**SUPPLEMENTAL MATERIALS**

**Table S1.** Numbers and percentages of pro- and anti-apoptosis genes that were up-regulated and down-regulated in THP-1 macrophages incubated with live or dead microsporidia.a

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **THP-1 treatment and replicate number** | **Pro-Apoptosis Genes** | | | **Anti-Apoptosis Genes** | | |
| **Number of genes (percent of up- vs down-regulated genes)** | | | **Number of genes (percent of up- vs down-regulated genes)** | | |
|  | **Up-regulated** |  | **Down regulated** | **Up-regulated** |  | **Down-regulated** |
| ***E. cuniculi* - dead** |  |  |  |  |  |  |
| 1 | 42 (93.3) |  | 3 (6.7) | 4 (21.1) |  | 15 (78.9) |
| 2 | 44 (93.6) |  | 3 (6.7) | 9 (42.9) |  | 12 (57.1) |
| 3 | 44 (93.6) |  | 3 (6.7) | 9 (42.9) |  | 12 (57.1) |
| **mean** | **43.3 (93.5)** |  | **3 (6.7)** | **7 (36.1)** |  | **13 (63.9)** |
| ***E. cuniculi* - live** |  |  |  |  |  |  |
| 1 | 7 (14) |  | 40 (85.1) | 11 (52.4) |  | 10 (47.6) |
| 2 | 19 (39.6) |  | 29 (60.4) | 17 (81) |  | 4 (19) |
| 3 | 13 (27.7) |  | 34 (72.3) | 15 (75) |  | 5 (25) |
| **mean** | **13 (27.5)** |  | **34 (72.5)** | **14 (69.4)** |  | **6 (30.6)** |
| ***V. corneae* - dead** |  |  |  |  |  |  |
| 1 | 16 (37.2) |  | 27 (62.8) | 8 (40) |  | 12 (60) |
| 2 | 23 (47.9) |  | 25 (52.1) | 10 (50) |  | 10 (50) |
| 3 | 26 (60.5) |  | 17 (39.5) | 10 (62.5) |  | 6 (37.5) |
| **mean** | **22 (48.5)** |  | **23 (51.5)** | **9 (50)** |  | **9 (50)** |
| ***V. corneae* - live** |  |  |  |  |  |  |
| 1 | 14 (31.1) |  | 31 (68.9) | 8 (40) |  | 12 (60) |
| 2 | 20 (43.5) |  | 26 (56.5) | 10 (52.6) |  | 9 (47.4) |
| 3 | 31 (67.4) |  | 15 (32.6) | 14 (73.7) |  | 5 (26.3) |
| **mean** | **22 (47.4)** |  | **24 (52.6)** | **11 (55.2)** |  | **9 (44.8)** |

a  The apoptosis RT2 Profiler PCR Array kit was used to assay gene expression of treated THP-1 compared to medium-treated controls. Genes that increased or decreased at least 2-fold relative to medium-treated macrophages were included. Gene expression was normalized against beta-2 microglobulin that was expressed at the same levels in treated and untreated samples. Number of pro-apoptosis genes = 47. Number of anti-apoptosis genes = 21. Number of apoptosis regulatory genes = 15

