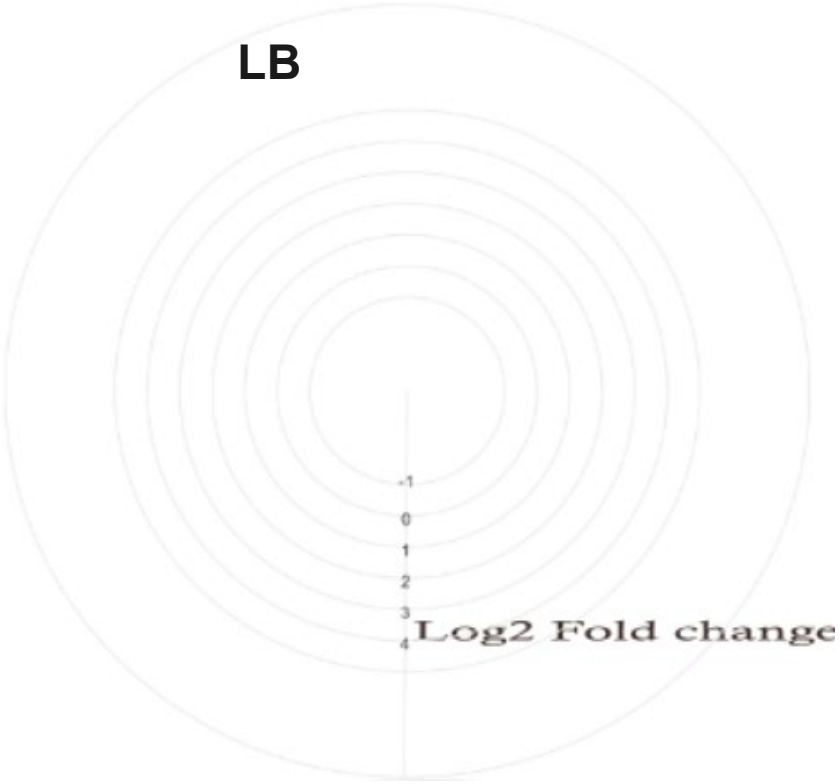
Th1, Th2 Th17 & Treg marker genes

L
D

LB





- Th1
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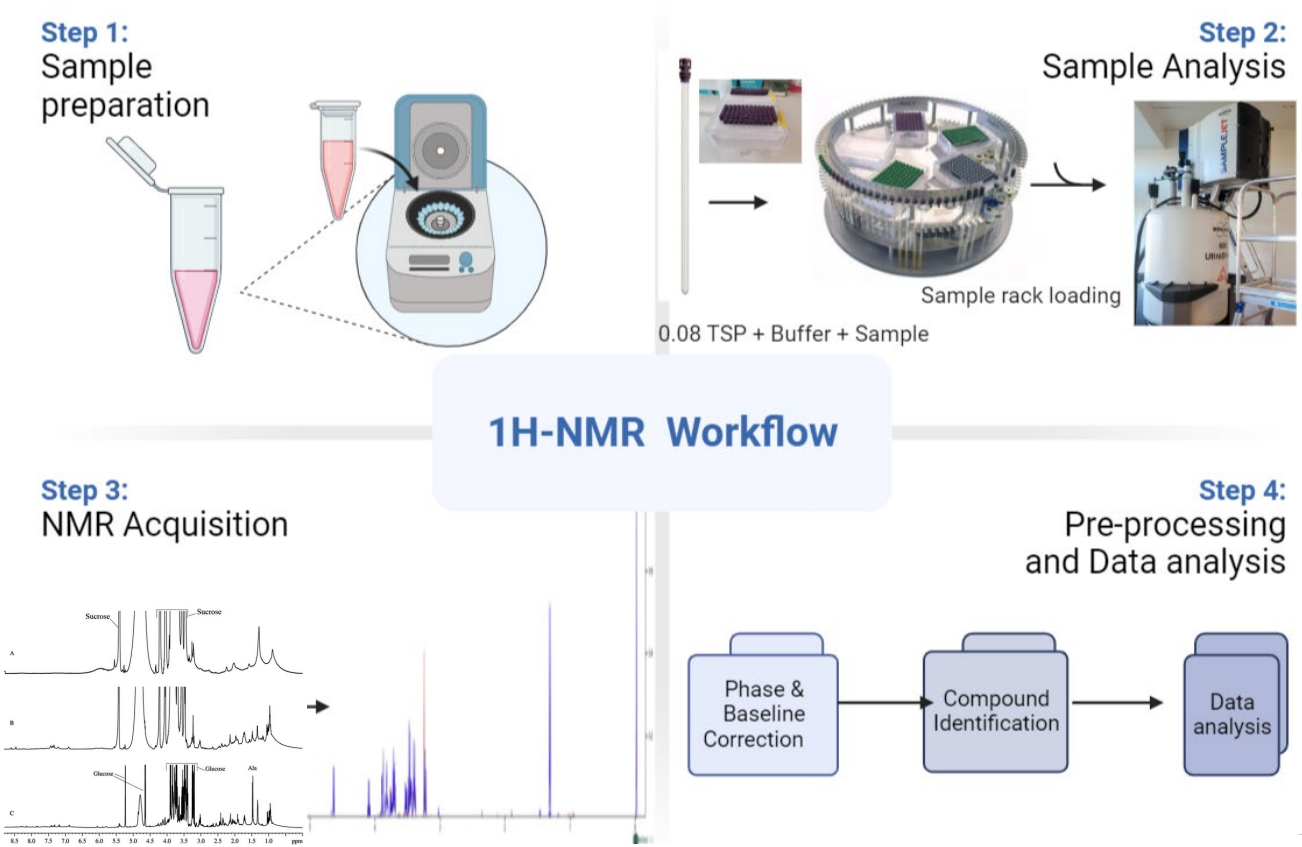
^{1}H-NMR Work-Flow



