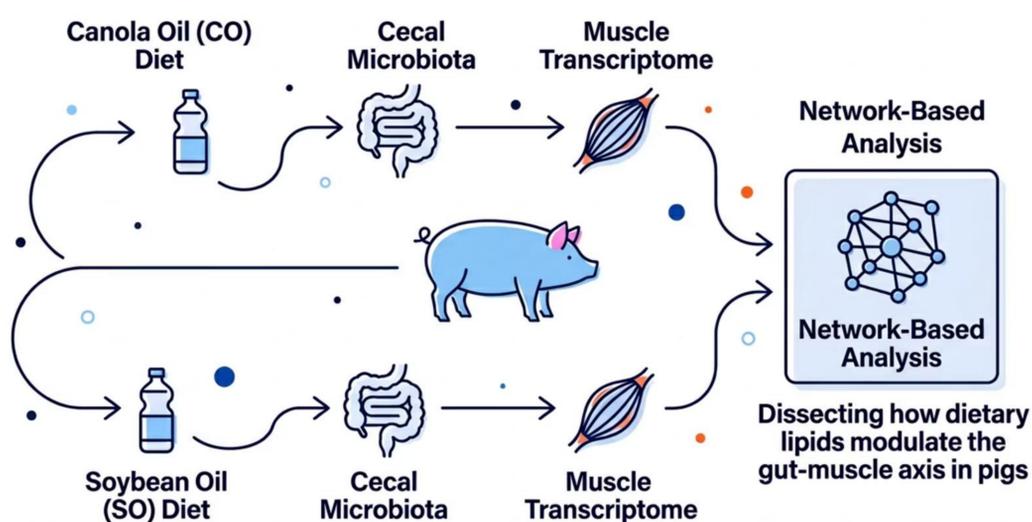


Dietary lipid source unravels host-microbiota networks along the gut-muscle axis in pigs

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INTRODUCTION & AIM



METHOD

- **Diets** → Pigs were assigned to one of two dietary groups:
 - 3% canola oil (CO) – 14 Large White pigs
 - 3% soybean oil (SO) – 18 Large White pigs
- **Tissues & Sample Collection:**
 - Skeletal muscle (*Longissimus lumborum*) → RNA-Seq.
 - Cecal content → 16S rRNA gene sequencing of microbiota.
- **Datasets generated:**
 - Muscle transcriptome (~14 k genes, TPM values);
 - Cecal microbiota (447 ASVs, 50% prevalence).
- **Integrative analysis:** Diet-specific Weighted Gene Co-expression Network Analysis (WGCNA) to map interactions with the 19 most abundant cecal genera.
 - Relevant modules ($|r| > 0.7, p < 0.01$) → DAVID enrichment analysis.

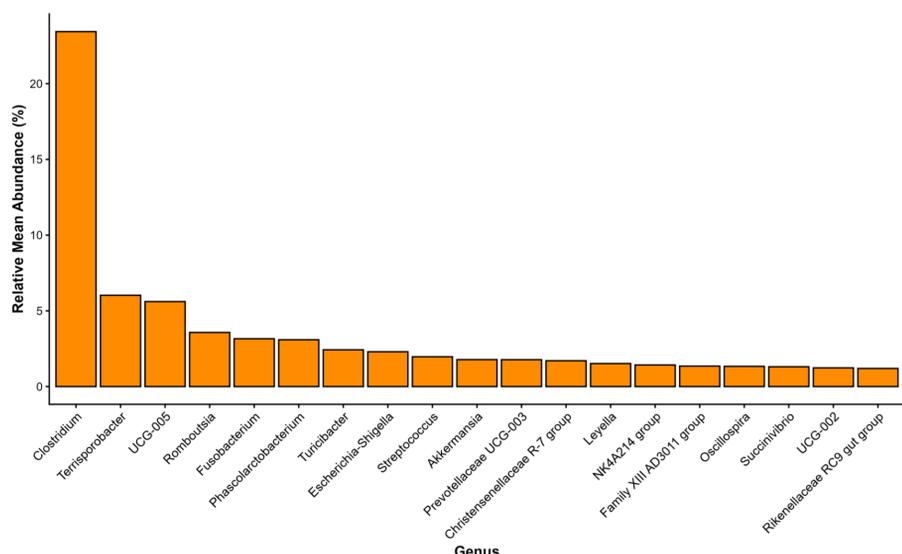


Figure 1. Mean relative abundance of the 19 most abundant genera (>1%) selected for the Weighted Gene Co-expression Network Analysis (WGCNA), excluding “*Incertae Sedis*”.

