Supplemental Information

Engineering the Biocatalytic Selectivity of Iridoid Production in *Saccharomyces*

cerevisiae

John M. Billingsley^a, Anthony B. DeNicola^a, Joyann S. Barber^b, Man-Cheng Tang^a, Joe

Horecka^{c,d}, Angela Chu^{c,d}, Neil K. Garg^b, Yi Tang^{a,b,}*

^a Department of Chemical and Biomolecular Engineering, University of California, Los Angeles, California 90095, United States

^b Department of Chemistry and Biochemistry, University of California, Los Angeles, California 90095, United States

^c Stanford Genome Technology Center, Stanford University, Palo Alto, CA, USA

^d Department of Biochemistry, Stanford University School of Medicine, Stanford, CA, USA

The Supplemental Information consists of 2 Supplementary Methods, 22 Supplementary Figures and 4 Supplementary Tables.

*Corresponding author. E-mail address: yitang@ucla.edu (Y. Tang)

Supplementary Method 1. Construction of JHY651

In order to improve the capacity of BY4742 [\(Brachmann et al., 1998\)](#page-20-0) for expression of heterologous natural product pathways, a number of genomic changes were implemented. Six previously identified quantitative trait loci (QTLs) were repaired to restore sporulation (MKT1(30G) RME1(INS-308A) TAO3(1493Q)) [\(Deutschbauer and](#page-20-1) [Davis, 2005\)](#page-20-1) and mitochondrial genome stability (SAL1+ CAT5(91M) MIP1(661T)) [\(Dimitrov et al., 2009\)](#page-20-2) in BY4742. Additionally, a Ty1 element which inactivates the HAP1 regulatory gene in S288c derived strains [\(Gaisne et al., 1999\)](#page-20-3) was repaired. The resulting strain, DHY214 was further modified by deletion of PRB1 and PEP4, which mediate the degradation of heterologous proteins [\(Jones, 1991\)](#page-20-4), resulting in the parent strain used in this study, JHY651 (S1). Strain modifications were performed using the previously described 50:50 method [\(Horecka and Davis, 2014\)](#page-20-5).

Supplementary Method 2. Synthesis of 8-hydroxygeraniol

Synthesis of **10**: To a solution of selenium dioxide (0.68 g, 6.12 mmol, 0.4 equiv) in CH2Cl² (77 mL) was added *tert*-butyl hydroperoxide (5.5 M in decane, 8.6 mL, 47.5 mmol, 3.1 equiv). The solution was then cooled to 0 °C and geranyl acetate (**9**, 3.3 mL, 15.3 mmol, 1.0 equiv) was added. After stirring for 7 h at 0 °C, EtOAc (200 mL) was added and the reaction was transferred to a separatory funnel. The layers were separated and the organic layer was washed successively with deionized water (2 x 75 mL), saturated aqueous NaHCO₃ (1 x 75 mL), deionized water (1 x 50 mL), and brine (1 x 80 mL). The organic layer was dried over MgSO4, filtered, and concentrated under reduced pressure. The resulting crude oil was purified by flash chromatography (9:1 \rightarrow 1:1 hexanes:EtOAc) to afford allylic alcohol **10** (1.99 g, 61% yield) as a light yellow oil. Allylic alcohol **10**: R*f* 0.44 (2:1 hexanes:EtOAc). Spectral data (Fig. S11) match those previously reported [\(Bogazkaya et al., 2014\)](#page-20-6).

Synthesis of 8-hydroxygeraniol **1**: To a solution of allylic alcohol **10** (1.99 g, 9.39 mmol, 1.0 equiv) in MeOH (60 mL) was added potassium hydroxide (1.56 g, 11.3 mmol, 1.2 equiv) as a solid in one portion. After stirring for 2.5 h at 23 °C, deionized water (40 mL) was added and the reaction was transferred to a separatory funnel. The layers were separated and the aqueous layer was extracted with $Et₂O$ (3 x 80 mL). The combined organic layers were washed successively with 0.5 M HCl (1 x 50 mL), saturated aqueous NaHCO₃ (1 x 100 mL), brine (1 x 50 mL), and deionized water (1 x 50 mL). The organic layers were then dried over MgSO4, filtered, and concentrated under reduced pressure. The resulting crude oil was purified by flash chromatography (1:1 hexanes:EtOAc) to afford 8-hydroxygeraniol (**1**, 1.29 g, 81% yield) as a light yellow oil. **1**: R*f* 0.14 (2:1 hexanes:EtOAc). Spectral data (Fig. S12) match those previously reported [\(Bogazkaya et al., 2014\)](#page-20-6).

Supplementary Fig. 1. The monoterpene indole alkaloid biosynthetic pathway.