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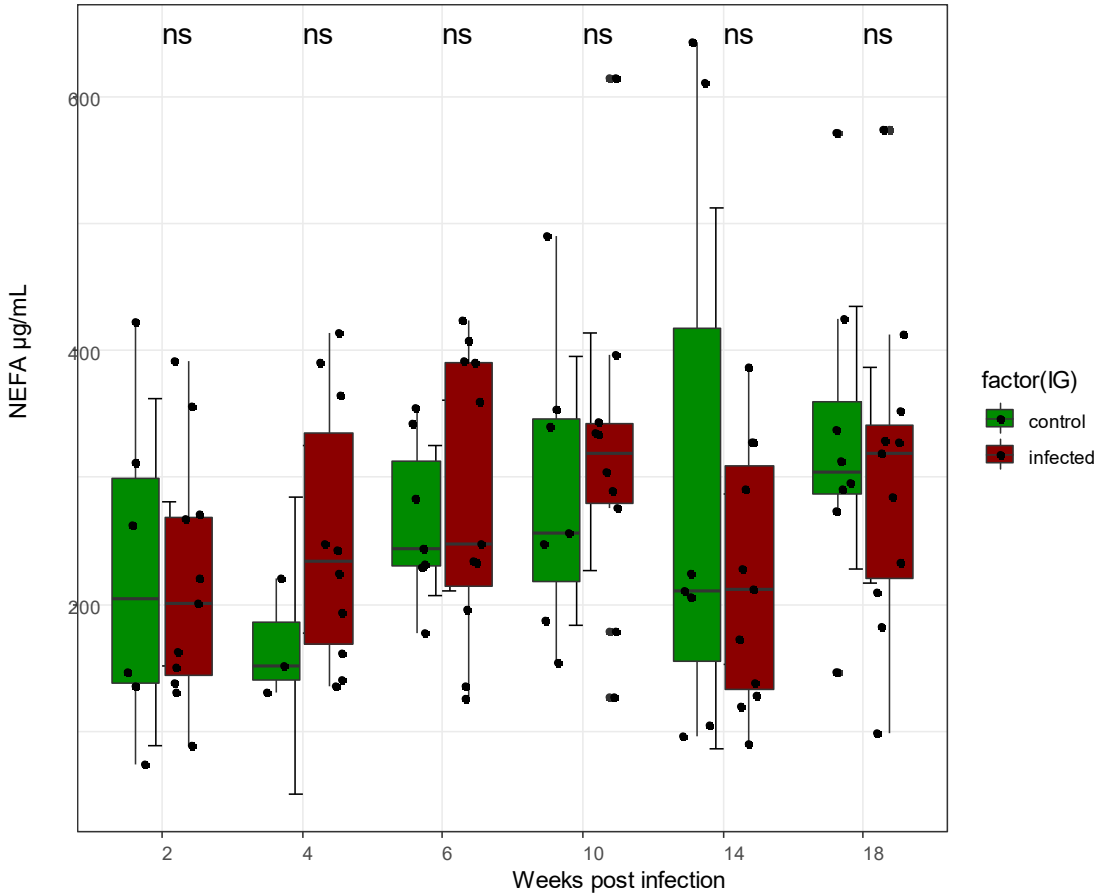
Non-Esterified Fatty Acids (NEFA)



