Supplementary File – for Online Publication Only

Effect of feed supplementation with live *Saccharomyces cerevisiae* on intestinal transcriptome profile of weaning pigs orally challenged with *Escherichia coli* F4

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Supplementary Table S1Comparison of the transcriptome profile of the intestinal mucosa, 24 hours after challenge with Escherichia coli F4ac (ETEC), in pigs supplemented (AB) or not (CO) with colistin.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene | AB1  (log2) | CO1  (log2) | Fold  Change | *P*-value  (AB vs.  CO) | Full name | Biological function |
| Genes up-regulated in AB group | | | | | | |
| ENPP7 | 7.2 | 5.35 | 3.6 | 0.02 | Ectonucleotide pyrophosphatase / phosphodiesterase 7 | Digests sphingomyelin |
| SEC14L2 | 6.92 | 5.31 | 3.07 | 0.04 | SEC14-like protein 2 | Lipid-binding protein |
| CA12 | 7.48 | 5.89 | 3.01 | 0.04 | Carbonic anhydrases 12 | Catalyses the reversible hydration of  carbon dioxide |
| DNASE1L3 | 8.4 | 6.84 | 2.95 | 0.04 | Deoxyribonuclease I-Like 3 | DNA breakdown during apoptosis |
| SLC5A4 | 7.94 | 6.44 | 2.82 | 0.04 | Solute carrier family 5 member 4 |  |
| GPT2 | 7.93 | 6.5 | 2.7 | 0.01 | Glutamic pyruvate transaminase (alanine aminotransferase) 2 | Arginine metabolism |
| SCD | 8.98 | 7.87 | 2.16 | <0.01 | Stearoyl-CoA desaturase | Cell growth and differentiation |
| APOC3 | 10.51 | 9.43 | 2.12 | 0.03 | Apolipoprotein C-III | Synthesis of lipids |
| Genes down-regulated in AB group | | | | | | |
| GCNT3 | 9.6 | 10.62 | -2.02 | 0.02 | Glucosaminyl (N-Acetyl) Transferase 3,  Mucin Type | Mucin biosynthesis |
| GPR126 | 8.45 | 9.51 | -2.09 | 0.05 | G-protein coupled receptor 126 | Up-regulated by bacterial lipopolysaccharides (LPS). |
| CCL20 | 5.95 | 7.56 | -3.05 | 0.03 | Chemokine (C-C Motif) Ligand 20 | Response to infection by various enteropathogenic bacteria or exposure to bacterial flagellin |
| DUOX2 | 5.36 | 7.18 | -3.53 | 0.02 | Dual oxidase 2 | Activation of bactericidal molecule |

1AB: Colistin + challenge with ETEC; CO: no live yeast + challenge with ETEC.

