Supplementary Material

# Supplementary Data

**Table 1**

Summary of values of water chemistry data for all treatments.The results are presented as means ± standard deviation.

|  |  |  |  |
| --- | --- | --- | --- |
| variable | Coral | Coral exposed to algae | Coral contact with algae |
| 27oC | 30oC | 27oC | 30oC | 27oC | 30oC |
| Temperature [oC] | 27.1±0.1 | 30±0.2 | 27.1±0.1 | 30±0.2 | 27.1±0.1 | 30±0.2 |
| PH | 8.0±0.03 | 8.0±0.04 | 8.0±0.03 | 8.0 | 8.0±0.03 | 8.0 |
| Salinity | 32.1±0.4 | 32.1±0.4 | 32.1±0.4 | 32±0.3 | 32±0.3 | 32±0.2 |

**Table 2**

Two way ANOVA output of different variables for *A.hyacinthus* with bold values indicating significant effects on the variable. *F=F-value; p=p-value(significance <0.05).*

|  |  |  |  |
| --- | --- | --- | --- |
| Variable | Source of variation | F | p |
| Growth Rate | Algae | F(2,8) = 0.7 | 0.4 |
| Temperature | F(1,4) = 0.7 | 0.5 |
| Interaction | F(2,8) = 0.3 | 0.7 |
| Zooxanthellae | Algae | F(2,8) = 2.1 | 0.18 |
| Temperature | F(1,4) = 6.2 | 0.07 |
| Interaction | F(2,8) = 6.9 | **0.02** |
| Chl *a* | Algae | F(2,8) = 1.4 | 0.3 |
| Temperature | F(1,4) = 5.1 | 0.09 |
| Interaction | F(2,8) = 10.8 | **<0.01** |
| Protein | Algae | F(2,8) = 0.8 | 0.46 |
| Temperature | F(1,4) = 1.8 | 0.25 |
| Interaction | F(2,8) = 4.3 | 0.05 |
| SOD | Algae | F(2,8) = 0.17 | 0.86 |
| Temperature | F(1,4) = 0.03 | 0.86 |
| Interaction | F(2,8) = 6.3 | **0.02** |
| CAT | Algae | F(2,8) = 16.4 | **<0.01** |
| Temperature | F(1,4) = 2.8 | 0.17 |
| Interaction | F(2,8) = 43.5 | **<0.01** |

**Table 3**

Data of various physiological indicators, the results are presented as means ± standard deviation. The results are presented as means ± standard deviation.