**Table S2.** Mean expression levels of apoptosis-related genes by THP-1 macrophages cultured with live or dead *E. cuniculi* or *V. corneae* spores.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene Name** | **Gene Description** | **Experimental treatmenta** | | | |
| **E.c.live** | **E.c. dead** | **V.c. live** | **V.c. dead** |
| *ABL1* | C-abl oncogene 1, receptor tyrosine kinase | **+4.65** | -1.48 | +2.20 | -1.92 |
| *AKT1* | V-akt murine thymoma viral oncogene hom.1, Ser/Thr kinase | +1.43 | -1.07 | **+4.38** | **-7.90** |
| *BAD* | BCL2-associated agonist of cell death | -1.58 | +1.83 | **+10.72** | **-3.36** |
| *BAG1* | BCL2-associated athanogene | **+2.60** | -0.38 | +1.7 | -1.24 |
| *BAG3* | BCL2-associated athanogene 3 | **+2.17** | **-2.51** | +1.52 | -0.35 |
| *BAG4* | BCL2-associated athanogene 4 | -1.45 | +0.83 | -0.94 | **+2.79** |
| *BAK1* | BCL2-antagonist/killer 1 | **-2.70** | +1.52 | -0.17 | +1.91 |
| *BAX* | BCL2-associated X protein | +1.75 | +1.04 | **+7.67** | +1.1 |
| *BCL2* | B-cell CLL/lymphoma 2 | +2.04 | **-1.91** | +2.36 | -3.13 |
| *BCL2L1* | BCL2-like 1 | -1.52 | +2.14 | **+4.41** | **-3.20** |
| *BCL2L11* | BCL2-like 11 (apoptosis facilitator) | -1.80 | **+2.96** | **+4.13** | **-5.08** |
| *BCLAF1* | BCL2-associated transcription factor 1 | -1.96 | **+2.93** | **-2.20** | +1.70 |
| *BIRC2* | Baculoviral IAP repeat-containing 2 | **+**0.52 | -1.13 | -2.04 | **+2.89** |
| *BIRC6* | Baculoviral IAP repeat-containing 6 | +1.89 | **-2.79** | +1.56 | -0.98 |
| *BNIP3* | BCL2/adenovirus E1B 19kDa interacting protein 3 | **-2.62** | +1.92 | +1.60 | -2.18 |
| *BNIP3L* | BCL2/adenovirus E1B 19kDa interacting protein 3-like | **+4.48** | **-2.30** | +0.52 | +0.07 |
| *CARD8* | Caspase recruitment domain family, member 8 | **-2.94** | +2.18 | -1.9 | +1.7 |
| *CASP1* | Caspase 1, apoptosis-related cysteine peptidase | **-4.78** | **+2.82** | **+8.17** | **-12.44** |
| *CASP3* | Caspase 3, apoptosis-related cysteine peptidase | -1.88 | +1.84 | **-3.83** | **+3.68** |
| *CASP4* | Caspase 4, apoptosis-related cysteine peptidase | -2.24 | +2.03 | **+3.32** | **-3.21** |
| *CASP9* | Caspase 9, apoptosis-related cysteine peptidase | **-5.33** | +2.29 | -0.66 | +1.37 |
| *CIDEA* | Cell death-inducing DFFA-like effector a | **-3.91** | -1.22 | +2.46 | -0.84 |
| *CRADD* | CASP2 and RIPK1 domain with death domain adaptor | +1.58 | **+3.64** | +0.11 | +1.40 |
| *DARK1* | Death-associated protein kinase 1 | -1.48 | **+2.97** | **-2.49** | n/d4 |
| *DFFA* | DNA fragmentation factor, 45kDa, alpha polypeptide | -1.67 | **-1.80** | -2.02 | +1.26 |
| *FADD* | Fas (TNFRSF6)-associated via death domain | -1.69 | **+3.14** | -2.19 | **+3.09** |
| *GADD45A* | Growth arrest and DNA-damage-inducible, alpha | +1.47 | **-2.12** | -0.48 | +1.99 |
| *LTA* | Lymphotoxin alpha (TNF superfamily, member 1) | **-2.66** | +2.51 | **-5.85** | **+7.72** |
| *NOL3* | Nucleolar protein 3 (apoptosis repressor with CARD domain) | +1.69 | **-2.55** | +0.08 | -0.91 |
| *PYCARD* | ­PYD and CARD domain containing | +1.10 | **+3.15** | +0.73 | -0.53 |
| *CD27* | TNFR family, CD27 molecule | +1.76 | **-2.36** | **-3.99** | **+5.24** |
| *CD40LG* | TNFR family, CD40 ligand | **+2.74** | **-5.56** | **-4.33** | **+4.94** |
| *FAS* | Fas (TNF receptor superfamily, member 6) | **-2.32** | +1.64 | 0.32 | -1.88 |
| *TNFRSF11B* | Tumor necrosis factor receptor superfamily, member 11b | **-3.05** | **+2.61** | **+3.94** | **-3.87** |
| *TNFRSF1A* | Tumor necrosis factor receptor superfamily, member 1A | **+2.81** | -1.63 | **-3.01** | **+4.25** |
| *TNFRSF21* | Tumor necrosis factor receptor superfamily, member 21 | **+2.16** | **-1.72** | -2.02 | +2.32 |
| *TP53* | Tumor protein p53 | **+2.46** | +1.59 | **+100.6** | **-46.4** |
| *TP53BP2* | Tumor protein p53 binding protein, 2 | **-2.87** | **+2.65** | **-2.98** | **+3.91** |
| *TP73* | Tumor protein p73 | **+2.11** | **+2.75** | **-3.15** | **+10.16** |
| *TRADD* | TNFRSF1A-associated via death domain | **-2.78** | +1.57 | **-2.56** | +1.86 |
| *TRAF2* | TNF receptor-associated factor 2 | +0.29 | -2.04 | +3.25 | **-3.58** |
| *TRAF4* | TNF receptor-associated factor 4 | -1.82 | +2.40 | **+3.58** | **-3.38** |

a Mean log2-fold expression of genes are shown in comparison to gene expression in medium-treated macrophages averaged from three replicates per group. The 10 maximal up- and down-regulated genes in each group are indicated in bold font. Anti-apoptotic genes are shown in non-highlighted fields, pro-apoptotic genes are highlighted in dark grey fields and regulatory genes are highlighted in light grey fields. E.c. = *Encephalitozoon cuniculi*;V.c. = *Vittaforma corneae.*