# Supporting Information

## Addition of vegetable oil to improve triterpenoids production in liquid fermentation of medicinal fungus *Antrodia cinnamomea*

Biaobiao Luo[1, †], Linghui Meng1[, †], Yang Yang[1], Mohammad Omar Faruque[2], Jiuliang Zhang[3], Xiaohua Li[1], and Xuebo Hu[1, *]

[1]Laboratory of Natural Medicine and Molecular Engineering, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan, 430070, China

[2]Ethnobotany and Pharmacognosy Laboratory, Department of Botany, University of Chittagong, Chittagong, Bangladesh, 4331, Bangladesh

[3]Department of Food and Nutrition, College of Food Science and Technology, Huazhong Agricultural University, Wuhan, 430070, China

[†]These authors contribute equally to this work

[*]Correspondence: xuebohu@mail.hzau.edu.cn; Tel.: 0086-180-6250-3982

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## Table S1. Differential gene expression analysis under oil treatment

| GeneID | Diff | $log_2FC$ | P value | Annotation |
|---|---|---|---|---|
| ACg009074 | Up | 2.4764384 | 6.24E-41 | *N/A* |
| ACg008441 | Up | 1.9032387 | 2.52E-263 | MFS multidrug transporter |
| ACg007137 | Up | 1.8273310 | 2.91E-151 | FAD-binding domain |
| ACg007232 | Up | 1.3742482 | 6.09E-94 | *N/A* |
| ACg006971 | Up | 1.3313856 | 3.35E-65 | *N/A* |
| ACg003473 | Up | 1.0991426 | 1.23E-59 | Contributes to surface hydrophobicity, which is important for processes such as association of hyphae in reproductive structures, dispersal of aerial spores and adhesion of pathogens to host structures |
| ACg007233 | Up | 1.2536028 | 3.77E-59 | *N/A* |
| ACg007080 | Up | 1.0477856 | 2.52E-58 | Glycosyl hydrolase family 71 |
| ACg007231 | Up | 1.2236576 | 3.43E-57 | *N/A* |
| ACg004204 | Up | 1.1993258 | 5.50E-54 | Lipase, hormone-sensitive |
| ACg001758 | Up | 1.8775421 | 1.19E-51 | Transporter |
| ACg008756 | Up | 1.3238808 | 4.06E-48 | Riboflavin aldehyde-forming enzyme |
| ACg008408 | Up | 1.0155715 | 1.30E-45 | Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| ACg007935 | Up | 1.1143509 | 3.24E-43 | Glycoside hydrolase family 18 |
| ACg002304 | Up | 1.3127590 | 4.13E-31 | DnaJ |
| ACg001962 | Up | 1.0074369 | 5.82E-24 | *N/A* |
| ACg001023 | Up | 1.1127260 | 2.44E-18 | Major royal jelly protein |
| ACg007004 | Up | 1.1074562 | 6.39E-06 | *N/A* |
| ACg000642 | Up | 1.1132242 | 6.93E-04 | *N/A* |
| ACg005259 | Up | 1.3883839 | 1.24E-02 | *N/A* |
| ACg006389 | Up | 4.2664892 | 1.24E-02 | *N/A* |
| ACg000159 | Down | -2.6447621 | 2.67E-39 | GMC oxidoreductase |
| ACg005309 | Down | -1.9272622 | 6.61E-214 | Flavin-binding monooxygenase-like |
| ACg004077 | Down | -1.7686331 | 3.41E-213 | Putative cyclase |
| ACg008952 | Down | -1.9389313 | 2.19E-190 | Occurs in almost all aerobically respiring organisms and serves to protect cells from the toxic effects of hydrogen peroxide |
| ACg008851 | Down | -1.9482786 | 5.87E-179 | Inherit from NOG: Conserved hypothetical, protein |
| ACg005974 | Down | -2.0091623 | 8.64E-171 | Transporter |
| ACg005318 | Down | -1.8888673 | 2.36E-161 | Alpha-glucosidase |
| ACg003983 | Down | -1.6388108 | 1.49E-159 | *N/A* |
| ACg001915 | Down | -2.0403733 | 1.73E-159 | Tripeptidyl peptidase |
| ACg001732 | Down | -2.0431351 | 3.41E-150 | *N/A* |
| ACg004524 | Down | -1.4515484 | 1.32E-136 | Glucosylceramidase |
| ACg008852 | Down | -2.0514382 | 6.34E-134 | *N/A* |
| ACg003815 | Down | -1.3891564 | 2.16E-133 | Carboxylesterase family |