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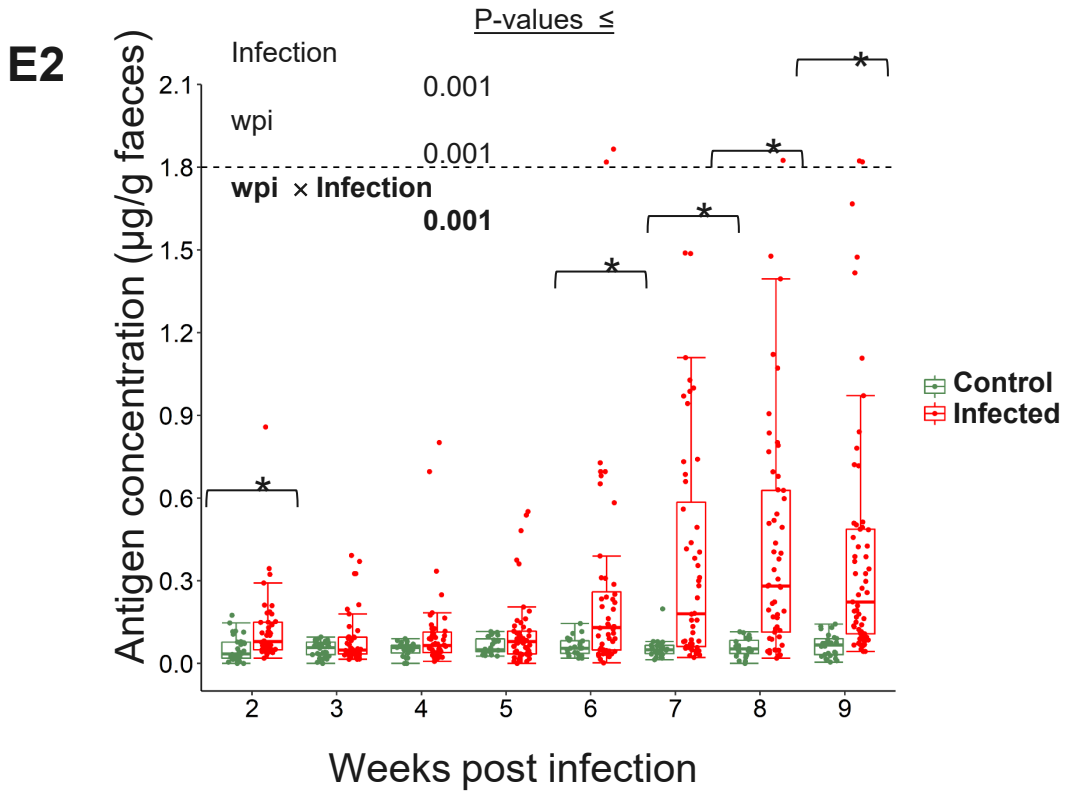
Faecal antigen concentration



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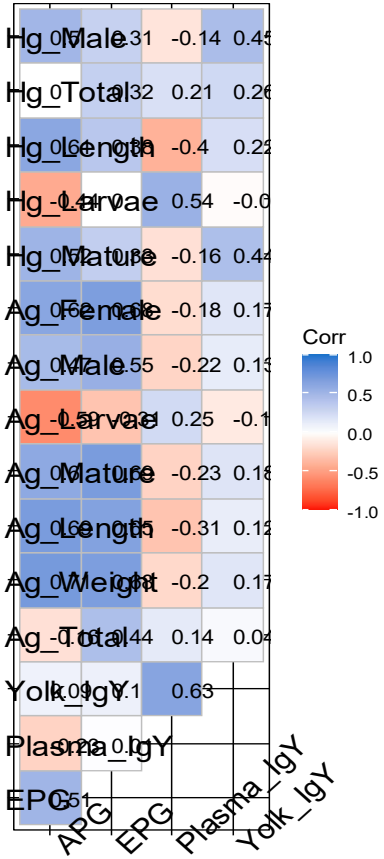
Correlations with worm burdens in E1



