**Deeper Understanding of the Mechanism Promoting Gall Formation of** ***Zizania latifolia* under Fenaminosulf Treatment.**

**Fang Li1, Juefeng Zhang1, Haiying Zhong1, Jianming Chen1\***

1 State Key Laboratory for Managing Biotic and Chemical Threats to the Quality and Safety of Agro-products, Hangzhou, 310021, China; Institute of Plant Protection and Microbiology, Zhejiang Academy of Agricultural Sciences, Hangzhou, 310021, China

**\* Correspondence:**

Jianming Chen

chenjm63@163.com

**Supplementary tables**

**Table S1** Pairedprimers used for qRT-PCR in *Ustilago esculenta*.

|  |  |  |
| --- | --- | --- |
| **Primers** | **Paired sequences (5′-3′) \*** | **Purpose** |
| qβ-actin-F/ R | CAATGGTTCGGGAATGTGC/GGGATACTTGAGCGTGAGGA | Detecting of *β-actin* transcript |
| q*mfa*1.2-F/ R | TGTTCTCCATCTTCACTCA/CGACAATACATGTGGAGTAG | Detecting of *mfa*1.2 transcript |
| q*mfa*1.3-F/R | GGACGCTCTTACTCTCTT/GCAACGATACATCCAGAA | Detecting of *mfa*1.3 transcript |
| q*pra*1-F/R | CGTTATGTCAGGCTTCTC/AGATGTAGGCGGATAGAG | Detecting of *pra*1 transcript |
| q*mfa*2.1-F/R | TCACTATCTTCGAGACTGTT/AGTAGTTGGCAAGCTGTC | Detecting of *mfa*2.1 transcript |
| q*mfa*2.3-F/R | TCGCCATTTTCTCTTTCTCGATGATGCAACCGCTAGA | Detecting of *mfa*2.3 transcript |
| q*pra*2-F/R | ATAGGCTTGTGCTGTAGT/CGACGAAGAATAACGGAAT | Detecting of *pra*2 transcript |
| q*ubc*2-F/R | TGGAGGAAGACGACGAAAGCT/CATGCTCATGGACTACCAGAGT | Detecting of *ubc*2 transcript |
| q*gpa*3-F/R | TGGGTAATTGCCTTTCTTCGAC/TGGATGATCTTCATCTGCTTGA | Detecting of *gpa*3 transcript |
| q*pkaC*-F/R | CATGAAGGAGGTCAAGGT/GCACATACACATCCAAGG | Detecting of *pkaC* transcript |
| q*kss*1-F/R | AATCCACGCAACATTCTC/ATCTTCTTGATGGCTACCT | Detecting of *kss*1 transcript |
| q*mkk*-F/R | CCATTCCATCAGCATCAG/CAAGTCGTGTTGTTGTAATC | Detecting of *mkk* transcript |
| q*ssk*-F/R | ACACATCTCGCAAGTAAG/GGCTTCCTTCTGGTATTG | Detecting of *ssk* transcript |
| q*chs*1-F/R | TCGTATCCTCCTCACATC/CATCATATCGTCATCGTCAT | Detecting of *chs*1 transcript |
| q*chs*2-F/R | GCCGACCTACATTATCATC/TCTTGACTTCCACCATCT | Detecting of *chs*2 transcript |
| q*chs*3-F/R | GGTGGTGTATGTGTTGTG/CGGTATCGTTGTGGAATC | Detecting of *chs*3 transcript |
| q*chs*4-F/R | ACTGCCTACTCTGAATCTT/GTCTCGTTGTCGTAATCG | Detecting of *chs*4 transcript |
| q*chs*5-F/R | TACATCTCACACCACCTC/ACCAGCGTAGTCAAGTAT | Detecting of *chs*5 transcript |