|  |  |
| --- | --- |
| Variable | Zooxanthellae×106 (cell cm-2) |
|  | 27℃ | Mean±sd | 30℃ | Mean±sd |
| Coral | 0.29 | 0.33 | 0.32 | 0.32±0.02 | 0.03 | 0.06 | 0.06 | 0.05±0.02 |
| Coral exposed to algae | 0.24 | 0.11 | 0.11 | 0.15±0.07 | 0.07 | 0.21 | 0.18 | 0.15±0.07 |
| Coral contact with algae | 0.15 | 0.22 | 0.36 | 0.24±0.11 | 0.12 | 0.28 | 0.28 | 0.23±0.09 |
|  | Chl *a* (µg cm-2) |
|  | 27℃ | Mean±sd | 30℃ | Mean±sd |
| Coral | 5.3 | 4.1 | 6.7 | 5.34±1.3 | 0.25 | 0.47 | 0.27 | 0.33±0.12 |
| Coral exposed to algae | 1.8 | 1.8 | 1.1 | 1.54±0.4 | 0.29 | 3.47 | 3.35 | 2.37±1.8 |
| Coral contact with algae | 3.8 | 2.5 | 4.0 | 3.43±0.8 | 1.28 | 4.89 | 1.31 | 2.47±2.1 |
|  | Protein (mg cm-2) |
|  | 27℃ | Mean±sd | 30℃ | Mean±sd |
| Coral | 1.17 | 0.72 | 0.59 | 0.83±0.3 | 0.33 | 0.31 | 0.48 | 0.37±0.09 |
| Coral exposed to algae | 0.54 | 0.71 | 0.29 | 0.52±0.21 | 0.38 | 0.64 | 0.75 | 0.59±0.19 |
| Coral contact with algae | 0.78 | 0.39 | 0.42 | 0.53±0.22 | 0.44 | 0.49 | 0.35 | 0.43±0.07 |
|  | Growth Rate (mg cm-2 d-1) |
|  | 27℃ | Mean±sd | 30℃ | Mean±sd |
| Coral | 0.45 | 1.06 | 1.74 | 1.09±0.64 | 0.51 | 1.2 | 0.79 | 0.83±0.22 |
| Coral exposed to algae | 1.13 | 0.42 | 0.73 | 0.76±0.35 | 0.56 | 1.5 | 0.46 | 0.84±0.58 |
| Coral contact with algae | 0.97 | 0.77 | 0.53 | 0.76±0.22 | 0.41 | 0.49 | 0.61 | 0.5±0.1 |
|  | SOD (U mgprot-1) |
|  | 27℃ | Mean±sd | 30℃ | Mean±sd |
| Coral | 149.1 | 231.1 | 241.6 | 207.3±50.6 | 426.9 | 635.4 | 341.3 | 467.8±151.3 |
| Coral exposed to algae | 316.8 | 282.3 | 515.3 | 371.5±125.8 | 213 | 288.4 | 227.7 | 243±40 |
| Coral contact with algae | 501.1 | 417.3 | 261.3 | 393.3±121.7 | 282.7 | 273.3 | 286.8 | 280.9±7 |
|  | CAT (U mgprot-1) |
|  | 27℃ | Mean±sd | 30℃ | Mean±sd |
| Coral | 3.76 | 8.92 | 12.64 | 8.44±4.46 | 27.01 | 17.34 | 33.18 | 25.84±7.99 |
| Coral exposed to algae | 6.14 | 12.49 | 25.71 | 14.78±9.98 | 51.01 | 41.34 | 43.29 | 45.21±5.11 |
| Coral contact with algae | 48.54 | 53.79 | 51.73 | 51.35±2.64 | 14.46 | 24.4 | 25.03 | 21.3±5.93 |

**Tab.4**

Statistics summary of RNA-Seq of *A. hyacinthus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Samples | Clean reads | Mapped reads | Comparison rate | Q30 | GC content |
| LD | 21 476 650 | 14 574 005 | 67.9% | 96% | 46.1% |
| LH | 20 347 432 | 13 261 939 | 65.2% | 94.6% | 46.5% |
| LM | 20 993 422 | 13 807 161 | 65.8% | 94.4% | 47.1% |
| HD | 21 290 828 | 14 314 966 | 67.3% | 95.9% | 43.9% |
| HH | 21 142 687 | 14 068 385 | 66.6% | 95.9% | 46.4% |
| HM | 21 336 087 | 14 179 496 | 66.5% | 96% | 45.5% |
| Total | 126 587 106 |  |  |  |  |

Notes：Q30 represent 0.1% probabilities of base error，respectively

**Tab. 5**

qPCR Primer sequences

|  |  |  |  |
| --- | --- | --- | --- |
| Gene | Primer sequence（5’-3’） | Size（bp） | Reference |
| β-Actin | F:ATGACAGAGGATGAGGGTAGAAA | 194 | Designed by author |
| R:GAGAAGAGGTCCCGACGAATA |
| SODC | F：TGATACCAACCTGCCTCT | 186 | Designed by author |
| R：TGCGTGAACTTGAAATAAC |
| CATE | F：TGGAAACAATACGCCAATCT | 124 | Designed by author |
| R：AGTGATGAAATCCCAGAACAT |
| CYP3A | F：ATCGCCGCAGAAATCGTG | 163 | Designed by author |
| R：CGTAGCCAGCCAATAGAAAG |
| HSP90 | F：GCTGTTTGCCGAAGTGAC | 144 | Designed by author |
| R：GAGGCTGAAGAATGGTATCT |
| HSP40 | F：TGGTCAGATGCCAAGTCC | 96 | Designed by author |
| R：CGGCTAAATACAGGGTGC |
| CalM | F：ACCTCTTTCGTTTCGCTGAC | 145 | Designed by author |
| R：CTTCCTGAATCGCTGTTGCT |
| Casp8 | F：GCACAGCCTACGACATTG | 108 | Designed by author |
| R：GACACGACCGTTCATTCA |
| Casp7 | F：TTCAGTTCCCTTGCGTTTA | 175 | Designed by author |
| R：CCTCCCTTCCATCTACACC |
| ALG9 | F：TCGTTATGGCTCCAAGAATC | 193 | Designed by author |
| R：ACCGTCGTGAGAACAGTTTC |
| Galaxin | F：CGATGCCACCCTTTCCC | 137 | Designed by author |
| R：CTGGTACGCCTACAGGTTTGT |
| GPX | F：GAATCATCTCGCCACCTGAC | 96 | Designed by author |
| R：GCATACTTCGGAGCCTACTGA |
| ATG5 | ACTGTAAACCGACGCCTGAT | 173 | Designed by author |
| GGAACAAACTCCCGCAACA |