| | | | | |
|---|---|---|---|---|
| ACg001538 | Down | -1.5607301 | 4.12E-133 | Acetohydroxy acid isomer reductase, catalytic domain |
| ACg008856 | Down | -1.9944572 | 1.75E-132 | *N/A* |
| ACg008849 | Down | -2.4582420 | 1.28E-125 | Tryptophan dimethylallyl transferase |
| ACg006871 | Down | -1.4637502 | 2.77E-122 | Alcohol dehydrogenase GroES-like domain |
| ACg007557 | Down | -1.3410480 | 3.12E-121 | Chitinase |
| ACg002632 | Down | -1.4393805 | 3.10E-119 | Protein of unknown function (DUF3421) |
| ACg008931 | Down | -1.6389817 | 3.47E-117 | Sugar (and other) transporter |
| ACg002220 | Down | -1.6840855 | 1.27E-116 | Sugar (and other) transporter |
| ACg002874 | Down | -2.0513526 | 1.60E-112 | *N/A* |
| ACg007041 | Down | -1.3149942 | 6.83E-112 | Alpha/beta hydrolase fold |
| ACg004095 | Down | -1.7989585 | 3.33E-108 | Potassium voltage-gated channel, shaker-related subfamily, beta member |
| ACg004345 | Down | -1.3329592 | 1.01E-95 | carnitine |
| ACg008854 | Down | -1.2516958 | 1.39E-91 | Mono-carboxylate |
| ACg000818 | Down | -1.2058513 | 3.03E-91 | Short chain dehydrogenase |
| ACg001328 | Down | -1.5625523 | 4.90E-90 | Glycoside hydrolase family 5 |
| ACg000668 | Down | -1.1708956 | 2.17E-86 | Sugar (and other) transporter |
| ACg005777 | Down | -1.3716691 | 9.59E-86 | Catechol dioxygenase |
| ACg005832 | Down | -1.2883867 | 1.08E-84 | Synthetase |
| ACg005818 | Down | -1.1699218 | 1.80E-83 | *N/A* |
| ACg005663 | Down | -1.4005451 | 2.49E-78 | AMP-binding enzyme |
| ACg004913 | Down | -1.1310721 | 1.73E-77 | Phenol 2-monooxygenase |
| ACg003553 | Down | -2.1912079 | 4.11E-76 | L-fucose permease |
| ACg007125 | Down | -1.3822664 | 3.11E-74 | Sterol 24-c-methyltransferase |
| ACg006921 | Down | -1.1075541 | 6.97E-73 | HMG (high mobility group) box |
| ACg003531 | Down | -1.0530572 | 7.97E-72 | *N/A* |
| ACg003902 | Down | -1.3584996 | 1.72E-71 | Short chain dehydrogenase |
| ACg007556 | Down | -1.0857264 | 3.90E-70 | LysM domain |
| ACg007106 | Down | -1.0456316 | 4.17E-69 | Mitochondrial |
| ACg000575 | Down | -1.3913229 | 6.43E-69 | *N/A* |
| ACg006920 | Down | -1.0155080 | 2.26E-67 | Arginyl-tRNA synthetase |
| ACg007009 | Down | -1.2633044 | 2.31E-66 | *N/A* |
| ACg001117 | Down | -1.2774508 | 1.24E-65 | Domain protein |
| ACg002692 | Down | -1.0162451 | 4.17E-65 | Dienelactone hydrolase family protein |
| ACg003331 | Down | -1.6113675 | 7.12E-64 | *N/A* |
| ACg002589 | Down | -1.2067805 | 1.76E-63 | Disrupter of telomere silencing protein Dot5 |
| ACg004240 | Down | -1.4517098 | 4.14E-62 | Inherit from fuNOG: NF-X1 finger and helicase domain protein |
| ACg004264 | Down | -1.0622700 | 7.10E-58 | Alanine--glyoxylate aminotransferase 2 |
| ACg008798 | Down | -1.1849239 | 8.83E-57 | Mannitol-1-phosphate dehydrogenase |
| ACg003543 | Down | -1.1426180 | 9.50E-56 | Acyl-CoA dehydrogenase, middle domain |
| ACg000540 | Down | -1.2463001 | 1.04E-55 | *N/A* |
| ACg008853 | Down | -1.2468301 | 7.70E-55 | Cytochrome P450 |