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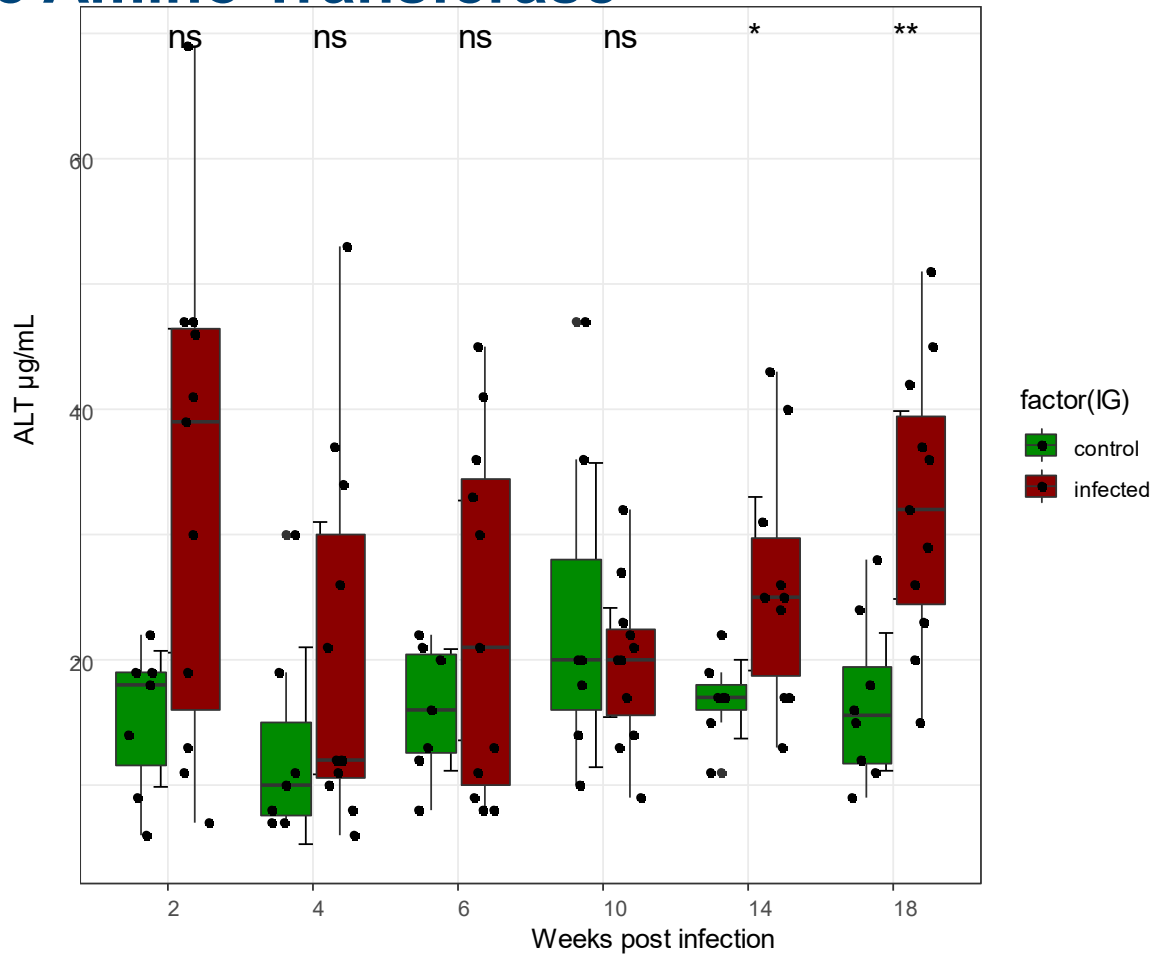
Alanine Amino Transferase



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Effect of infection on laying hens

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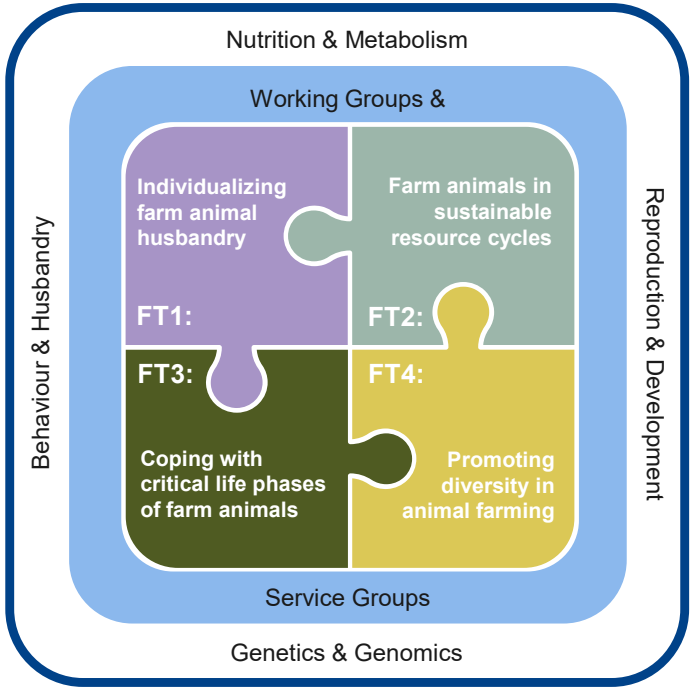

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