**Tab. 6**

DEGs statistics in all treatments. Select FDR < 0.001 and shown as LH, LM and HD groups vs LD group, HH and HM groups vs HD group.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| DEGs  | LH groups | LM groups  | HD groups | HH groups | HM groups |
| Up-regulated | 5 621 | 5 313 | 1 590 | 16 | 15 |
| Down-regulated | 6 413 | 7 160 | 11 | 2 861 | 313 |

**Tab. 7**

FPKM expression map of different biological processes regulated by DEGs. The results are presented as means ± standard deviation.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| DEGs | LD groups | LH groups | LM groups | HD groups | HH groups | HM groups |
| Rab5 | 75.3±7.5 | 10.6±0.3 | 13.1±4.9 | 91.8±18.9 | 74.5±5.5 | 64.4±36.8 |
| Rab10 | 0.5±0.1 | 42.7±6.8 | 32.7±6.5 | 0.6±0.5 | 0.5±0.2 | 16.9±28.6 |
| Rab22 | 54±8.8  | 0.7±0.2 | 0.6±0.2 | 66.5±4.2 | 52.4±13.3 | 41.1±34.0 |
| Rab11A | 13.3±3.2 | 79.1±6.0 | 58.9±7.1 | 12.9±0.6 | 8.9±3.1 | 44.3±51.4 |
| ATG5 | 0.2±0.1 | 12.5±2.4 | 10.7±2.7 | 0.4±0.1 | 0.2±0.1 | 3.8±6.0 |
| ATG10 | 17.4±11.4 | 0.8±0.2 | 1.3±0.1 | 8.6±4.9 | 16.5±15.2 | 10.1±8.9 |
| CalM | 71.2±7.8 | 3.9±0.6 | 2.7±0.3 | 97.7±6.4 | 54.7±10.0 | 54.3±43.8 |
| Galaxin | 5.9±1.2 | 0.9±0.8 | 0.7±0.9 | 48.5±10.0 | 9.4±12.0 | 11.1±12.5 |
| SODC | 38.4±17.4 | 8.8±12.2 | 20.1±1.1 | 107.2±34.8 | 33.5±14.0 | 24.1±19.4 |
| CAT | 4.6±1.9 | 12.8±2.0 | 14.0±4.1 | 11.3±4.2 | 11.7±9.1 | 23.6±19.0 |
| GPX | 0.9±0.1 | 0.04±0.08 | 0.03±0.05 | 1.5±0.6 | 0.6±0.1 | 0.4±0.2 |
| Hsp70 | 16.8±5.8 | 3.8±0.6 | 3.3±1.1 | 26.3±5.4 | 11.8±3.5 | 10.7±4.3 |
| HSP40 | 7.2±0.72 | 27.2±8.4 | 20.8±4.9 | 11.2±1.0 | 7.5±1.2 | 14.6±10.1 |
| CYP3A | 9.5±1.9 | 0.1±0.1 | 0.2±0.2 | 20.9±3.1 | 12.3±2.5 | 7.6±6.6 |
| TNFRSF14 | 3.1±3.0 | 0.7±0.1 | 0.4±0.2 | 8.7±5.3 | 2.8±3.4 | 1.4±0.8 |
| TLR2 | 2.6±0.1 | 10.4±2.6 | 13.3±0.7 | 6.1±1.6 | 2.7±1.3 | 8.3±7.9 |
| TRAF3 | 5.3±2.0 | 0.3±0.2 | 0.2±0.2 | 19.0±1.5 | 2.5±2.3 | 7.3±7.6 |
| IFI47 | 3.2±0.2 | 3.3±0.1 | 4.4±0.9 | 15.1±9.5 | 3.4±0.5 | 5.5±1.2 |
| TRAF5 | 2.9±2.9 | 0.9±1.0 | 0.8±0.8 | 9.1±7.1 | 0.9±0.2 | 5.4±7.7 |
| MYD88 | 18.3±4.4 | 2.1±0.1 | 1.3±0.4 | 38.7±5.1 | 19.1±7.2 | 17.7±13.4 |
| Casp3 | 0.3±0.1 | 10.0±0.8 | 9.7±0.6 | 1.2±0.6 | 0.3±0.1 | 5.4±8.2 |
| Casp8 | 20.7±1.9 | 3.0±1.0 | 0.9±1.5 | 25.6±1.3 | 18.9±5.7 | 15.9±11.3 |
| Casp7 | 4.3±1.0 | 11.0±3.0 | 5.0±3.3 | 9.9±3.5 | 4.4±1.6 | 9.1±5.7 |
| FADD | 7.8±1.7 | 5.0±0.7 | 4.7±0.7 | 11.5±0.7 | 7.0±1.5 | 7.1±1.5 |
| HIRA2 | 1.1±0.4 | 9.9±2.3 | 8.1±1.6 | 1.6±0.2 | 0.75±0.3 | 4.9±6.7 |

