

Table 1 Suppl. Primers used in this study.

| Primer name | Primer sequence (5'-3') |
|-----------------------|--|
| cDNA synthesis primer | TTTTGTACAAGCTT ₃₀ NN |
| Adaptor 1 | CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGT |
| PCR primer 1 | CTAATACGACTCACTATAGGGC |
| Nested PCR primer 1 | TCGAGCGGCCGCCCGGGCAGGT |
| Adaptor 2R | CTAATACGACTCACTATAGGGCAGCGTGGTCGCGGCCGAGGT |
| Nested PCR primer 2 | AGCGTGGTCGCGGCCGAGGT |
| CsWRKY1_F | AAAGTGGTTAAGGGCAATCCAA |
| CsWRKY1_R | TCGTTCGGCGTGTTTCC |
| Cs4CL1_F | GGGCGTAATCAGTCCGGTGAAA |
| Cs4CL1_R | TAGCCAGCCATCTTTGTCGATCG |
| CsC4H1_F | CTTGGAAGAGGAGTCTAAGGTGGA |
| CsC4H1_R | GGGCTTTTCTCGCTTGTTTAGTT |
| CsHSP1_F | CACTGCCCCAAACCACCATC |
| CsHSP1_R | GCATCCCTCAAACACTTCTCAAC |
| CsSOD1_F | TGAGGATGATCTCGGAAAAGG |
| CsSOD1_R | AGTCAAACCAACAACACCACAAG |
| 18S_F | CCTGAATGCCGAGTCTTTCTCT |
| 18S_R | GGGCTTTTCTCGCTTGTTTAGTT |