**Table S2** List of differentially expressed genesin *Zizania latifolia* under fenaminosulf stress.

|  |  |  |
| --- | --- | --- |
| Locus tag | Annotation | log2FoldChange |
| KEGG:zma04626 Plant-pathogen interaction  Sample number/Background number:18/209 Corrected P-value:0.000788571 | | |
| Zlat\_10034518 | WRKY transcription factor 2 WRKY2 | 1.8221 |
| Zlat\_10027326 | WRKY transcription factor 22 WRK22 | -2.296 |
| Zlat\_10006341 | WRKY transcription factor 27 WRK27 | -2.5964 |
| Zlat\_10028790 | WRKY transcription factor 33 WRK33 | -2.1091 |
| Zlat\_10017671 | WRKY transcription factor 33 WRK33 | -2.0059 |
| Zlat\_10004543 | Calcium-dependent protein kinase 14 CDPK14 | -3.4139 |
| Zlat\_10028613 | Calcium-dependent protein kinase 30 CDPK30 | -1.7203 |
| Zlat\_10008743 | Calcium-binding protein CML14 | -2.0117 |
| Zlat\_10041370 | Calcium-binding protein CML24 | -2.6476 |
| Zlat\_10006767 | Calcium-binding protein CML27 | -1.7111 |
| Zlat\_10004561 | Calcium-binding protein CML31 | -1.5199 |
| Zlat\_10006578 | Disease resistance protein 2 RPS2 | -1.8883 |
| Zlat\_10030262 | Chitin elicitor-binding protein | -1.7397 |
| Zlat\_10048179 | Respiratory burst oxidase homolog protein C | -1.8535 |
| Zlat\_10026801 | Respiratory burst oxidase homolog protein E | -1.7885 |
| Zlat\_10019842 | RPM1-interacting protein 4 RIN4 | -1.4583 |
| Zlat\_10038158 | PTI1-like tyrosine-protein kinase 3 PTI13 | -1.925 |
| Zlat\_10036946 | -//- | -1.8764 |
| KEGG:zma00940 Phenylpropanoid biosynthesis  Sample number/Background number:19/242 Corrected P-value: 0.000788571 | | |
| Zlat\_10041351 | Cationic peroxidase 1 PER1 | -3.1259 |
| Zlat\_10036307 | Peroxidase 1 PER1 | 2.246 |
| Zlat\_10007768 | Peroxidase 19 PER19 | 2.0968 |
| Zlat\_10029728 | Peroxidase 47 PER47 | -12.011 |
| Zlat\_10001910 | Peroxidase 52 PER52 | 2.1065 |
| Zlat\_10046751 | Peroxidase 52 PER52 | 2.9818 |
| Zlat\_10003203 | Peroxidase 72 PER72 | -2.7887 |
| Zlat\_10007582 | Cinnamyl alcohol dehydrogenase 5 CADH5 | -2.262 |
| Zlat\_10037056 | Cinnamyl alcohol dehydrogenase 6 CADH6 | -3.0534 |
| Zlat\_10004185 | Cinnamyl alcohol dehydrogenase 9 CADH9 | -1.9164 |
| Zlat\_10048065 | Probable inactive beta-glucosidase 14 BGL14 | -4.5313 |
| Zlat\_10047787 | Beta-glucosidase 30 BGL30 | 8.1727 |
| Zlat\_10045750 | Cytochrome P450 CYP73A100 | -2.0429 |
| Zlat\_10045747 | Cytochrome P450 CYP73A100 | -2.6201 |
| Zlat\_10015120 | Cinnamoyl-CoA reductase 1 CCR1 | -3.867 |
| Zlat\_10035005 | 4-coumarate--CoA ligase 5 4CL5 | -1.6962 |
| Zlat\_10016473 | Tricin synthase 1 | -1.9036 |
| Zlat\_10008844 | Cationic peroxidase SPC4 | -1.4769 |
| Zlat\_10045749 | Trans-cinnamate 4-monooxygenase | -2.7848 |
| KEGG:zma00908 Zeatin biosynthesis  Sample number/Background number:7/31 Corrected P-value: 0.000788571 | | |
| Zlat\_10001161 | Cytokinin dehydrogenase 4 CKX4 | -1.9672 |
| Zlat\_10032604 | Cytokinin dehydrogenase 5 CKX5 | -1.753 |
| Zlat\_10029015 | Cytokinin dehydrogenase 5 CKX5 | -1.9567 |
