Article title: Promotion of Phenolic Compounds Production in Salvia miltiorrhiza

Hairy Roots by Six Strains of Rhizosphere Bacteria

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Materials and methods

Total RNAs were extracted from *S. miltiorrhiza* hairy roots using RNAisoTM Plus

(Takara, Tokyo, Japan) according to the manufacturer's protocol. The first strand

cDNA was synthesized from 500 ng total RNA with PrimeScript[™] RT reagent Kit

(Takara, Tokyo, Japan). Primers with the following sequences, FPAL

(5'-GGCGGCGATTGAGAGCAGGA-3') and RPAL (5'-

ATCAGCAGATAGGAAGAGGAGCACC-3'), F4CL

(5'- TCGCCAAATACGACCTTTCC -3') and R4CL (5'-

TGCTTCAGTCATCCCATACCC-3'), FC4H (5'-

CCAGGAGTCCAAATAACAGAGCC-3') and RC4H (5'-

GAGCCACCAAGCGTTCACCAA-3'), FTAT (5'-

TTCAACGGCTACGCTCCAACT-3') and RTAT (5'-

AAACGGACAATGCTATCTCAAT-3'), FHPPR

(5'- GACTCCAGAAACAACCCACATT-3') and RHPPR (5'-

CCCAGACGACCCTCCACAAGA-3'), FRAS (5'-

CGCCCTAGTTGAGTTCTACCCTTACGC-3') and RRAS (5'-

TCGGATAGGTGGTGCTCGTTTGC-3'), were used to detect the gene expression of

smPAL, sm4CL, smC4H, smTAT, smHPPR and smRAS, respectively. The 18S rRNA

with specific primers F18S (5'-ATGATAACTCGACGGATCGC-3') and R18S

(5'-CTTGGATGTGGTAGCCGTTT-3') were used as control. Real-time PCR was

performed on the Bio-Rad CFX96 system (Bio-Rad, USA) with SYBR® Premix Ex

TaqTM II (Tli RNaseH Plus, Takara). The reaction mixture was incubated for 30 s at

95 °C, and for 40 cycles of 5 s at 95 °C and 30 s at 60 °C.

Figure legends

Fig. S1 The way of isolating the components of fermentation broth of strain LNHR13. **Fig. S12** Effects of bacteria LNHR13 on the expression level of six key enzyme genes (*smPAL*, *sm4CL*, *smC4H*, *smTAT*, *smHPPR* and *smRAS*) of RA and SAB biosynthesis pathway (phenylpropanoid pathway and the tyrosine pathway) in *S. miltiorrhiza* hairy roots at sixth day after treatment. Values are presented as mean \pm SD, n = 3. The asterisks indicate significant differences at P < 0.05, P < 0.01, and P < 0.001, marked as *, **, and ***, respectively.