**Tab. 8**

The log2FoldChange value of qRT-PCR and RNA-seq. Compared with LD group, DEGs verification of LH, LM and HD groups . And compared with HD group, the DEGs verification of HH and HM. The results are presented as means ± standard deviation.

|  |  |  |  |
| --- | --- | --- | --- |
| Group | DEGs | qRT-PCR | RNA-seq |
| LH | Casp8 | -1.4±1.2 | -2.9 |
| Casp7 | 1.1±0.6 | 1.3 |
| CYP3A | -2.0±2.9 | -3.3 |
| ATG5 | 3.1±0.5 | 5.9 |
| LM | Casp8 | -1.6±0.4 | -6.3 |
| Hsp90 | -1.1±0.3 | -1.3 |
| ATG5 | 3.2±0.4 | 5.5 |
| HD | CAT | 0.6±0.6 | 2.3 |
| SODC | 2.3±0.7 | 2.5 |
| CYP3A | 1.3±0.9 | 2.1 |
| CalM | 1.2±0.7 | 1.9 |
| Galaxin | 5±0.8 | 3.9 |
| Casp7 | 3.5±0.4 | 2.2 |
| HH | SODC | -2.9±0.4 | -3.0 |
| CYP3A | -1.8±0.2 | -2.0 |
| Hsp40 | -1.6±1.1 | -2.0 |
| CalM | -1.6±0.7 | -2.1 |
| CASP7 | -3.2±1.2 | -2.7 |
| HM | ALG9 | -1.3±0.4 | -3.0 |
| CalM | -1.6±0.7 | -2.1 |
| GPX | -1.6±2.4 | -2.8 |

