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Feed stress-induced transcriptomic changes in the liver of Krškopolje pigs reared in the outdoor system

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INTRODUCTION

Krškopolje pig – the only autochthonous breed in Slovenia

- reared in diverse production systems (extensive to intensive)
- low muscle and high fat deposition
- well adapted to local environmental conditions and (?) poor feed resources
- lower protein requirements



AIM OF THE STUDY

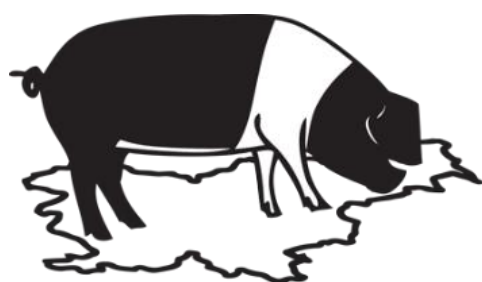
The present study aimed to evaluate the effect of feed stress on **liver** transcriptome of Krškopolje pig's reared in the outdoor production system.



The GEroNIMO project has received funding from European Union's Horizon 2020 research and innovation program under Grant Agreement No 101000236.

EXPERIMENTAL DESIGN

OUTDOOR SYSTEM



n = 20

Low protein diet (LP)¹
(n = 10)

Standard protein diet (HP)²
(n = 10)

Isoenergetic
diet

¹ 15% crude protein from 20 to 60 kg and 10% crude proteins from 60 kg to slaughter

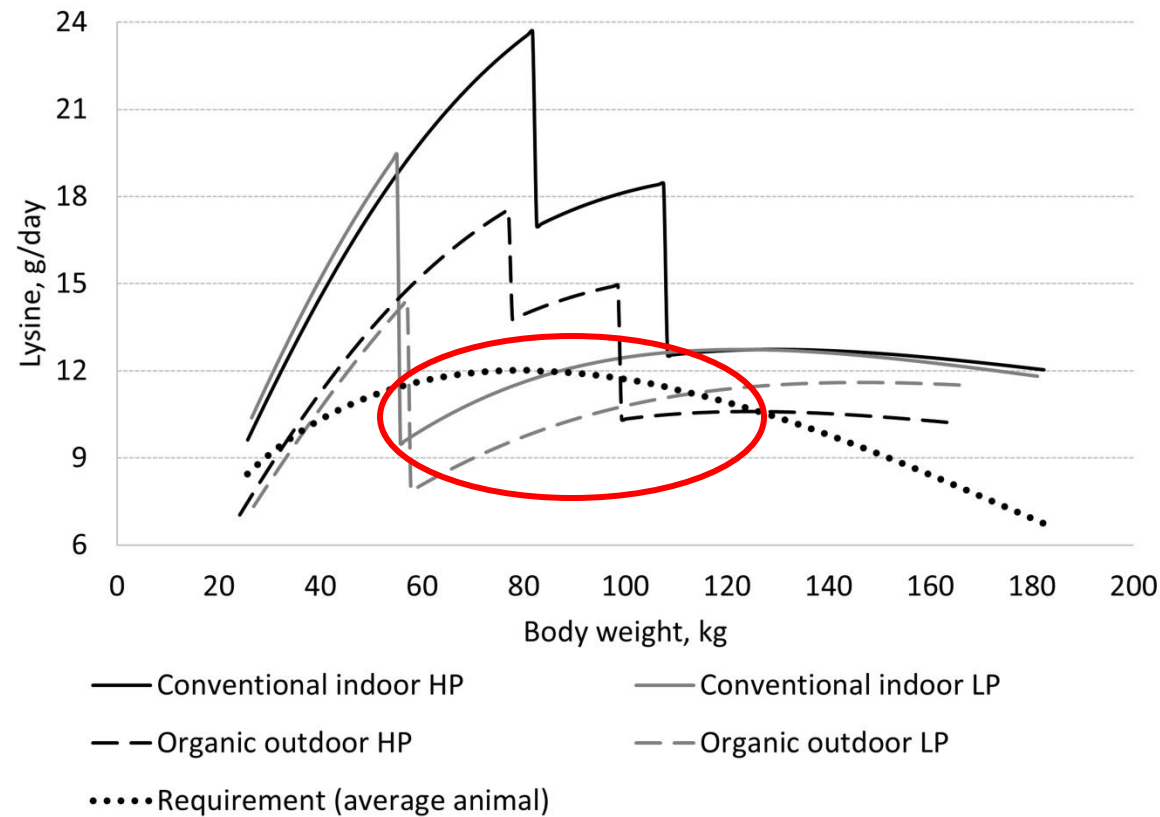
² 15, 12.5 and 10% crude protein from 20 to 80 kg, from 80 to 100 kg and from 100 kg to slaughter, respectively