| Zlat\_10029016 | Cytokinin dehydrogenase 5 CKX5 | -2.1255 |
| Zlat\_10003044 | Cytokinin dehydrogenase 11 CKX11 | -1.6667 |
| Zlat\_10017743 | Cis-zeatin O-glucosyltransferase 1 CZOG1 | -2.8285 |
| Zlat\_10003321 | Adenylate isopentenyltransferase 1 IPT1 | -1.6601 |
| KEGG:zma04075 Plant hormone signal transduction  Sample number/Background number:20/355 Corrected P-value: 0.018559854 | | |
| Zlat\_10037646 | Indole-3-acetic acid-amido synthetase GH3.8 GH38 | -1.9171 |
| Zlat\_10005384 | Serine/threonine-protein kinase At4g35230 | 1.8145 |
| Zlat\_10007749 | serine/threonine-protein kinase At4g35230 | 2.4567 |
| Zlat\_10005792 | Auxin response factor 11 ARF11 | 7.5341 |
| Zlat\_10005787 | Auxin-induced protein X10A AX10A | -3.8671 |
| Zlat\_10015482 | Auxin transporter-like protein 2 LAX2 | 2.1862 |
| Zlat\_10017452 | Transcription factor APG | 1.6209 |
| Zlat\_10009390 | Transcription factor MYC2 | -1.596 |
| Zlat\_10022833 | bZIP transcription factor TRAB1 | -1.4779 |
| Zlat\_10040352 | Transport inhibitor response 1-like protein TIR1A | 2.0898 |
| Zlat\_10035141 | TGACG-sequence-specific DNA-binding protein TGA-2.1 TGA21 | -2.5162 |
| Zlat\_10022265 | protein phosphatase 2C 37 P2C37 | -1.6287 |
| Zlat\_10026591 | Protein TIFY 3A TIF3A | -1.5511 |
| Zlat\_10022690 | Regulatory protein NPR3 | -1.6198 |
| Zlat\_10006293 | Protein TIFY 10A TI10A | -1.6425 |
| Zlat\_10018497 | Cyclin-D3-2 CCD32 | 2.1198 |
| Zlat\_10000572 | -//- | 3.6105 |
| Zlat\_10026592 | -//- | -1.9869 |
| Zlat\_10000259 | -//- | 2.5918 |
| KEGG:zma00941 Flavonoid biosynthesis  Sample number/Background number:6/44 Corrected P-value: 0.018934388 | | |
| Zlat\_10045747 | Cytochrome P450 CYP73A100 | -2.6201 |
| Zlat\_10045750 | Cytochrome P450 CYP73A100 | -2.0429 |
| Zlat\_10045749 | Trans-cinnamate 4-monooxygenase | -2.7848 |
| Zlat\_10016473 | Tricin synthase 1 | -1.9036 |
| Zlat\_10001216 | Anthocyanidin reductase | -3.0914 |
| Zlat\_10003508 | Chalcone--flavonone isomerase | 2.2501 |
| KEGG:zma01110 Biosynthesis of secondary metabolites  Sample number/Background number:56/1481 Corrected P-value: 0.022291996 | | |
| Zlat\_10032403 | Serine hydroxymethyltransferase 7 GLYC7 | -2.1046 |
| Zlat\_10041351 | Cationic peroxidase 1 PER1 | -3.1259 |
| Zlat\_10036307 | Peroxidase 1 PER1 | 2.246 |
| Zlat\_10007768 | Peroxidase 19 PER19 | 2.0968 |
| Zlat\_10029728 | Peroxidase 47 PER47 | -12.011 |
| Zlat\_10001910 | Peroxidase 52 PER52 | 2.1065 |
| Zlat\_10046751 | Peroxidase 52 PER52 | 2.9818 |
| Zlat\_10003203 | Peroxidase 72 PER72 | -2.7887 |
| Zlat\_10008844 | Cationic peroxidase SPC4 | -1.4769 |
| Zlat\_10041502 | Peroxisomal (S)-2-hydroxy-acid oxidase GLO3 | -1.8284 |
| Zlat\_10007582 | Cinnamyl alcohol dehydrogenase 5 CADH5 | -2.262 |
| Zlat\_10037056 | Cinnamyl alcohol dehydrogenase 6 CADH6 | -3.0534 |
| Zlat\_10004185 | Cinnamyl alcohol dehydrogenase 9 CADH9 | -1.9164 |
| Zlat\_10048065 | Probable inactive beta-glucosidase 14 BGL14 | -4.5313 |