**Tab. 9**

Distribution of gene ontologies which were signifificantly enriched in KEGG pathways of LH , LM, HD, HH and HM treatments. The difference gourps selected as LH, LM and HD compared with LD, HH and HM compared with HD.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Group | Pathway | ko ID | DEGs in Pathway | All gene in Pathway | P-value |
| LH | FoxO signaling pathway | ko04068 | 102 | 193 | <0.01 |
| Inositol phosphate metabolism | ko00562 | 71 | 140 | <0.01 |
| mTOR signaling pathway | ko04150 | 139 | 311 | <0.01 |
| Endocytosis | ko04144 | 210 | 491 | <0.01 |
| Autophagy - animal | ko04140 | 164 | 375 | <0.01 |
| Apoptosis - multiple species | ko04215 | 39 | 72 | <0.01 |
| Various types of N-glycan biosynthesis | ko00513 | 48 | 96 | <0.01 |
| Glycosphingolipid biosynthesis - lacto and neolacto series | ko00601 | 14 | 21 | <0.01 |
| Glycosaminoglycan biosynthesis - keratan sulfate | ko00533 | 7 | 8 | <0.01 |
| Neuroactive ligand-receptor interaction | ko04080 | 103 | 233 | <0.01 |
| Other glycan degradation | ko00511 | 27 | 50 | <0.01 |
| beta-Alanine metabolism | ko00410 | 42 | 85 | <0.01 |
| Glycosaminoglycan degradation | ko00531 | 33 | 64 | <0.01 |
| Cell adhesion molecules | ko04514 | 14 | 22 | <0.01 |
| TGF-beta signaling pathway | ko04350 | 50 | 105 | <0.01 |
| Other types of O-glycan biosynthesis | ko00514 | 28 | 54 | 0.01 |
| Lysine degradation | ko00310 | 64 | 142 | 0.01 |
| Notch signaling pathway | ko04330 | 54 | 118 | 0.02 |
| Mannose type O-glycan biosynthesis | ko00515 | 15 | 27 | 0.03 |
| Wnt signaling pathway | ko04310 | 115 | 278 | 0.03 |
| LM | mTOR signaling pathway | ko04150 | 151 | 311 | <0.01 |
| Autophagy - animal | ko04140 | 176 | 375 | <0.01 |
| Glycosaminoglycan degradation | ko00531 | 39 | 64 | <0.01 |
| FoxO signaling pathway | ko04068 | 97 | 193 | <0.01 |
| TGF-beta signaling pathway | ko04350 | 55 | 105 | <0.01 |
| Inositol phosphate metabolism | ko00562 | 69 | 140 | <0.01 |
| Endocytosis | ko04144 | 213 | 491 | <0.01 |
| Neuroactive ligand-receptor interaction | ko04080 | 107 | 233 | <0.01 |
| Glycosaminoglycan biosynthesis - keratan sulfate | ko00533 | 7 | 8 | <0.01 |
| Apoptosis - multiple species | ko04215 | 38 | 72 | <0.01 |
| Glycosphingolipid biosynthesis - lacto and neolacto series | ko00601 | 14 | 21 | <0.01 |
| Various types of N-glycan biosynthesis | ko00513 | 48 | 96 | <0.01 |
| Other types of O-glycan biosynthesis | ko00514 | 29 | 54 | 0.01 |
| Cell adhesion molecules | ko04514 | 14 | 22 | 0.01 |
| ECM-receptor interaction | ko04512 | 67 | 144 | 0.02 |
| Other glycan degradation | ko00511 | 26 | 50 | 0.03 |
| Glycosaminoglycan biosynthesis - heparan sulfate / heparin | ko00534 | 19 | 35 | 0.03 |
| Wnt signaling pathway | ko04310 | 119 | 278 | 0.04 |
| Mannose type O-glycan biosynthesis | ko00515 | 15 | 27 | 0.04 |
| Lysosome | ko04142 | 182 | 440 | 0.05 |
| HD | ErbB signaling pathway | ko04012 | 7 | 19 | <0.01 |
| Cytosolic DNA-sensing pathway | ko04623 | 5 | 20 | <0.01 |
| TNF signaling pathway | ko04668 | 5 | 22 | <0.01 |
| Cell adhesion molecules | ko04514 | 5 | 22 | <0.01 |
| Herpes simplex virus 1 infection | ko05168 | 11 | 107 | 0.01 |
| Toll-like receptor signaling pathway | ko04620 | 5 | 36 | 0.02 |