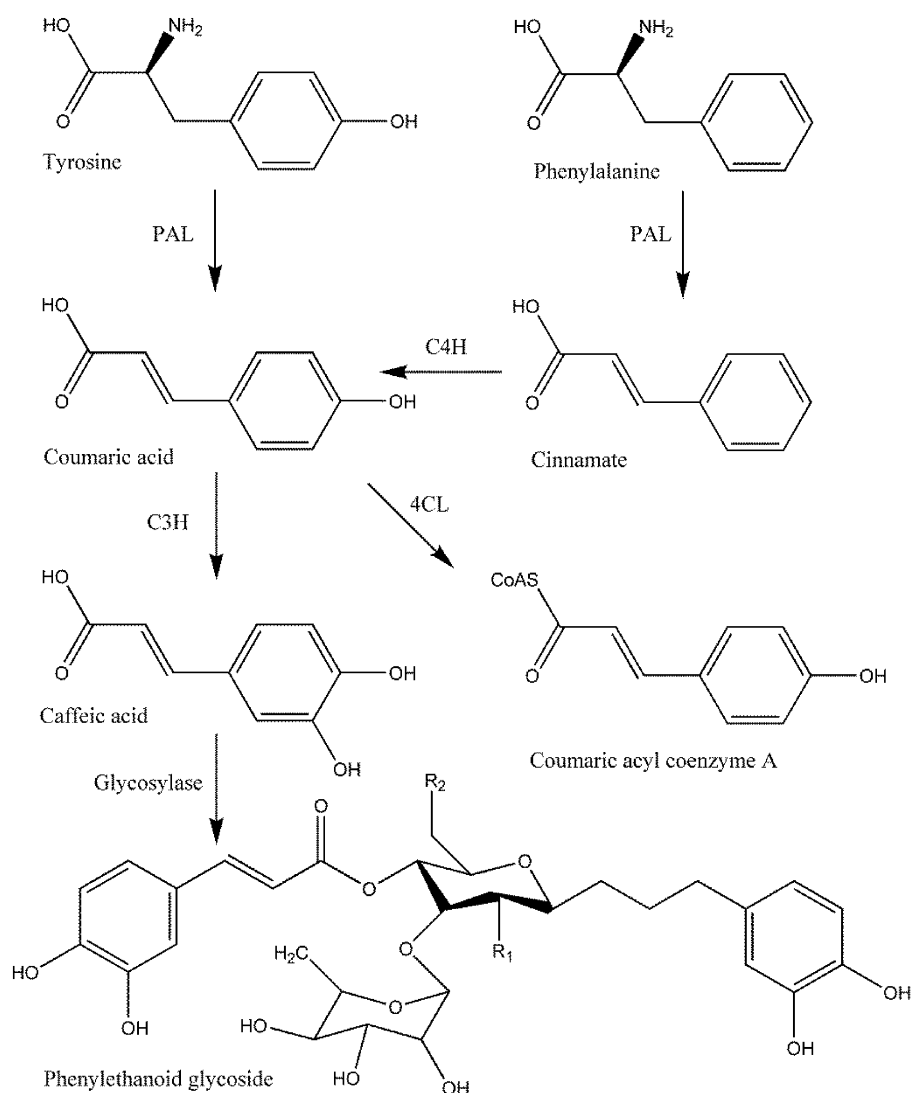


Fig. 1 Suppl. The phenylethanoid glycoside (PeG) biosynthesis pathway. PeG is derived from phenylalanine ammonia-lyase pathway metabolites, various PeGs are synthesized after glycosylation by different saccharides. When R_1 = hydroxyl and R_2 = glucosyl, the PeG is echinacoside; when R_1 = hydroxyl and R_2 = hydroxyl, the PeG is acteoside; when R_1 = acetyl and R_2 = hydroxyl, the PeG is acetylacteoside. PAL - phenylalanine ammonia-lyase, C4H - cinnamate-4-hydroxylase, C3H - coumarate-3-hydroxylase, 4CL - 4-coumarate: ligase.

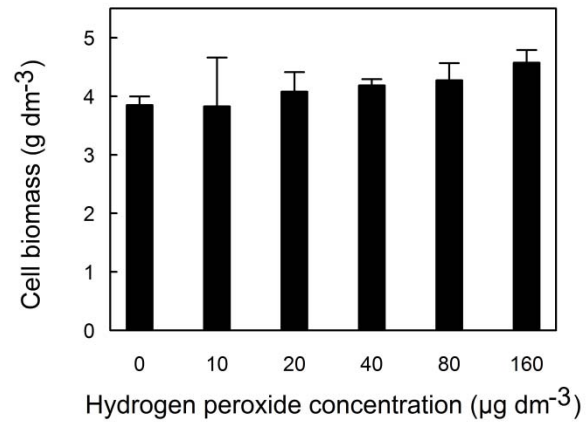


Fig. 2 Suppl. Hydrogen peroxide effects on cell growth. Every 5.0 ± 0.2 g of cells was inoculated in 50 cm^3 of a medium and then harvested after 10 d in suspension culture with or without hydrogen peroxide treatment. Data are shown as mean \pm SD of at least five samples of dry mass within three independent biological replications.