- Animals were slaughtered at the age of 330 ± 2 days (mean \pm SE) and at the body weight of 166 ± 13.2 kg (mean \pm SE)
- **LIVER** and adipose tissue were sampled for RNA extraction
- RNA-seq library was prepared - 10 samples per group
- Sequencing on Illumina NovaSeq 6000 (generation of 150 bp pair-end reads)
- Bioinformatic analysis (slaughter batch was included as a fixed effect)



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Previous results



A tendency to larger average backfat thickness in LP group.

* Modelling with INRAPorc®

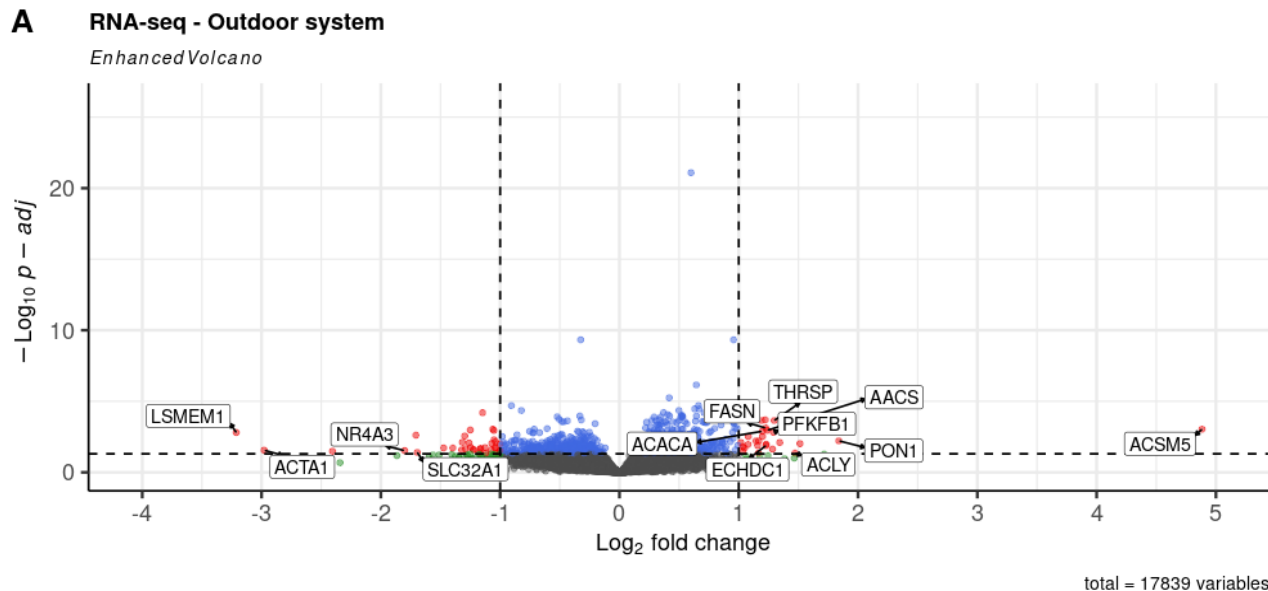
Krškopolje pigs receiving the LP diet were deficient in lysine from 60 kg to 120 kg.



