Table 1: Effects of dietary treatments on fatty acid profile of *Longissimus lumborum* intramuscular fat of pigs

|  |  |  |  |
| --- | --- | --- | --- |
| Fatty Acid (%) |  | Dietary treatment | |
| SOY1.5 | SOY3.0 | Pooled SEM2 | *p-value* |
| Saturated fatty acid (SFA) |  |  |  |  |
| Myristic acid (C14:0) | 1.14 | 1.19 | 0.04 | 0.20 |
| Palmitic acid (C16:0) | 25.50 | 25.01 | 0.21 | 0.21 |
| Stearic acid (C18:0) | 12.18 | 11.89 | 0.15 | 0.42 |
| Monounsaturated fatty acid (MUFA) |  |  |  |  |
| Palmitoleic acid (C16:1) | 2.86 | 3.17 | 0.13 | 0.02 |
| Eicosenoic acid (C20:1) | 0.51 | 0.55 | 0.03 | 0.11 |
| Oleic acid (C18:1 n-9) | 38.93 | 44.15 | 1.40 | <0.01 |
| Polyunsaturated fatty acid (PUFA) |  |  |  |  |
| Linoleic acid (C18:2 n-6) | 17.90 | 13.28 | 1.12 | <0.01 |
| Alpha-linolenic acid (C18:3 n-3) | 0.77 | 0.56 | 0.06 | <0.01 |
| Eicosapentaenoic acid (C20:5 n-3) | 0.30 | 0.15 | 0.09 | 0.12 |
| Docosahexaenoic acid (C22:6 n-3) | 0.36 | 0.16 | 0.08 | 0.03 |
| Total SFA | 38.83 | 38.09 | 0.65 | 0.26 |
| Total MUFA | 42.29 | 47.70 | 1.48 | <0.01 |
| Total PUFA | 19.28 | 14.80 | 1.72 | 0.02 |
| Total n-3 PUFA3 | 1.35 | 0.87 | 0.15 | <0.01 |
| Total n-6 PUFA4 | 17.90 | 13.28 | 1.12 | <0.01 |
| PUFA:SFA ratio5 | 0.50 | 0.39 | 0.05 | 0.03 |
| n-6:n-3 PUFA ratio6 | 14.20 | 17.29 | 1.70 | 0.10 |
| Atherogenic index | 0.49 | 0.48 | 0.09 | 0.43 |

1Pigs (*n* = 36) were fed either a corn-soybean meal diet containing 1.5% soybean oil (SOY1.5) or diet containing 3% soybean oil (SOY3.0). Values represent the least square means from a subset of pigs (*n*= 36; 18 pigs/treatment).

2SEM = standard error of the least square means.

3Total n-3 PUFA = {[C18:3 n-3] + [C20:5 n-3] + [C22:6 n-3]}.

4Total n-6 PUFA = C18:2 n-6.

5PUFA:SFA ratio = total PUFA/total SFA.

6Σ n-6/Σ n-3 PUFA ratio.

Table 2: Effects of dietary treatments on fatty acid profile of liver tissueof pigs

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Fatty acid (%) | Dietary treatment | | | | Pooled SEM2 | *p-value* |
| SOY1.5 | SOY3.0 |  |  |
| Saturated fatty acid (SFA) |  |  |  |  |  |  |
| Myristic acid (C14:0) | 0.73 | 0.98 |  |  | 0.05 | <0.01 |
| Palmitic acid (C16:0) | 20.92 | 22.98 |  |  | 0.40 | <0.01 |
| Stearic acid (C18:0) | 25.48 | 21.28 |  |  | 1.06 | <0.01 |
| Monounsaturated fatty acid (MUFA) |  |  |  |  |  |  |
| Palmitoleic acid (C16:1) | 0.66 | 0.93 |  |  | 0.05 | <0.01 |
| Oleic acid (C18:1 n-9) | 21.36 | 27.84 |  |  | 1.06 | <0.01 |
| Polyunsaturated fatty acid (PUFA) |  |  |  |  |  |  |
| Linoleic acid (C18:2 n-6) | 27.02 | 23.64 |  |  | 0.67 | <0.01 |
| Alpha-linolenic acid (C18:3 n-3) | 1.42 | 1.17 |  |  | 0.10 | 0.07 |
| Eicosapentaenoic acid (C20:5 n-3, EPA) | 0.58 | 0.27 |  |  | 0.11 | 0.04 |
| Docosahexaenoic acid (C22:6 n-3, DHA) | 1.18 | 0.99 |  |  | 0.11 | 0.17 |
| Total SFA | 46.69 | 45.24 |  |  | 1.03 | 0.31 |
| Total MUFA | 22.01 | 28.78 |  |  | 1.04 | <0.01 |
| Total PUFA | 30.79 | 26.06 |  |  | 0.55 | <0.01 |
| Total n-3 PUFA3 | 3.75 | 2.42 |  |  | 0.37 | <0.01 |
| Total n-6 PUFA4 | 27.02 | 23.64 |  |  | 0.67 | <0.01 |
| PUFA:SFA ratio5 | 0.67 | 0.58 |  |  | 0.02 | <0.01 |
| n-6:n-3 PUFA ratio6 | 8.51 | 9.90 |  |  | 0.50 | 0.05 |
| Atherogenic index | 0.42 | 0.51 |  |  | 0.01 | <0.01 |

1Pigs (*n* = 35) were fed either a corn-soybean meal diet containing 1.5% soybean oil (SOY1.5) or diet containing 3% soybean oil (SOY3.0). Values represent the least square means from a subset of pigs (*n*= 35; 17pigs/SOY1.5; 18 pigs/SOY3.0).

