Biosynthesis of plant hemostatic dencichine in Escherichia coli

Li et al.



Supplementary Figure 1. Production and optimization of *L*-DAP by strain BW1 and BW2. The bars indicate the titer of *L*-DAP and the lines indicate biomass at OD_{600} . Data shown are mean \pm SD (n=3 independent experiments). Source data are provided as a Source Data file.



Supplementary Figure 2. Biochemical analysis of Fpgloxdh and Scgloxdh. a SDS-PAGE analysis of nickel-affinity purified codon-optimized His-Fpgloxdh and wild-type His-Scgloxdh. This experiment was repeated independently twice with similar results. **b**, **c** Kinetic analysis of Gloxdh over a gradient of glyoxylate concentrations (n=2, data distribution is less than 7.84% in duplicate experiments). Enzyme activity was determined by measurement the production of cytochrome c reduced at 550 nm. M, marker II; S, soluble fraction; I, insoluble fraction; P, purified protein. Source data are provided as a Source Data file.



Supplementary Figure 3. Biochemical analysis of Anoah, Ssoah, Pcoah and Fpoah. a, b, c, d SDS-PAGE analysis of nickel-affinity purified Anoah, Ssoah, Pcoah and Fpoah. This experiment was repeated independently twice with similar results. **e, f** Kinetic analysis of Oah over a gradient of oxaloacetate concentrations (n=2, data distribution is less than 6.13% in duplicate experiments). Enzyme activity was determined by measurement the consumption of oxaloacetate at 255 nm. M, marker II; S, soluble fraction; I, insoluble fraction; P, purified protein. Source data are provided as a Source Data file.



Supplementary Figure 4. Biochemical analysis of PanE. a SDS-PAGE analysis of nickel-affinity purified PanE. This experiment was repeated independently twice with similar results. **b** Kinetic analysis of PanE over a gradient of glyoxylate concentrations (n=2, data distribution is less than 6.16% in duplicate experiments). Enzyme activity was determined by measurement the production of NADPH at 340 nm. M, marker II; S, soluble fraction; I, insoluble fraction; P, purified protein. Source data are provided as a Source Data file.



Supplementary Figure 5. Phylogenic relationships of LsBAHD in *L. sativus* **with sequences encoding highly homologous proteins.** Amino acid sequences were aligned and the Maximum Likelihood (ML) tree was built using MAFFT (version 7.407). The phylogeny was constructed with 1000 implementations of ultrafast bootstrap tests with IQ-TREE. The Model of substitution is JTT+I+G4 (Jones-Taylor-Thornton model, Has Invariant sites plus discrete Gamma model). The tree was further annotated by iTOL (Interactive Tree Of Life).



Supplementary Figure 6. Biochemical analysis of LsBAHD. a SDS-PAGE analysis of nickel-affinity purified LsBAHD. This experiment was repeated independently twice with similar results. **b** The *in vitro* assay substrates and products were monitored by HPLC analysis. A PanE-LsBAHD coupling assay was used due to the chemical oxalyl-CoA is not commercially available. From top to bottom are L-DAP standard, β -ODAP standard and the reaction at 0 h, 1 h and 2 h, respectively. **c** Kinetic analysis of LsBAHD over a gradient of L-DAP concentrations (n=2, data distribution is less than 1.97% in duplicate experiments). Enzyme activity was determined by measurement the production of NADPH at 340 nm. M, marker II; S, soluble fraction; I, insoluble fraction; P, purified protein. Source data are provided as a Source Data file.



Supplementary Figure 7. Solubility optimization of LsBAHD by conventional methods. Expression levels of a LsBAHD co-expressed with DnaKJ, GroSL and IbpAB and b fusion enzymes (MBP: maltose-binding protein-LsBAHD and GST: glutathione S-transferase) were identified through SDS–PAGE analysis. M, marker II; S, soluble fraction; I, insoluble fraction. This experiment was repeated independently twice with similar results. Source data are provided as a Source Data file.



Supplementary Figure 8. Block the degradation pathways of glyoxylate. a Cell growth with time. b Glyoxylate consumption with time. Data shown are mean \pm SD (n=3 independent experiments). Source data are provided as a Source Data file.