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Previous results on adipose tissue

RNA-sequencing of subcutaneous adipose tissue (LP compared to HP diet)



Upregulated genes in LP group were involved in:

- lipogenesis
 - FASN, ACACA, ACLY
 - THRSP - energy storage
 - MOGAT2
- fatty acid beta oxidation (e.g., ECHDC1)
- response to oxidative stress (e.g., PON1, XDH)

Downregulated genes in LP group were involved in:

- adipogenesis (e.g., NR4A3) - regulate lipid and carbohydrate metabolism, reduce deposition of white fat
- negative regulation of oxidative stress (e.g., TRPV4)



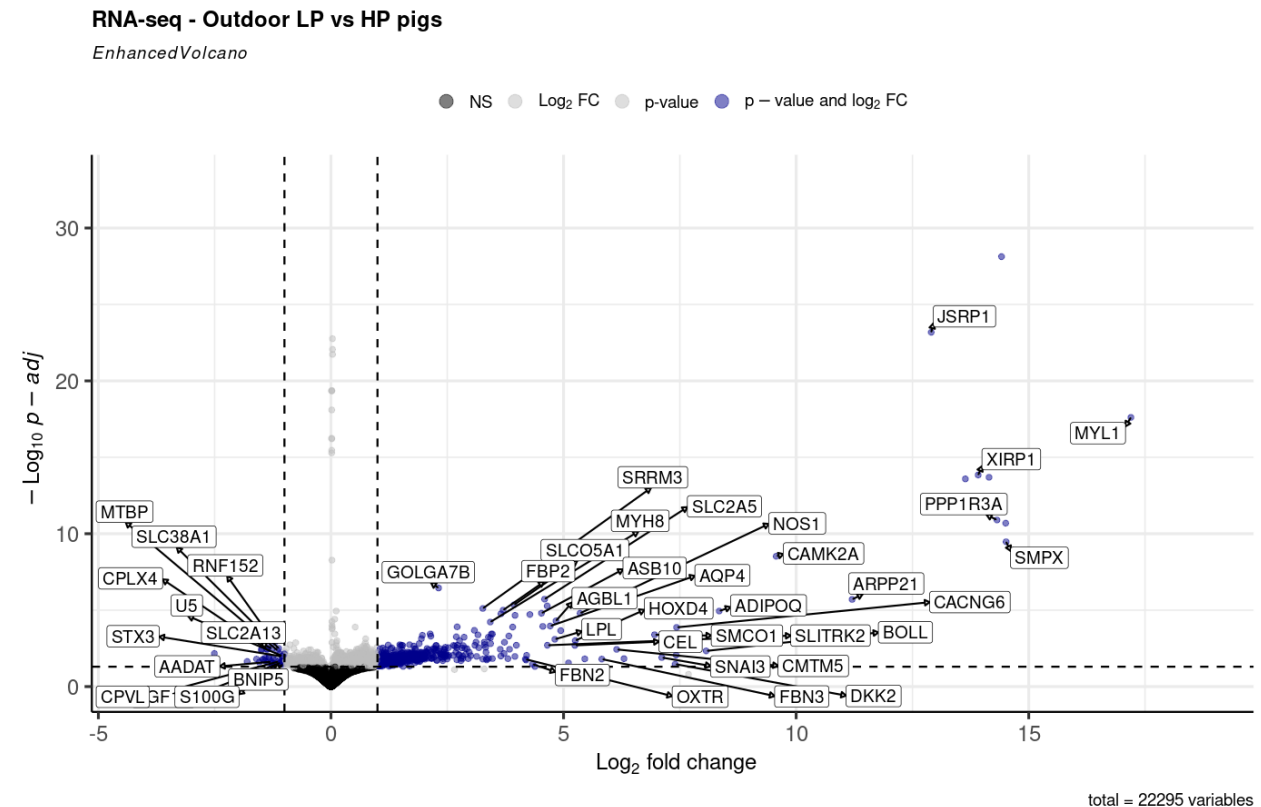
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Differential gene expression analysis - Liver

643 upregulated and 41 downregulated genes in LP compared to HP group.