| Zlat\_10047787 | Beta-glucosidase 30 BGL30 | 8.1727 |
| Zlat\_10045750 | Cytochrome P450 CYP73A100 | -2.0429 |
| Zlat\_10045747 | Cytochrome P450 CYP73A100 | -2.6201 |
| Zlat\_10034541 | Cytochrome P450 724B1 | 2.0021 |
| Zlat\_10037791 | 3-ketoacyl-CoA synthase 5 KCS5 | -100 |
| Zlat\_10018082 | 3-ketoacyl-CoA synthase 11 KCS11 | -4.2539 |
| Zlat\_10009486 | 3-ketoacyl-CoA synthase 12 KCS12 | -2.4227 |
| Zlat\_10015120 | Cinnamoyl-CoA reductase 1 CCR1 | -3.867 |
| Zlat\_10035005 | 4-coumarate--CoA ligase 5 4CL5 | -1.6962 |
| Zlat\_10026402 | Gibberellin 2-beta-dioxygenase 8 | -2.081 |
| Zlat\_10032857 | Gibberellin 2-beta-dioxygenase | -1.7147 |
| Zlat\_10031241 | Protein ECERIFERUM 1 CER1 | 1.7321 |
| Zlat\_10026392 | Protein ECERIFERUM 1 CER1 | 8.8863 |
| Zlat\_10017156 | Lipoxygenase 2.3 | -1.3266 |
| Zlat\_10003050 | Lipoxygenase 5 LOX5 | -1.7654 |
| Zlat\_10045844 | ATP-dependent 6-phosphofructokinase 3 PFKA3 | -1.9501 |
| Zlat\_10046954 | Fructose-bisphosphate aldolase cytoplasmic isozyme | -1.77 |
| Zlat\_10032926 | Fructose-1,6-bisphosphatase | -3.7715 |
| Zlat\_10020097 | Fructose-1,6-bisphosphatase | -3.2867 |
| Zlat\_10012970 | ATP-citrate synthase alpha chain protein 2 ACLA2 | 1.6908 |
| Zlat\_10043163 | Non-specific phospholipase C4 NPC4 | -1.9603 |
| Zlat\_10023644 | Glycerol-3-phosphate 2-O-acyltransferase 4 GPAT4 | -1.6075 |
| Zlat\_10045749 | Trans-cinnamate 4-monooxygenase | -2.7848 |
| Zlat\_10019656 | 4-hydroxyphenylacetaldehyde oxime monooxygenase | -2.4564 |
| Zlat\_10045635 | 12-oxophytodienoate reductase 1 OPR1 | -1.7521 |
| Zlat\_10016473 | Tricin synthase 1 | -1.9036 |
| Zlat\_10039160 | Malate dehydrogenase | -2.0036 |
| Zlat\_10020835 | 1-aminocyclopropane-1-carboxylate oxidase | -2.4359 |
| Zlat\_10028912 | Solanesyl-diphosphate synthase 1 SPS1 | 1.6388 |
| Zlat\_10003508 | Chalcone--flavonone isomerase | 2.2501 |
| Zlat\_10030369 | Obtusifoliol 14-alpha demethylase | -2.0888 |
| Zlat\_10001216 | Anthocyanidin reductase | -3.0914 |
| Zlat\_10025055 | Branched-chain-amino-acid aminotransferase 3 BCAT3 | -1.3997 |
| Zlat\_10012130 | Farnesyl pyrophosphate synthase | -2.3845 |
| Zlat\_10011777 | Pyruvate kinase isozyme A KPYA | 1.7043 |
| Zlat\_10018948 | Glycine cleavage system H protein | -2.2227 |
| Zlat\_10020498 | Salicylate carboxymethyltransferase | -2.0801 |
| Zlat\_10039130 | Allene oxide synthase 1 | -1.724 |
| Zlat\_10006128 | Isocitrate lyase | 100 |
| Zlat\_10003321 | Adenylate isopentenyltransferase 1 IPT1 | -1.6601 |
| Zlat\_10000934 | -//- | -2.6327 |
| Zlat\_10000435 | -//- | -1.8873 |
| KEGG:zma00945 Stilbenoid, diarylheptanoid and gingerol biosynthesis  Sample number/Background number:4/23 Corrected P-value: 0.039972715 | | |
| Zlat\_10045747 | Cytochrome P450 CYP73A100 | -2.6201 |
| Zlat\_10045750 | Cytochrome P450 CYP73A100 | -2.0429 |
| Zlat\_10045749 | Trans-cinnamate 4-monooxygenase | -2.7848 |
| Zlat\_10016473 | Tricin synthase 1 | -1.9036 |