RESULTS & DISCUSSION

Gene module	Terrisp.	Romb.	Akkerm.	Prevot.	Leyella	Riken.
CANOLA OIL (CO)						
Meyellow-green	-0.056 (0.9)	0.59 (0.03)	-0.62 (0.02)	0.48 (0.1)	0.13 (0.7)	0.7 (0.008)
MEsalmon	-0.26 (0.4)	-0.53 (0.06)	0.19 (0.5)	0.32 (0.3)	0.72 (0.005)	0.33 (0.3)
MEagenta	0.31 (0.3)	0.34 (0.3)	-0.71 (0.006)	0.58 (0.04)	-0.11 (0.7)	0.22 (0.5)
MEdarkgrey	-0.73 (0.004)	-0.7 (0.008)	0.39 (0.2)	0.024 (0.9)	0.31 (0.3)	0.34 (0.2)
SOYBEAN OIL (SO)						
Medark-orange	0.42 (0.1)	0.21 (0.4)	-0.24 (0.4)	0.82 (9e-05)	0.12 (0.7)	0.35 (0.2)
MElightcyan	0.81 (2e-04)	0.21 (0.4)	0.18 (0.5)	0.08 (0.8)	0.17 (0.5)	-0.067 (0.8)

Table 1. Diet-specific correlations (SO and CO) between muscle gene co-expression modules (MEs) and cecal genera. Only significant correlations with an absolute Pearson's $r > 0.7$ ($p < 0.01$) are shown. Values represent the correlation coefficient with p -values in parentheses.

- The opposite association of *Terrisporobacter*, a genus linked to SCFA production, oxidative stress, and immune modulation, suggests that fat source influences muscle metabolic and immune signaling. While no significant enrichment was observed for MEdarkgrey, MElightcyan showed enrichment for Proteasome and MAPK6/MAPK4 pathways.

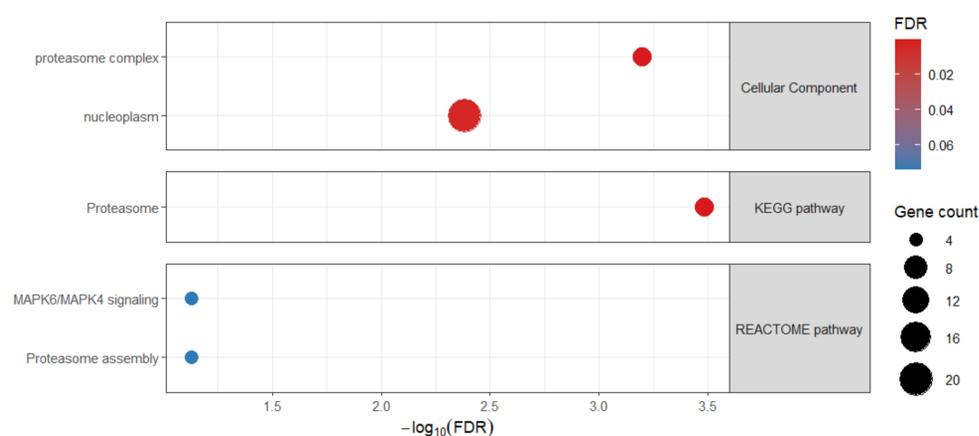


Figure 2. Functional enrichment of *MElightcyan* genes using DAVID (FDR < 0.10, Benjamini-Hochberg). The x-axis represents $-\log_{10}(\text{FDR})$; bubble size corresponds to gene count, and color indicates FDR. Terms are grouped by functional category.

CONCLUSION

- Dietary lipids reshape functional communication rather than the composition of the gut-muscle axis;
- This integrative framework offers a powerful tool for the sustainable development of targeted nutritional strategies to enhance muscle development and pork quality.

Acknowledgments:



Full CV:

