

Omega-6-associated gene modules reveal novel regulatory mechanisms in porcine liver

Simara Fanalli¹, Richard Crooijmans², Izally Gervásio³, Bárbara Silva-Vignato³, Vivian Almeida⁴, Aline Cesar^{1,3*}

¹School of Animal Science and Food Engineering, (FZEA), University of São Paulo, Pirassununga, São Paulo, Brazil; ²ABG, Wageningen University & Research, Wageningen, The Netherlands; ³Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, Brazil; ⁴College of Veterinary Medicine and Animal Science, Federal University of Goiás, Goiânia, Goiás, Brazil

INTRODUCTION & AIM

Identifying diets with desirable ratios of omega-6 (n-6) and omega-3 (n-3) fatty acids (FAs) plays a key role in regulating inflammation, maintaining membrane fluidity, facilitating β -oxidation, and promoting overall metabolic health.

Previously, we showed that pigs fed 1.5% soybean oil (SOY1.5) had greater hepatic linoleic acid (an n-6 FA) deposition than pigs fed 3.0% soybean oil (SOY3.0) (Fanalli et al., 2022). A balanced dietary ratio of n-6:n-3 FA is crucial to support optimal health and reduce the risk of chronic diseases.

This study aimed to identify gene co-expression modules correlated with n-6 deposited in hepatic tissue of pigs fed diets containing either SOY1.5 or SOY3.0.

METHOD

All animal experimental procedures were performed in accordance with the guidelines established by the Animal Care and Use Committee of Luiz de Queiroz College of Agriculture (University of São Paulo, Piracicaba, Brazil), under protocol number 2018.5.1787.11.6 and CEUA approval 2018–28.

RESULTS & DISCUSSION

In pigs fed SOY1.5, one gene cluster was negatively correlated with **linoleic acid** and **total n-6**. In pigs fed SOY3.0, however, another module was negatively correlated with the **n-6:n-3 ratio**. Functional enrichment analysis (FDR < 0.05) highlighted the fatty acid degradation pathway (**ssc00071**- Figure 1) in SOY1.5-fed pigs and Bile secretion pathway (**ssc04976**- Figure 2) in the SOY3.0 group.

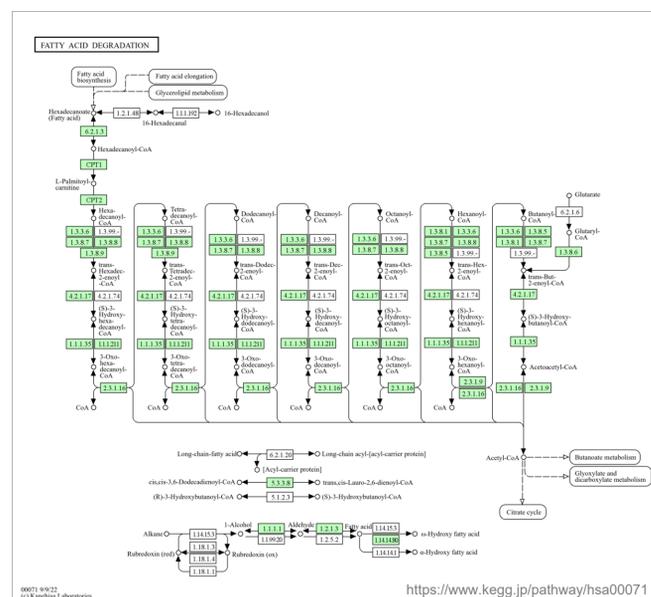


Figure 1. KEGG pathway ssc00071: Fatty acid degradation showing genes associated with fatty acid degradation identified in pigs fed a basal diet supplemented with 1.5% soybean oil. The genes ENSSSCG00000009889, ENSSSCG00000009151, ENSSSCG00000026153, ENSSSCG00000009184, ENSSSCG00000004510, and ENSSSCG00000006324 were mapped to this pathway, highlighting metabolic processes.

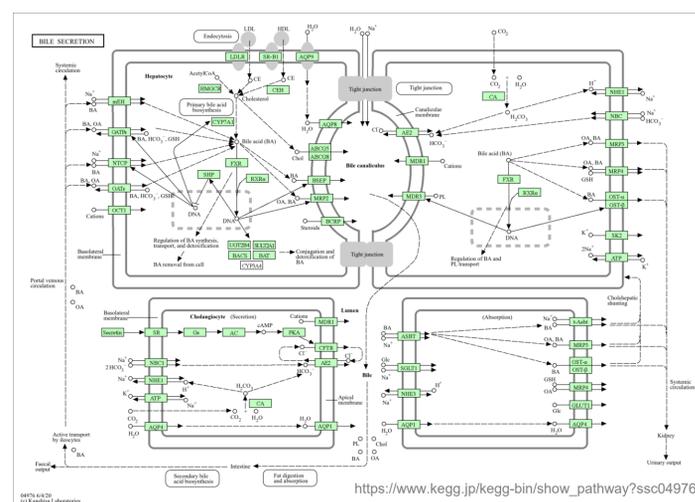
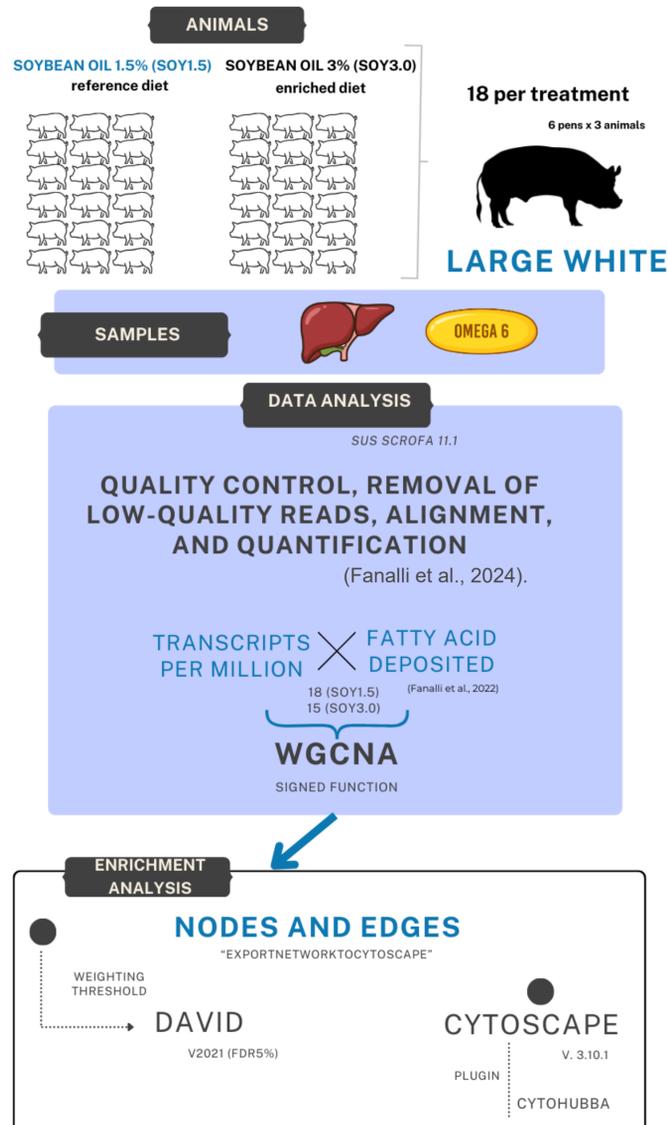


Figure 2. KEGG pathway ssc04976: Bile secretion showing genes associated with bile secretion identified in pigs fed a basal diet supplemented with 3% soybean oil. The genes ENSSSCG00000005398, ENSSSCG000000034735, ENSSSCG000000006238, and ENSSSCG00000004597 were mapped to this pathway, indicating potential involvement in hepatic lipid metabolism.

CONCLUSION

These findings suggest that dietary oil inclusion modulates distinct co-expression networks and metabolic pathways in porcine liver. These molecular insights can optimize nutritional strategies, thereby enhancing animal health and aligning with the FAO's One Health initiative.

FUTURE WORK / REFERENCES

Fanalli, S.L. et al. (2022). Differential Gene Expression Associated with Soybean Oil Level in the Diet of Pigs. *Animals* 2022, Vol. 12, Page 1632. <https://doi.org/10.3390/ANI12131632>
Fanalli, S.L. et al. (2024). Key co-expressed genes correlated with blood serum parameters of pigs fed with different fatty acid profile diets. *Front. Genet. Sec. Livestock Genomics*. <https://doi.org/10.3389/fgene.2024.1394971>.