Upregulated genes in LP group were involved in:

- **lipolysis** (e.g., LIPE, PNPLA2, LPL, CEL, GPIHBP1).
- **heat shock proteins** (e.g., CRYAB, HSPB1, HSP70.2, DNAJB5)



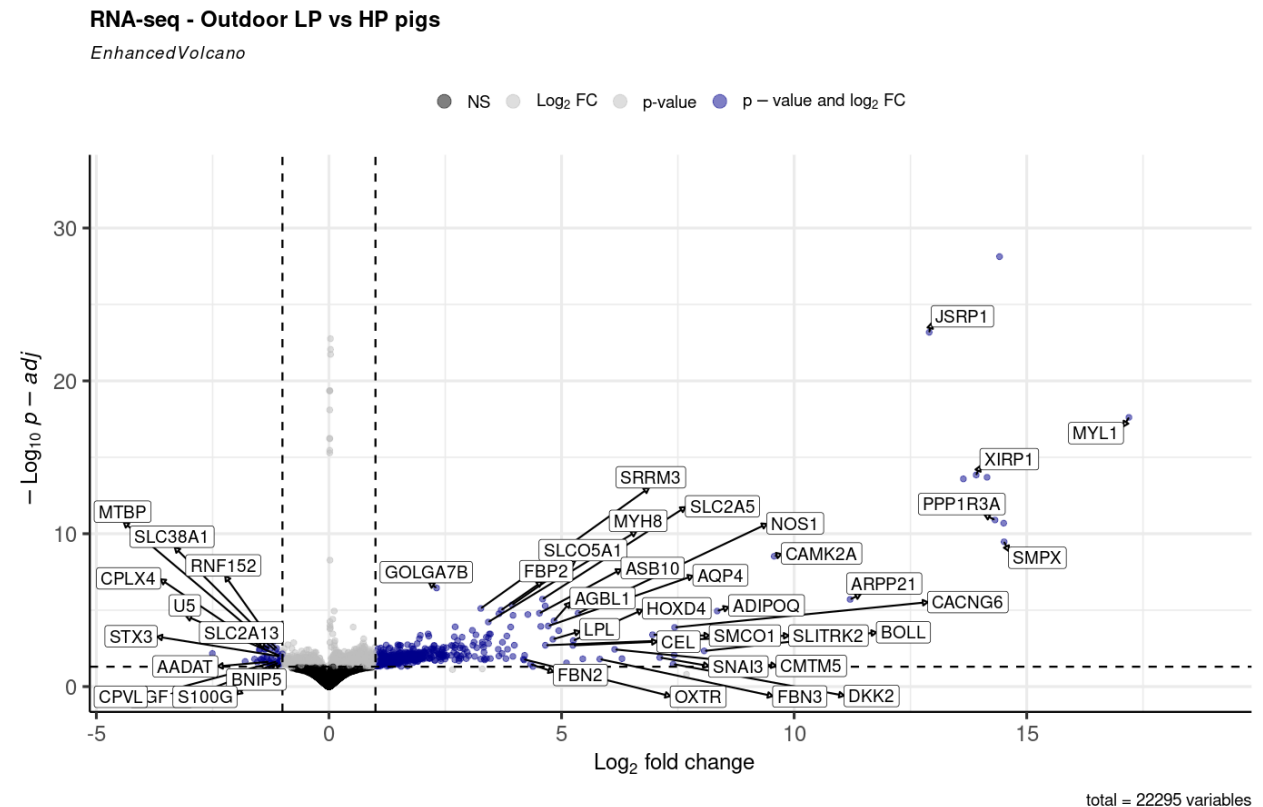
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Differential gene expression analysis - LIVER

643 upregulated and 41 downregulated genes in LP compared to HP group.