Supplementary Fig. 1 (continued). The monoterpene indole alkaloid biosynthetic pathway. 8-Hydroxygeraniol is converted to the dialdehyde by geraniol oxidoreductase (GOR). 8-oxogeranial undergoes reductive cyclization by iridoid synthase (ISY). The iterative P450 iridoid oxidase (IO) converts the C-4 methyl into a carboxy group. 7 deoxyloganitic acid glucosyltransferase (7-DLGT) stabilizes the hemiacetal. The P450 7-deoxyloganic acid hydroxylase (7-DLH) installs the hydroxyl, followed by Omethylation by loganic acid O-methyltransferase (LAMT). Secologanin synthase (SLS) then performs the oxidative cleavage of loganin. Meanwhile, tryptophan decarboxylase (TDC) produces the β-arylethylamine tryptamine. The Pictet-Spenglerase strictosidine synthase (STR) catalyzes the condensation of tryptamine with secologanin followed by ring closure to forge strictosidine.

__

ATGACTAAAACTAATTCTCCAGCCCCATCTGTCATTACTTGCAAGGCTGCTGTCGTTTGGAAATCCGGTGAACCACCAAAGGTCGAAGAGATCCAAGT TGATCCACCCAAGGCTTCTGAAGTTCGCATTAAGATGTTGTGTGCTTCCTTGTGCCACACCGATTTCTTGGCTTGTAATGGTCTGCCAGTTCCATTGT TTGGGTGAGTGTGGCGAATGCTTGAATTGCAAGTCCGGCAGGACTAACTTGTGTCATAAGTATCCGTTGGGTTTTTCTGGCCTGTTGTTGGATGGCAC TTCCAGGATGAGCATTGGCGAACAAAAAGTCTACCACCACTTCTCTTGTTCCACCTGGTCTGAATACATTGTTATTGAGGCCGCCTACGCAGTTAAAG TTGACCCAAGGGTTAGCTTGCCACATGCTTCTTTCCTGTGTTGCGGTTTTACTACTGGCTTTGGCGCCACTTGGAGAGATGTTAATGTTGTCAAAGGC TCTACTGTCGCTGTTTTGGGTTTAGGTGCCGTCGGTTTGGGTGCTGTTCAAGGCGCTAAATCTCAAGGTGCCTCCAGGATCATTGGTTTAGACATTAA CGATAAGAAGAGGGAGAAAGGCGAAGCTTTCGGCATGACCGAATTCATCAACCCCAAGGGCTCCAATAAGTCCATCTCCGAATTGATCAACGAAGCTA CTGGTGGTCTAGGTTTGGACTACGTTTATGAATGCACTGGTGTCCCAGCTCTGTTGAACGAAGCCATTGAGTCCTCTAAAGTTGGTCTGGGTACTGCC GCCAAAGTCCGACTTGCCAACTCTGATTGAGAAGTGCATTAACAAGGAGATTCCAATGGACGAGCTGATGACCCATGAGGTGTCTCTGTCCGAGATCA ACAAGGGTTTCGAGTACTTGAAGCACCCAGACTGTGTCAAAGTTGTTATTAAGTTCTAA

> codon optimized ISY gene sequence

ATGTCCTGGTGGTGGAAAAGGTCTATTGGTGCTGGCAAAAACTTGCCAAACCAAAACAAGGAAAACGGTGTCTGCAAGTCTTACAAATCTGTCGCCTT GGTCGTCGGTGTTACTGGTATTGTTGGTTCTTCTCTGGCTGAGGTTTTGAAGTTGCCAGATACTCCAGGTGGTCCATGGAAAGTTTATGGTGTTGCTA GAAGACCATGTCCAGTCTGGTTGGCTAAGAAGCCAGTCGAGTACATCCAGTGTGACGTCTCCAATAACCAAGAAACCATTTCTAAGCTGTCTCCCCTG AAAGACATCACTCACATCTTCTATGTCTCCTGGATTGGCTCTGAGGATTGCCAGACTAATGCCACCATGTTCAAGAACATCTTGAACTCCGTTATCCC AAATGCTTCCAACTTGCAGCACGTCTGCCTACAAACCGGCATTAAGCATTACTTCGGCATTTTCGAAGAGGGTTCCAAAGTCGTTCCACATGATTCCC CCTTTACCGAAGATTTGCCACGCTTGAACGTCCCAAACTTTTATCACGACCTGGAAGACATTTTGTACGAGGAGACAGGCAAAAATAACCTAACCTGG TCCGTTCACAGGCCAGCTTTGGTTTTCGGTTTTCCCCATGCTCCATGATGATATCGTCTCTCTACTCTGTGCGTCTACGCTACTATTTGCAAGCATGA GAACAAGGCTCTGGTTTACCCAGGTTCCAAGAATTCCTGGAATTGCTATGCTGATGCTGTCGATGCTGACTTGGTTGCTGAGCATGAAATTTGGGCTG ATCGAGATGGTCGGTTATGTTGAAGGCAAAGAACAGGTCAGCCTGGCCGAATTGATGAAAGATAAGGATCAAGTCTGGGACGAAATCGTCAAGAAAAA CAACCTGGTGCCAACTAAGTTGAAGGAGATTGCCGCCTTCTGGTTTGCCGATATCGCCTTTTGCTCTGAAAACTTGATCTCTTCCATGAACAAGTCCA

Supplementary Fig. 2. Gene sequences of GOR and ISY synthesized by Gen9.

> codon optimized GOR gene sequence

Supplementary Fig. 3. Monoterpene standard curve.

