**SUPPLEMENTAL MATERIALS**

**Table S1.** GenBank accession number, hybridization position, sequence and amplicon size of primers *for Bos taurus* used to analyze gene expression by qPCR.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Accession no. | Symbol | Primers | Primers (5’-3’) | Amplicon size (bp) |
| EU276074.1 | *IL10* | F.171 | GAAGGACCAACTGCACAGCTT | 98 |
|  |  | R.268 | AAAACTGGATCATTTCCGACAAG |  |
| NM\_174093.1 | *IL1B* | F.453 | TCCACCTCCTCTCACAGGAAA | 100 |
|  |  | R.552 | TACCCAAGGCCACAGGAA |  |
| NM\_001040555.1 | *IRAK1* | F.950 | CCTCAGCGACTGGACATCCT | 103 |
|  |  | R.1052 | GGACGTTGGAACTCTTGACATCT |  |
| NM\_001039957.1 | *ITGAM* | F. 268 | GGCTTGTCTCTTGCATTTGCT | 95 |
|  |  | R. 362 | CCATTTGCATAGGTGTTCTCCTT |  |
| NM\_001113298.2 | *MPO* | F. 1311 | AGCCATGGTCCAGATCATCAC | 105 |
|  |  | R. 1415 | ACCGAGTCGTTGTAGGAGCAGTA |  |
| NM\_001014382.2 | *MYD88* | F. 367 | GGAGGACTGCCAAAAGTATATTCTG | 105 |
|  |  | R. 471 | GCCATGTCATTTATCCGAGTTATG |  |
| NM\_001076409.1 | *NFKB1* | F.172 | TCAACCGGAGATGCCACTAC | 95 |
|  |  | R.266 | ACACACGTAACGGAAACGAAATC |  |
| NM\_001011678.2 | *NRF2* | F.135 | AGGACATGGATTTGATTGAC | 272 |
|  |  | R.406 | TACCTGGGAGTAGTTGGCA |  |
| NM\_174182.1 | *SELL* | F.588 | CTCTGCTACACAGCTTCTTGTAAACC | 104 |
|  |  | R.691 | CCGTAGTACCCCAAATCACAGTT |  |
| NM\_174615.2 | *SOD1* | F.355 | TGTTGCCATCGTGGATATTG | 143 |
|  |  | R.497 | CAGCGTTGCCAGTCTTTGTA |  |
| NM\_201527.2 | *SOD2* | F. 620 | TGTGGGAGCATGCTTATTACCTT | 95 |
|  |  | R. 714 | TGCAGTTACATTCTCCCAGTTGA |  |
| NM\_001034661.2 | *TRAF6* | F. 675 | AGAACAGATGCCCAATCACTATGAT | 100 |
|  |  | R. 774 | GTGATTCCTCTGCATCTTTTCATG |  |
| NM\_001205428.3 | *TLN1* | F. 942 | TTCCTGCCCAAGGAGTATGTG | 100 |
|  |  | R. 1041 | AGCGTACCTTGGCCTCAATCT |  |
| NM\_174197.2 | *TLR2* | F.1201 | AAGAGTCACAATAGAAAG | 102 |
|  |  | R.1302 | GCTATTTATGACACATCCAA |  |
| NM\_174198.6 | *TLR4* | F.102 | GCTGTTTGACCAGTCTGATTGC | 102 |
|  |  | R.203 | GGGCTGAAGTAACAACAAGAGGAA |  |
| EU276079.1 | *TNFA* | F.438 | TCTCAAGCCTCAAGTAACAAGCC | 100 |
|  |  | R.537 | CCATGAGGGCATTGGCATAC |  |
| NM\_001191370.1 | *VCL* | F. 1778 | CATCTCAGCTCCAAGACTCCTTAAA | 103 |
|  |  | R. 1880 | TTGATGGGAGTCGTGGTATCAC |  |
| XM\_005194417.3 | *ZBP1* | F. 88 | CCCAGGAGACACAGACCTTGA | 100 |
|  |  | R. 187 | GGGCACTTGGAATTTCTTTAACA |  |

**Table S2.** Genes selected for transcript profiling in bovine polymorphonuclear leukocytes (PMNL) and their biological functions1

|  |  |  |
| --- | --- | --- |
| Gene Name | Symbol | Function |
| Tumor Necrosis Factor Alpha | *TNFA* | This gene encodes a multifunctional pro-inflammatory cytokine that belongs to the tumor necrosis factor (TNF) superfamily. This cytokine is mainly secreted by macrophages. |
| Nuclear Factor Of Kappa Light Polypeptide Gene Enhancer In B-Cells 1 | *NFKB1* | NFKB is a transcription regulator that is activated by various intra- and extracellular stimuli such as cytokines, oxidant-free radicals, ultraviolet irradiation, and bacterial or viral products. Activated NFKB translocates into the nucleus and stimulates the expression of genes involved in a wide variety of biological functions. |
| Interleukin 1 B | *IL1B* | Produced by activated macrophages, IL-1 stimulates thymocyte proliferation by inducing IL-2 release, B-cell maturation and proliferation, and fibroblast growth factor activity. Potent pro-inflammatory cytokine. |
| Interleukin 10 | *IL10* | Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T-cells. |
| TNF receptor associated factor 6 | *TRAF6* | This protein mediates signaling from members of the TNF receptor superfamily as well as the Toll/IL-1 family. This protein functions as a signal transducer in the NF-kappaB pathway. |
| Myeloid differentiation primary response 88 | *MYD88* | This gene encodes a cytosolic adapter protein that plays a central role in the innate and adaptive immune response. This protein functions as an essential signal transducer in the interleukin-1 and Toll-like receptor signaling pathways. |
| Toll-like receptor 2 | *TLR2* | The protein encoded by this gene is a member of the Toll-like receptor (TLR) family which plays a fundamental role in pathogen recognition and activation of innate immunity. |
| Toll-like receptor 4 | *TLR4* | This receptor has also been implicated in signal transduction events induced by lipopolysaccharide (LPS) found in most gram-negative bacteria. |
| Selectin-L | *SELL* | Mediates the adherence of lymphocytes to endothelial cells of high endothelial venules in peripheral lymph nodes. Promotes initial tethering and rolling of leukocytes in endothelia. |
| Interleukin 1 receptor associated kinase 1 | *IRAK1* | This gene is partially responsible for IL1-induced upregulation of the transcription factor NF-kappa B. |
| Z-DNA biding protein 1 | *ZBP1* | The encoded protein plays a role in the innate immune response by binding to foreign DNA and inducing type-I interferon production. |
| Integrin subunit alpha M | *ITGAM* | This gene encodes the integrin alpha M chain. The alpha M beta 2 integrin is important in the adherence of neutrophils and monocytes to stimulated endothelium, and also in the phagocytosis of complement coated particles. |
| Talin 1 | *TLN1* | This gene encodes a cytoskeletal protein that is concentrated in areas of cell-substratum and cell-cell contacts. |
| Vinculin | *VCL* | Vinculin is a cytoskeletal protein associated with cell-cell and cell-matrix junctions, where it is thought to function as one of several interacting proteins involved in anchoring F-actin to the membrane. |
| Nuclear factor erythroid 2-related factor 2 | *NRF2* | The encoded transcription factor regulates genes which contain antioxidant response elements (ARE) in their promoters; many of these genes encode proteins involved in response to injury and inflammation which includes the production of free radicals. |
| Superoxide dismutase 1 | *SOD1* | The protein encoded by this gene binds copper and zinc ions and is one of two isozymes responsible for destroying free superoxide radicals in the body. The encoded isozyme is a soluble cytoplasmic protein. |
| Superoxidase dismutase 2 | *SOD2* | This gene is a member of the iron/manganese superoxide dismutase family. It encodes a mitochondrial protein that forms a homotetramer and binds one manganese ion per subunit. |
| Myeloperoxidase | *MPO* | Myeloperoxidase (MPO) is a heme protein synthesized during myeloid differentiation that constitutes the major component of neutrophil azurophilic granules. This enzyme produces hypohalous acids central to the microbicidal activity of neutrophils. |

1Entrez Gene; National Center for Biotechnology Information (https://www.ncbi.nlm.nih.gov/gene/).



**Figure S1.** Independent analysis of the Parity × treatment effect in polymorphonuclear leukocyte mRNA expression of interleukin 10 (gene symbol *IL10*; *P* = 0.04), Z-DNA binding protein 1 (gene symbol *ZBP1*; *P* < 0.01), vinculin (gene symbol *VCL*; *P* = 0.02), superoxide dismutase 1 (gene symbol *SOD1*; *P* = 0.05). Difference in mRNA expression between YC cows and control in 2nd lactation cows is denoted by an asterisk (\*) for *IL10* (*P* = 0.01), *ZBP1* (*P* < 0.01), *VCL* (*P* = 0.01), and *SOD1* (*P* = 0.02). Values are least square means; error bars represent standard errors.



**Figure S2.** Percent change in blood albumin and gamma-glutamyl transferase (GGT) relative to -30 DIM in cows (n = 8/treatment) supplemented with a basal diet (Control) or a basal diet plus yeast culture fermentation production (YC) from -31 ± 6 d relative to parturition through 50 DIM. Mean separations between treatments at a given time point were evaluated when a treatment × time (Trt × T) interaction (P ≤ 0.05) was observed, and differences (\*) were declared at a Tukey-adjusted P ≤ 0.05. Values are means, and SE are represented by vertical bars.