Supplementary Table S2Comparison of the transcriptome profile of the intestinal mucosa, 24 hours after challenge with Escherichia coli F4ac (ETEC), in pigs supplemented for all the experimental period (PR) or not (CO) with S. cerevisiae CNCM I-4407.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Gene | PR1  (log2) | CO1  (log2) | Fold  Change | *P-*value  (PR vs. CO) | Full name | Biological function |
| Genes up-regulated in PR group | | | | | | |
| TAF7 | 6.45 | 5.27 | 2.27 | 0.04 | Transcription initiation factor TFIID subunit 7 | participate in the assembly of the [transcription](http://en.wikipedia.org/wiki/Transcription_(biology)) preinitiation [complex](http://en.wikipedia.org/wiki/Protein_complex) |
| SCD | 8.99 | 7.87 | 2.17 | 0.02 | Stearoyl-CoA desaturase (delta-9-desaturase) | cell growth and differentiation |
| CD69 | 5.77 | 4.77 | 1.99 | 0.05 | Cluster of Differentiation 69 | lymphocyte proliferation |
| GZMK | 7.31 | 6.43 | 1.84 | 0.04 | Granzyme K | Innate immune response |
| PRKCQ | 6.58 | 5.72 | 1.82 | <0.01 | Protein kinase C theta type | cellular signalling pathways |
| NLN | 6.86 | 6.07 | 1.73 | <0.01 | Neurolysin (Metallopeptidase M3 Family) | gastrointestinal motility |
| IKZF3 | 6.85 | 6.1 | 1.68 | 0.03 | Ikaros family zinc finger protein 3 | B lymphocyte proliferation and  differentiation |
| RASGRP1 | 7.45 | 6.76 | 1.62 | 0.03 | RAS guanyl-releasing protein 1 | T and B-cells development/ homeostasis/differentiation. |
| CD8A | 7.24 | 6.56 | 1.6 | 0.02 | Cluster of Differentiation 8a | Co-receptor on T lymphocytes  to recognize antigens |
| IKZF1 | 6.48 | 5.85 | 1.54 | 0.02 | Ikaros family zinc finger protein 1 | lymphocyte differentiation. |
| SH3KBP1 | 7.2 | 6.6 | 1.52 | 0.05 | SH3-Domain Kinase Binding Protein 1 | protein-protein interactions |
| FASN | 7.36 | 6.76 | 1.51 | 0.04 | Fatty Acid Synthase | catalyse the synthesis of palmitate |
| Genes down-regulated in PR group | | | | | | |
| IFRD1 | 9.16 | 9.81 | -1.57 | 0.001 | Interferon-related developmental regulator 1 | cell differentiation |
| PFKFB3 | 8.32 | 9.01 | -1.61 | 0.05 | 6-Phosphofructo-2-Kinase/Fructose-2,6-Biphosphatase 3 | protects against inflammatory response |
| LIPH | 8.49 | 9.19 | -1.62 | 0.02 | Lipase member H | cell proliferation and motility |
| VEGFA | 5.86 | 6.55 | -1.62 | 0.02 | Vascular Endothelial Growth Factor A | cell growth/promoting cell migration/inhibiting apoptosis |
| P2RY4 | 6.6 | 7.4 | -1.74 | 0.02 | P2Y purinoceptor 4 | G-protein-coupled receptor signalling |
| TFF3 | 8.17 | 9.01 | -1.79 | 0.03 | Trefoil factor 3 | stabilize the mucus layer/affects healing of the epithelium |
| CCL20 | 5.97 | 7.56 | -3.02 | 0.04 | Chemokine (C-C Motif) Ligand 20 | Bacterial recognition |

1PR: preventive administration pattern of live yeast (5x1010 CFU/kg of feed from day 0 to sacrifice) + challenge with ETEC; CO: no live yeast + challenge with ETEC.