| Inositol phosphate metabolism | ko00562 | 12 | 140 | 0.03 |
| MAPK signaling pathway | ko04010 | 9 | 95 | 0.03 |
| FoxO signaling pathway | ko04068 | 15 | 193 | 0.04 |
| Phenylalanine metabolism | ko00360 | 5 | 41 | 0.04 |
| Glyoxylate and dicarboxylate metabolism | ko00630 | 10 | 115 | 0.04 |
| Tryptophan metabolism | ko00380 | 10 | 121 | >0.05 |
| Glycosaminoglycan degradation | ko00531 | 6 | 64 | >0.05 |
| Phosphatidylinositol signaling system | ko04070 | 16 | 238 | >0.05 |
| Ubiquitin mediated proteolysis | ko04120 | 23 | 367 | >0.05 |
| Ether lipid metabolism | ko00565 | 5 | 52 | >0.05 |
| Butanoate metabolism | ko00650 | 5 | 54 | >0.05 |
| N-Glycan biosynthesis | ko00510 | 6 | 70 | >0.05 |
| Autophagy - animal | ko04140 | 23 | 375 | >0.05 |
| Protein processing in endoplasmic reticulum | ko04141 | 28 | 472 | >0.05 |
| HH | Endocytosis | ko04144 | 67 | 491 | <0.01 |
| TNF signaling pathway | ko04668 | 7 | 22 | <0.01 |
| NOD-like receptor signaling pathway | ko04621 | 17 | 93 | <0.01 |
| Apoptosis - multiple species | ko04215 | 14 | 72 | <0.01 |
| ErbB signaling pathway | ko04012 | 6 | 19 | <0.01 |
| Vitamin digestion and absorption | ko04977 | 3 | 5 | <0.01 |
| Cell adhesion molecules | ko04514 | 6 | 22 | 0.01 |
| Lysosome | ko04142 | 53 | 440 | 0.01 |
| Ether lipid metabolism | ko00565 | 10 | 52 | 0.01 |
| Sulfur relay system | ko04122 | 4 | 13 | 0.02 |
| Glycosaminoglycan biosynthesis - heparan sulfate / heparin | ko00534 | 7 | 35 | 0.03 |
| Basal transcription factors | ko03022 | 10 | 59 | 0.03 |
| Glycerophospholipid metabolism | ko00564 | 20 | 151 | 0.04 |
| ECM-receptor interaction | ko04512 | 19 | 144 | 0.049 |
| Phosphonate and phosphinate metabolism | ko00440 | 4 | 18 | >0.05 |
| MAPK signaling pathway | ko04010 | 13 | 95 | >0.05 |
| FoxO signaling pathway | ko04068 | 23 | 193 | >0.05 |
| N-Glycan biosynthesis | ko00510 | 10 | 70 | >0.05 |
| Amino sugar and nucleotide sugar metabolism | ko00520 | 15 | 117 | >0.05 |
| Toll-like receptor signaling pathway | ko04620 | 6 | 36 | >0.05 |
| HM | Neuroactive ligand-receptor interaction | ko04080 | 5 | 233 | 0.02 |
| Cytokine-cytokine receptor interaction | ko04060 | 1 | 8 | 0.049 |
| Arachidonic acid metabolism | ko00590 | 3 | 140 | >0.05 |
| Apoptosis - multiple species | ko04215 | 2 | 72 | >0.05 |
| Glutathione metabolism | ko00480 | 3 | 182 | >0.05 |
| Herpes simplex virus 1 infection | ko05168 | 2 | 107 | >0.05 |
| Phenylalanine, tyrosine and tryptophan biosynthesis | ko00400 | 1 | 26 | >0.05 |
| Vitamin B6 metabolism | ko00750 | 1 | 26 | >0.05 |
| Taurine and hypotaurine metabolism | ko00430 | 1 | 27 | >0.05 |
| Pyrimidine metabolism | ko00240 | 2 | 114 | >0.05 |
| Influenza A | ko05164 | 1 | 28 | >0.05 |
| Ubiquinone and other terpenoid-quinone biosynthesis | ko00130 | 1 | 28 | >0.05 |
| Notch signaling pathway | ko04330 | 2 | 118 | >0.05 |
| Peroxisome | ko04146 | 3 | 263 | >0.05 |
| Phenylalanine metabolism | ko00360 | 1 | 41 | >0.05 |
| ECM-receptor interaction | ko04512 | 2 | 144 | >0.05 |
| Nucleotide excision repair | ko03420 | 2 | 145 | >0.05 |
| Riboflavin metabolism | ko00740 | 1 | 42 | >0.05 |
| Purine metabolism | ko00230 | 3 | 278 | >0.05 |
| Thiamine metabolism | ko00730 | 1 | 49 | >0.05 |