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|---|---|---|---|---|
| ACg004062 | Down | -1.1058458 | 1.51E-47 | BTB/POZ domain |
| ACg003358 | Down | -1.1853109 | 1.78E-47 | Hydrolase family 10 |
| ACg007894 | Down | -1.0622058 | 1.95E-47 | Cytochrome p450 |
| ACg002169 | Down | -1.1017845 | 4.04E-47 | Sugar (and other) transporter |
| ACg002889 | Down | -1.0743323 | 6.82E-47 | Alpha beta hydrolase |
| ACg005148 | Down | -1.6833600 | 1.59E-46 | *N/A* |
| ACg000141 | Down | -1.2171070 | 2.80E-46 | Flavin containing amine oxidoreductase |
| ACg002089 | Down | -1.0318278 | 6.50E-46 | Acyl-CoA dehydrogenase, N-terminal domain |
| ACg008857 | Down | -2.5154666 | 8.18E-45 | *N/A* |
| ACg006199 | Down | -1.0017287 | 4.59E-43 | Protease, serine, 16 (thymus) |
| ACg001118 | Down | -1.0395905 | 4.13E-39 | Domain protein |
| ACg000529 | Down | -1.0253118 | 4.98E-37 | *N/A* |
| ACg006397 | Down | -1.2844515 | 5.30E-37 | Major Facilitator Superfamily |
| ACg005648 | Down | -1.1033594 | 1.37E-36 | Trehalase |
| ACg000195 | Down | -1.0828408 | 6.82E-36 | *N/A* |
| ACg002633 | Down | -1.1709579 | 4.29E-35 | Receptor |
| ACg006019 | Down | -1.2800294 | 5.39E-33 | *N/A* |
| ACg001071 | Down | -1.5184314 | 8.51E-33 | *N/A* |
| ACg002511 | Down | -1.0736893 | 3.18E-27 | *N/A* |
| ACg001964 | Down | -1.8960253 | 3.73E-27 | Inherit from fuNOG: fumarylacetoacetate hydrolase |
| ACg002896 | Down | -1.1677912 | 4.34E-23 | *N/A* |
| ACg002895 | Down | -2.0335373 | 2.85E-21 | *N/A* |
| ACg000821 | Down | -1.3903883 | 7.63E-20 | Short chain dehydrogenase |
| ACg006829 | Down | -1.3909792 | 8.93E-20 | Sugar (and other) transporter |
| ACg005150 | Down | -1.2701456 | 1.92E-19 | *N/A* |
| ACg000075 | Down | -1.1377992 | 5.60E-19 | Sugar (and other) transporter |
| ACg008451 | Down | -1.0639441 | 2.17E-18 | *N/A* |
| ACg000925 | Down | -1.4204323 | 1.88E-16 | *N/A* |
| ACg006427 | Down | -1.2455964 | 3.16E-16 | GDSL lipase acylhydrolase family protein |
| ACg003097 | Down | -1.0146153 | 2.45E-12 | Heat shock protein |
| ACg008090 | Down | -1.0354521 | 1.02E-08 | *N/A* |
| ACg008447 | Down | -1.0445379 | 3.75E-05 | Caspase domain |
| ACg008767 | Down | -1.3394176 | 1.80E-04 | *N/A* |
| ACg009239 | Down | -2.0768630 | 5.97E-04 | Inherit from COG: Retrotransposon protein |
| ACg000050 | Down | -1.7330041 | 6.68E-04 | *N/A* |
| ACg000808 | Down | -1.8046440 | 3.57E-03 | *N/A* |
| ACg005753 | Down | -1.1933009 | 5.53E-03 | *N/A* |
| ACg006627 | Down | -4.0019067 | 5.96E-03 | Inherit from fuNOG: reverse transcriptase |
| ACg003560 | Down | -4.3256940 | 9.48E-03 | *N/A* |

## Table S2. Amino acid sequences of hydrophobins

| Gene | Amino acid sequence |
|---|---|
| ACg003473 | MMFRTVLVLAFALSALSAPQSSSSQCDSGTIQCCDTVAPAYSASVAPVLKALKINVDDENK QVALGCGGSAVGVGAGSSCTSAPICCENNYFGLIGIGCISITL |
| ACg007231 | MMFRAVTFLTFALSALAVPQAPYVDQCNPGSVLCCDSVYSPSSVYATSLVKALQIDNVPQ DKQIATGCGGGGINVGGGSTCNSNPVCCERDGLGGLIGIGCAAIPVSI |
| ACg007232 | LRNPFILPSRTAIRTPSYIALSSHQAHRPLSFTIMMFRAVALLTFALSALAVPQYGPTSQCDS GSELCCDSVYSPGTVYATSLIKALNIDNVPVGHIATGCGGGGVNVGGGSTCNTNPVCCQG NALGGLIGVGCAAIPVSI |
| ACg007233 | MRLSLSLLSLALPLLALAAPQTFGPGPQCDGGPVECCDATYRADSPEGSAIMKAMKIDAR NVTGSTIIAAACGGGGVNVGGGSTCNNIPVCCNNTYFGLIGVGCASIPVSI |