Supplementary Table S3Comparison of the transcriptome profile of the intestinal mucosa, 24 hours after challenge with Escherichia coli F4ac (ETEC), in pigs supplemented from the day of the infection (CM) or not (CO) with S. cerevisiae CNCM I-4407.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | CM1  (log2) | CO1  (log2) | Fold Change | *P*-value  (CM vs. CO) | Full name | | Biological function |
| Genes up-regulated in CM group | | | | | | | |
| SCD | 9.2 | 7.87 | 2.51 | 0.001 | Stearoyl-CoA desaturase | cell growth and differentiation | |
| PCK1 | 5.01 | 3.97 | 2.07 | 0.01 | Phosphoenolpyruvate carboxykinase 1 | [gluconeogenesis](http://en.wikipedia.org/wiki/Gluconeogenesis) | |
| IGF1 | 6.66 | 5.64 | 2.02 | 0.03 | Insulin-like growth factor 1 | cell growth and proliferation | |
| NLN | 6.86 | 6.07 | 1.74 | 0.01 | Neurolysin (metallopeptidase M3 family) | gastrointestinal motility | |
| PRR19 | 4.32 | 3.59 | 1.66 | <0.01 | Proline-Rich Protein 19 | diseases associated with PRR19 include gastric cancer | |
| UNC5CL | 8.44 | 7.72 | 1.65 | <0.001 | Unc-5 Homolog C (C. Elegans)-Like | epithelial inflammation and immunity | |
| PPARGC-1 | 6.74 | 6.04 | 1.63 | 0.05 | Peroxisome proliferator-activated receptor gamma coactivator 1-alpha | inhibits pro-inflammatory cytokine production | |
| PEMT | 6.31 | 5.62 | 1.62 | 0.05 | phosphatidylethanolamine N-methyltransferase | cell membrane | |
| SLC6A20 | 9.42 | 8.73 | 1.62 | <0.01 | Solute carrier family 6, member 20 | cellular transport | |
| CMTM7 | 7.63 | 6.94 | 1.61 | 0.04 | Chemokine-Like Factor  Superfamily Member 7 | chemokine-like factor | |
| PDCL | 6.73 | 6.06 | 1.59 | 0.02 | Phosducin-like protein | regulate G-protein signalling | |
| STEAP4 | 5.36 | 4.7 | 1.58 | 0.02 | Six-transmembrane epithelial antigen of prostate 4 | regulation of inflammatory cytokines | |
| FBXW5 | 7.6 | 6.94 | 1.57 | <0.01 | F-box/WD repeat-containing protein 5 | phosphorylation-dependent | |
| NNT | 9.13 | 8.5 | 1.55 | 0.04 | NAD(P) transhydrogenase | production of NADPH | |
| BCKDK | 7.25 | 6.63 | 1.54 | 0.03 | Branched Chain Ketoacid  Dehydrogenase Kinase | amino acids catabolism in the  mitochondrion | |
| THOC5 | 6.87 | 6.26 | 1.52 | 0.03 | THO complex subunit 5 homolog | cell differentiation processes | |
| SOX6 | 6.03 | 5.42 | 1.52 | 0.03 | Transcription factor SOX-6 | transcriptional activator | |
| ALDH6A1 | 8.47 | 7.88 | 1.51 | 0.03 | Aldehyde Dehydrogenase 6 Family,  Member A1 | valine and pyrimidine catabolic  pathways | |
| Genes down-regulated in CM group | | | | | | | |
| CENPK | 6.42 | 7.03 | -1.52 | 0.02 | Centromere protein K | | mitotic progression |
| TRPC1 | 4.67 | 5.32 | -1.57 | <0.01 | Transient receptor potential channel 1 | | nonspecific cation channel |
| FGL2 | 7.52 | 8.17 | -1.57 | 0.01 | Fibrinogen-like protein 2 | | immunoregulatory - effector cytokine  of Treg cells |
| SAMD9 | 8.48 | 9.13 | -1.57 | 0.04 | Sterile Alpha Motif Domain  Containing 9 | | cellular proliferation |
| IL7R | 4.94 | 5.6 | -1.58 | 0.02 | Interleukin 7 Receptor | | survival factor for mature T cells  and IEC |
| ABCC2 | 8.54 | 9.21 | -1.59 | 0.02 | ATP-Binding Cassette,  Sub-Family C (CFTR/MRP), Member 2 | | oxidative stress |
| CPT1A | 6.9 | 7.61 | -1.64 | 0.01 | Carnitine palmitoyltransferase I | | mitochondrial enzyme |
| FABP1 | 9.64 | 10.46 | -1.77 | 0.03 | Fatty acid-binding protein 1 | | bind bile acids |
| PLIN2 | 7.47 | 8.39 | -1.9 | 0.02 | Perilipin 2 | | [adipocyte](http://en.wikipedia.org/wiki/Adipocyte) differentiation |
| CD163 | 5.13 | 6.43 | -2.47 | 0.04 | (Cluster of Differentiation 163 | | induction of local inflammation |

1CM: Competitive administration of live yeast (5x1010 CFU/kg of feed for 1 day after ETEC challenge) + challenge with ETEC; CO: no live yeast + challenge with ETEC