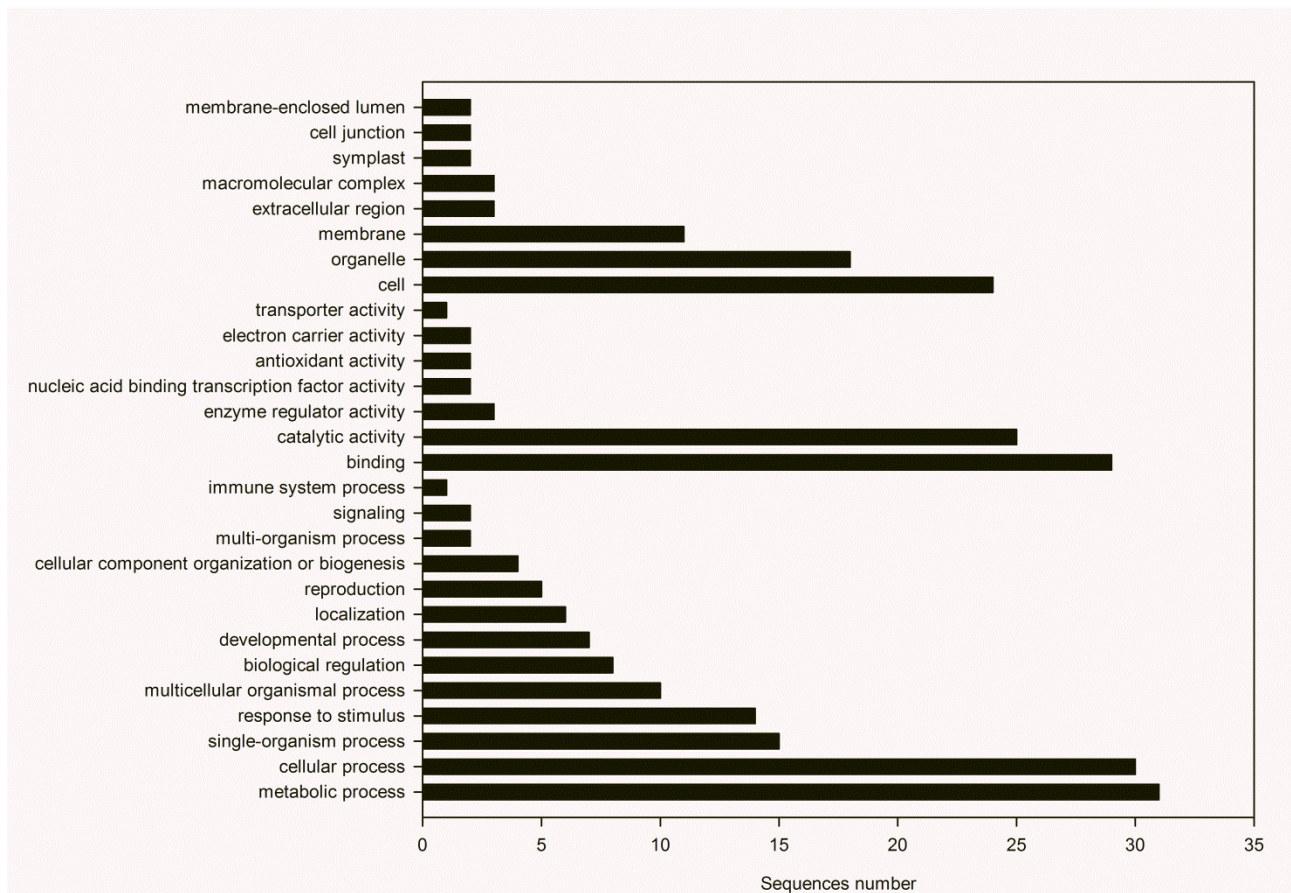


Fig. 3 Suppl. Annotated gene ontology (GO) distribution. The annotated genes identified by *Blast2GO* were further analyzed for GO distribution. Ontology IDs are as follows: GO:0008152, metabolic process; GO:0009987, cellular process; GO:0044699, single-organism process; GO:0050896, response to stimulus; GO:0032501, multicellular organismal process; GO:0065007, biological regulation; GO:0032502, developmental process; GO:0051179, localization; GO:0000003, reproduction; GO:0071840, cellular component organization or biogenesis; GO:0051704, multi-organism process; GO:0023052, signaling; GO:0002376, immune system process; GO:0005488, binding; GO:0003824, catalytic activity; GO:0030234, enzyme regulator activity; GO:0001071, nucleic acid binding transcription factor activity; GO:0016209, antioxidant activity; GO:0009055, electron carrier activity; GO:0005215, transporter activity; GO:0005623, cell; GO:0043226, organelle; GO:0016020, membrane; GO:0005576, extracellular region; GO:0032991, macromolecular complex; GO:0055044, symplast; GO:0030054, cell junction; GO:0031974, membrane-enclosed lumen.