2SEM = standard error of the least square means.

3Total n-3 PUFA = {[C18:3 n-3] + [C20:5 n-3] + [C22:6 n-3]}.

4Total n-6 PUFA = C18:2 n-6.

5PUFA:SFA ratio = total PUFA/total SFA.

6Σ n-6/Σ n-3 PUFA ratio.

Table 3. Common differentially expressed genes between the two tissues comparisons, in the skeletal muscle and liver tissue of pigs fed with two different levels of soybean oil in the diet (1.5 % and 3.0 % of soybean oil).

|  |  |  |
| --- | --- | --- |
| **Gene common** | **Description** | **Reference** |
| ENSSSCG00000009578  Cyclin dependent kinase 20 (*CDK20)* | Cell cycle related kinase. Its expression is related to the activation of β-catenin-TCF signaling and cell cycle progression. Can activate cyclin-dependent kinase 2 which is related to cell growth. | [39]  [40] |
| ENSSSCG00000014903  Coiled-coil domain containing 90B *(CCDC90B)* | Paralog of the MCUR1 gene (Mitochondrial Calcium Uniporter Regulator 1) which is related to the Ca, cAMP and lipid signaling pathways. | [40] |
| ENSSSCG00000022842  LOC100525692 | Protein encoding gene. | [40] |
| ENSSSCG00000022842  Alpha-1,3-Glucosyltransferase  *(ALG6)* | Related to N-Linked Glycosylation. | [40] |
| ENSSSCG00000017914  Glycolipid Transfer Protein Domain-Containing Protein 2  *GLTPD2* | Participates in the transfer of glycolipids. | [40] |
| ENSSSCG00000051557 | - | - |

Table 4. Pathway maps by MetaCore software (*p-value* <0.10) from the list of differentially expressed genes (FDR 10%) in the skeletal muscle of pigs fed with two different levels of soybean oil in the diet

|  |  |  |
| --- | --- | --- |
| **Pathway maps** | ***p-value*** | **DEG¹** |
| Fatty Acid Omega Oxidation | 3,33E-02 | *AL3A2* |
| Leukotriene 4 biosynthesis and metabolism | 4,42E-02 | *AL3A2* |
| *TNF-alpha, IL-1* beta induces dyslipidemia and inflammation in obesity and type 2 diabetes in adipocytes | 4,64E-02 | *AZGP1* |
| Breakdown of CD4+ T cell peripheral tolerance in type 1 diabetes mellitus | 5,39E-02 | *CD4* |
| Triacylglycerol metabolism p.1 | 6,56E-02 | *AL3A2* |
| Oxidative stress in adipocyte dysfunction in type 2 diabetes and metabolic syndrome X | 6,99E-02 | *AL3A2* |
| Peroxisomal branched chain fatty acid oxidation” | 9,08E-02 | *AL3A2* |

¹ Differentially expressed genes (DEG).

Table 5. Process Networks by MetaCore software (*p-value* <0.10) from the list of differentially expressed genes (FDR 10%) in the skeletal muscle of pigs fed with two different levels of soybean oil in the diet

|  |  |  |
| --- | --- | --- |
| **Process Networks** | ***p-value*** | **DEG¹** |
| Chemostaxis | 1,80E-03 | *CCR10, GPCRs, CD4* |
| Cell adhesion\_Leucocyte chemostaxis | 3,78E-03 | *CCR10, GPCRs, CD4* |
| Immune response\_Antigen presentation | 4,60E-03 | *CD4, AZGP1* |
| Signal transduction\_Leptin signaling | 1,56E-02 | *A2M, T-A2MG* |
| Inflammation\_Kallikrein-kinin system | 4,43E-02 | *A2M, T-A2MG* |
| Reproduction\_Male sex differentiation | 6,99E-02 | *Tektin 1, AKAP3* |

¹ Differentially expressed genes (DEG).

Table 6: Pathway maps with DEG between SOY1.5 vs SOY3.0 in liver tissue enriched in significant pathways (p <0.10)

|  |  |  |
| --- | --- | --- |
| **Pathway maps** | ***p-value*** | **DEG¹** |
| HSP70 and HSP40-dependent folding in Huntington's disease | 1.034E-2 | *BAG-1, ST13 (Hip)* |
| Inhibition of remyelination in multiple sclerosis: regulation of cytoskeleton proteins | 3.022E-2 | *MAPT, MELC* |
| Tau pathology in Alzheimer disease | 4.543E-2 | *MAPT, PP2C* |
| Mitochondrial dysfunction in neurodegenerative diseases | 5.153E-2 | *ANT* |
| Dual role of *p53* in transcription deregulation in Huntington's Disease | 7.179E-2 | *p21* |
| LRRK2 in neuronal apoptosis in Parkinson's disease | 9.869E-.0.2 | *ANT* |

¹ Differentially expressed genes (DEG).