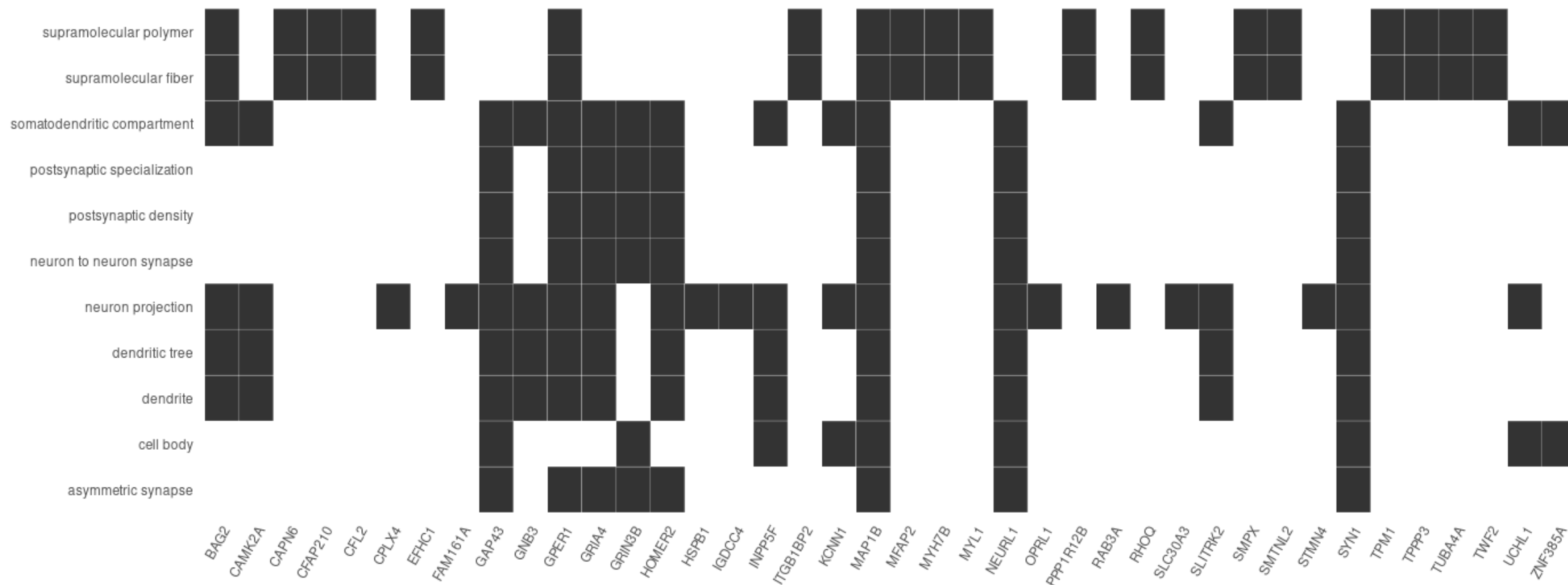
Upregulated genes in LP group were involved in: - regulation of glucose/energy homeostasis and lipid metabolism

- **PRKAG3** – an energy sensor protein kinase,
- **PPAR** – key regulator of adipocyte differentiation and glucose homeostasis,
- **CPT1B** – rate-controlling enzyme of the fatty acid beta-oxidation pathway,
- **FITM1** – binding to triglyceride and diacylglycerol, and hydrolysis of fatty acyl-CoA,
- **APOO** – fatty acid transport,
- **PPP1R1A** – hormonal regulation of glycogen metabolism,
- **GYS1** – glycogen synthesis



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Gene ontology analysis



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GERONMO



Conclusions

Protein restriction affects the expression of liver genes involved in:

- glucagon, insulin signalling pathways
- fatty acid oxidation and transport
- regulation of energy homeostasis

Feed and environmental stress

Potential risks of LP diet?



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