Strains	Description	Source
E coli DW25112	$rrnBT14 \Delta lacZWJ16 hsdR514 \Delta araBADAH33$	Coli genome
<i>E. coll</i> Bw25115	$\Delta rhaBADLD78$	stock center
E. coli XL-1 Blue	recA1 endA1gyrA96thi-1hsdR17supE44relA11ac	Stratagene
<i>E. coli</i> BL21 Star (<i>DE3</i>)	$F^{-} ompT hsdS_B (r_B^{-}m_B^{-}) gal dcm (DE3)$	Invitrogen
BW1	BW25113, pZE-sbnAB	This study
BW2	BW25113∆ <i>serB</i> , pZE-sbnAB	This study
BW3	BW25113, pCS-LsBAHD-panE	This study
BW4	BW25113, pCS-LsBAHD-ScAAE-Scgloxdh	This study
BW5	BW25113, pCS-LsBAHD-ScAAE-Fpoah	This study
BW6	BW25113, pCS-LsBAHD*-panE	This study
BW7	BW25113, pCS-LsBAHD*-ScAAE-Scgloxdh	This study
BW8	BW25113, pCS-LsBAHD*-ScAAE-Fpoah	This study
$BW\Delta 5$	$BW25113\Delta ace B\Delta glc B\Delta ycd W\Delta ghr B\Delta gcl$	This study
BW9	BW∆5, pCS-LsBAHD*-panE	This study
BW10	BW∆5, pCS-LsBAHD*-ScAAE-Scgloxdh	This study
BW11	BW∆5, pZE-sbnAB, pCS-LsBAHD*-panE	This study
BW12	BW Δ 5, pZE-sbnAB, pCS-LsBAHD*-ScAAE-Scgloxdh	This study
BW13	BW25113, pZE-sbnAB, pCS-LsBAHD*-ScAAE-Fpoah	This study
	BW∆5, pZE-sbnAB,	This study
D W 14	pCS-LsBAHD*-ScAAE-Fpoah-Scgloxdh	
BW15	BW $\Delta 5\Delta serB$, pZE-sbnAB,	This study
	pCS-LsBAHD*-ScAAE-Fpoah-Scgloxdh	
BW16	BW $\Delta 5\Delta serB$, pZE-sbnAB,	This study
	pCS-LsBAHD*-ScAAE-Fpoah-Scgloxdh, pSA-aceA	

Supplementary Table 1. Strains used in this study.

Plasmids	Description [*]	Source
pZE12-luc	P _L lacO1, <i>colE ori</i> , <i>luc</i> , <i>Amp^R</i>	Ref. 1
pCS27	P_L lacO1, <i>p15A ori</i> , <i>Kan^R</i>	Ref. 1
pSA74	P_L lacO1, <i>pSC101 ori</i> , Cl^R	Ref. 1
pETDuet-1	PT7, $pBR322 \text{ ori, } Amp^R$	Ref. 2
pMAL-c2x	Ptac, <i>pBR322 ori</i> , MBP tag, <i>Amp^R</i>	Ref. 3
pGEX-6p-1	Ptac, $pBR322 \text{ ori}$, GST tag, Amp^R	Solarbio
pZE-sbnAB	pZE12-luc, <i>sbnA</i> and <i>sbnB</i> from <i>S</i> . <i>aureus</i>	This study
pET-Fpgloxdh	pETDuet-1, Fpgloxdh from F. palustris	This study
pET-Scgloxdh	pETDuet-1, Scgloxdh from S. cerevisiae	This study
pET-Anoah	pETDuet-1, Anoah from A. niger	This study
pET-Pcoah	pETDuet-1, Pcoah from P. chrysogenum	This study
pET-Fpoah	pETDuet-1, Fpoah from F. palustris	This study
pET-Ssoah	pETDuet-1, Ssoah from S. sclerotiorum	This study
pET-panE	pETDuet-1, panE from M. extorquens	This study
pET-LsBAHD	pETDuet-1, Lsbahd from L. sativus	This study
pCS-dnaKJ	pCS27, <i>dnaK</i> and <i>dnaJ</i> from <i>E. coli</i>	This study
pCS-groSL	pCS27, groS and groL from E. coli	This study
pCS-ibpAB	pCS27, <i>ibpA</i> and <i>ibpB</i> from <i>E</i> . <i>coli</i>	This study
pMAL-LsBAHD	pMAL-c2x, Lsbahd	This study
pGEX-LsBAHD	pGEX-6p-1, Lsbahd	This study
pET-LsBAHD*	pETDuet-1, Lsbahd	This study
pCS-LsBAHD-panE	pCS27, <i>Lsbahd</i> and <i>panE</i>	This study
pCS-LsBAHD-ScAAE- Scgloxdh	pCS27, Lsbahd, ScAAE and Scgloxdh	This study
pCS-LsBAHD-ScAAE- Fpoah	pCS27, Lsbahd, ScAAE and Fpoah	This study
pCS-LsBAHD*-panE	pCS27, <i>Lsbahd</i> * and <i>panE</i>	This study
pCS-LsBAHD*-ScAAE -Scgloxdh	pCS27, <i>Lsbahd</i> *, <i>ScAAE</i> and <i>Scgloxdh</i>	This study
pCS-LsBAHD*-ScAAE -Fpoah	pCS27, <i>Lsbahd</i> *, <i>ScAAE</i> and <i>Fpoah</i>	This study
pCS-LsBAHD*-ScAAE -Fpoah-Scgloxdh	pCS27, Lsbahd*, ScAAE, Fpoah and Scgloxdh	This study
pSA-aceA	pSA74, <i>aceA</i>	This study

Supplementary Table 2. Plasmids used in this study.

*Amp^R, ampicillin resistant; Kan^R, kanamycin resistant; Cl^R, chloramphenicol resistant.

Supplementary references

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- 3. Chen Z, Li Y, Sun X, Yuan Q. Improvement of expression level of polysaccharide lyases with new tag GAPDH in *E. coli. J. Biotechnol.* **236**, 159-165 (2016).