**Table S3** List of differentially expressed genesin *Ustilago esculenta* under fenaminosulf stress.

|  |  |  |
| --- | --- | --- |
| Locus tag | Annotation | log2FoldChange |
| KEGG:uma00052 Galactose metabolism  Sample number/Background number:2/13 Corrected P-value: 0.173689177061 | | |
| g813 | Putative invertase | -1.842 |
| g3269 | Alpha-glucosidase | -3.3883 |
| KEGG:uma00650 Butanoate metabolism  Sample number/Background number:2/20 Corrected P-value: 0.183258712357 | | |
| g5895 | Acetoacetyl-CoA synthetase | 3.1926 |
| g352 | 5-aminovalerate aminotransferase | 2.1351 |
| KEGG:uma00500 Starch and sucrose metabolism  Sample number/Background number:2/26 Corrected P-value: 0.192927294722 | | |
| g813 | Putative invertase | -1.842 |
| g3269 | Alpha-glucosidase | -3.3883 |
| KEGG:uma00400 Phenylalanine, tyrosine and tryptophan biosynthesis  Sample number/Background number:1/15 Corrected P-value: 0.371552252837 | | |
| g748 | Phospho-2-dehydro-3-deoxyheptonate aldolase | -100 |
| KEGG:uma00630 Glyoxylate and dicarboxylate metabolism  Sample number/Background number:1/15 Corrected P-value: 0.371552252837 | | |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| KEGG:uma00410 beta-Alanine metabolism  Sample number/Background number:1/16 Corrected P-value: 0.371552252837 | | |
| g352 | 5-aminovalerate aminotransferase | 2.1351 |
| KEGG:uma00640 Propanoate metabolism  Sample number/Background number:1/17 Corrected P-value: 0.371552252837 | | |
| g352 | 5-aminovalerate aminotransferase | 2.1351 |
| KEGG:uma00051 Fructose and mannose metabolism  Sample number/Background number:1/19 Corrected P-value: 0.371552252837 | | |
| g2684 | L-rhamnose-1-dehydrogenase | 2.5426 |
| KEGG:uma00250 Alanine, aspartate and glutamate metabolism  Sample number/Background number:1/22 Corrected P-value: 0.371552252837 | | |
| g352 | 5-aminovalerate aminotransferase | 2.1351 |
| KEGG:uma00020 Citrate cycle (TCA cycle)  Sample number/Background number:1/23 Corrected P-value: 0.371552252837 | | |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| KEGG:uma01230 Biosynthesis of amino acids  Sample number/Background number:2/90 Corrected P-value: 0.371552252837 | | |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| g748 | 2-methylcitrate synthase | -2.3563 |
| KEGG:uma01210 2-Oxocarboxylic acid metabolism  Sample number/Background number:1/25 Corrected P-value: 0.371552252837 | | |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| KEGG:uma04146 Peroxisome  Sample number/Background number:1/39 Corrected P-value: 0.49571460689 | | |
| g6523 | Peroxisomal targeting signal 1 receptor | 2.0429 |
| KEGG:uma04111 Cell cycle - yeast  Sample number/Background number:1/59 Corrected P-value: 0.576271557971 | | |
| g5909 | Structural maintenance of chromosomes protein 2 | 4.4313 |
| KEGG:uma01100 Metabolic pathways  Sample number/Background number:6/555 Corrected P-value: 0.576271557971 | | |
| g980 | 5-hydroxyisourate hydrolase | -5.6573 |
| g352 | 5-aminovalerate aminotransferase | 2.1351 |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| g748 | Phospho-2-dehydro-3-deoxyheptonate aldolase | -100 |
| g813 | Putative invertase | -1.842 |
| g3269 | Alpha-glucosidase | -3.3883 |
| KEGG:uma03013 RNA transport  Sample number/Background number:1/73 Corrected P-value: 0.576271557971 | | |
| g4739 | -//- | 4.133 |
| KEGG:uma00230 Purine metabolism  Sample number/Background number:1/74 Corrected P-value: 0.576271557971 | | |
| g980 | 5-hydroxyisourate hydrolase | -5.6573 |
| KEGG:uma01200 Carbon metabolism  Sample number/Background number:1/78 Corrected P-value: 0.576271557971 | | |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| KEGG:uma03040 Spliceosome  Sample number/Background number:1/80 Corrected P-value: 0.576271557971 | | |
| g2750 | Small nuclear ribonucleoprotein G | -100 |
| KEGG:uma01110 Biosynthesis of secondary metabolites  Sample number/Background number:2/208 Corrected P-value: 0.609968042106 | | |
| g2660 | 2-methylcitrate synthase | -2.3563 |
| g748 | Phospho-2-dehydro-3-deoxyheptonate aldolase | -100 |