Supplementary Fig. 4. SDS-PAGE gel of purified enzymes used for *in vitro* **assays.**

Monoterpene profile in engineered strains

Supplementary Fig. 5. Monoterpene profile after bioconversion assay. (i) S1 with pJB031, (ii) S1 with pJB033, (iii) S4 with pJB033, (iv) S4 with pJB034.

Supplementary Fig. 6. GOR and OYE cofactor dependence, (i) 8-hydroxygeraniol standard, (ii) 8-hydroxytetrahydrogeraniol standard, (iii) 8-hydroxygeraniol + GOR + OYE2, without NAD⁺, (iv) 8-hydroxygeraniol + OYE2, without NADPH, (v) 8hydroxygeraniol + OYE3, without NAD⁺, (vi) 8-hydroxygeraniol + GOR + OYE2, without NADPH.

Supplementary Fig. 7. ARI1, ADH6, ADH7 cofactor dependence. (i) 8 hydroxygeraniol + ARI1 + NAD⁺, (ii) 8-hydroxygeraniol + ADH6 + NAD⁺, (iii) 8hydroxygeraniol + ADH7 + NAD⁺, (iv) 8-hydroxygeraniol + ARI1 + NADP⁺, (v) 8hydroxygeraniol + ADH6 + NADP⁺, (vi) 8-hydroxygeraniol + ADH7 + NADP⁺.

Supplementary Fig. 8. Mass spectra of compound 7 produced from 4 *in vitro* **through the action of GOR and OYE.**

Supplementary Fig. 9. Mass spectra of compound 8 produced from 4 *in vitro* **through the action of ISY and ADH.**

Supplementary Fig. 10. Additional fermentation data. Means and standard errors are reported for plasmid stability.

Supplementary Table 1. Primers used in this study.

Supplementary Table 2. gBlocks used for HICRISPR

Supplementary Fig. 11 1H NMR of **10**.

Supplementary Fig. 12 1H NMR of **1**.

.

Supplementary Table 3. NMR data for compound **4**. ¹H NMR spectrum (500 MHz), ¹³C NMR spectrum (125 MHz), CDCl₃

OH HO.

compound 4

ЭH HO[']

Key HMBC Correlations

Supplementary Table 4. NMR data for the isolated saturated acid. ¹H NMR spectrum (500 MHz), ¹³C NMR spectrum (125 MHz), CDCl₃

8-hydroxy-2,6-dimethyloctanoic acid

òн

Key HMBC Correlations

OH. HO

8-hydroxy-3,7-dimethyloctanoic acid

DН

Key HMBC Correlations

Supplementary Fig. 14. ¹³C NMR Spectrum of Compound **4** in CDCl3.

Supplementary Fig. 15. ¹H-¹H COSY Spectrum of Compound 4 in CDCl₃.

Supplementary Fig. 18. ¹H NMR Spectrum of the isolated saturated acid in CDCl₃.

Supplementary Fig. 21. ¹³C NMR Spectrum of the isolated saturated acid in CDCl₃.

Supplementary Fig. 20. ¹H-¹H COSY Spectrum of the isolated saturated acid in CDCl₃.

Supplementary Fig. 21. HSQC Spectrum of the isolated saturated acid in CDCl3.

Supplementary Fig. 22. HMBC Spectrum of the isolated saturated acid in CDCl3.

Supplemental Information References

- Bogazkaya, A. M., von Buhler, C. J., Kriening, S., Busch, A., Seifert, A., Pleiss, J., Laschat, S., Urlacher, V. B., 2014. Selective allylic hydroxylation of acyclic terpenoids by CYP154E1 from *Thermobifida fusca* YX. Beilstein journal of organic chemistry. 10**,** 1347-1353.
- Brachmann, C. B., Davies, A., Cost, G. J., Caputo, E., Li, J., Hieter, P., Boeke, J. D., 1998. Designer deletion strains derived from *Saccharomyces cerevisiae* S288C: a useful set of strains and plasmids for PCR-mediated gene disruption and other applications. Yeast. 14**,** 115-32.
- Deutschbauer, A. M., Davis, R. W., 2005. Quantitative trait loci mapped to singlenucleotide resolution in yeast. Nature genetics. 37**,** 1333-40.
- Dimitrov, L. N., Brem, R. B., Kruglyak, L., Gottschling, D. E., 2009. Polymorphisms in multiple genes contribute to the spontaneous mitochondrial genome instability of *Saccharomyces cerevisiae* S288C strains. Genetics. 183**,** 365-83.
- Gaisne, M., Becam, A. M., Verdiere, J., Herbert, C. J., 1999. A 'natural' mutation in *Saccharomyces cerevisiae* strains derived from S288c affects the complex regulatory gene HAP1 (CYP1). Current genetics. 36**,** 195-200.
- Horecka, J., Davis, R. W., 2014. The 50:50 method for PCR-based seamless genome editing in yeast. Yeast. 31**,** 103-12.
- Jones, E. W., 1991. Tackling the protease problem in *Saccharomyces cerevisiae*. Methods in enzymology. 194**,** 428-53.