

Supporting Information

D-2-Hydroxyglutarate dehydrogenase plays a dual role in L-serine biosynthesis and D-malate utilization in the bacterium *Pseudomonas stutzeri*

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Running title: Dual role of D-2-hydroxyglutarate dehydrogenase

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Keywords: D-2-hydroxyglutarate, dehydrogenase, D-malate, serine, TCA cycle, enzyme kinetics, *Pseudomonas*, phosphoglycerate dehydrogenase, D-2-hydroxyglutarate dehydrogenase, oxaloacetate

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TABLE S1.

Strains and plasmids used in this study.

Strain/plasmid	genotype or relevant characteristics
Strain	
<i>E. coli</i> DH5 α	F ⁻ , ϕ 80 <i>lacZ</i> Δ M15, Δ (<i>lacZYA-argF</i>) U169, <i>recA1</i> , <i>endA1</i> , <i>hsdR17</i> , <i>phoA</i> , <i>supE44</i> λ ⁻ , <i>thi</i> ⁻¹ , <i>gyrA96</i> , <i>relA1</i>
<i>E. coli</i> BL21 (DE3)	F ⁻ <i>ompT gal dcm lon hsdS_B</i> (rB ⁻ mB ⁻) λ (DE3), used for protein expression
<i>P. stutzeri</i> A1501-WT	wild strain of <i>P. stutzeri</i> A1501
<i>P. stutzeri</i> A1501-pk18- <i>d2hgdh'</i>	<i>P. stutzeri</i> A1501 strain harboring chromosomal integration with pk18- <i>d2hgdh'</i> plasmid; Km ^r *
<i>P. stutzeri</i> A1501-pk18- <i>etf'</i>	<i>P. stutzeri</i> A1501 strain harboring chromosomal integration with pk18- <i>etf'</i> plasmid; Km ^r *
<i>P. stutzeri</i> A1501- Δ <i>d2hgdh</i>	<i>P. stutzeri</i> A1501 strain mutant obtained by exchanging the <i>d2hgdh</i> gene with the <i>d2hgdh'</i>
<i>P. stutzeri</i> A1501- Δ <i>etf</i>	<i>P. stutzeri</i> A1501 strain mutant obtained by exchanging the <i>etf</i> gene with the <i>etf'</i>
<i>P. stutzeri</i> A1501- Δ <i>d2hgdh-d2hgdh</i> ⁺	A1501- Δ <i>d2hgdh</i> strain harboring the plasmid pBBR1MCS-5- <i>d2hgdh</i> ; Gm ^r *
<i>P. stutzeri</i> A1501- Δ <i>etf-etf</i> ⁺	A1501- Δ <i>etf</i> strain harboring the plasmid pBBR1MCS-5- <i>etf</i> ; Gm ^r *
<i>P. stutzeri</i> A1501- Δ <i>d2hgdh-dmlA</i> ⁺	A1501- Δ <i>d2hgdh</i> strain harboring the plasmid pBBR1MCS-5- <i>dmlA</i> ; Gm ^r *
<i>P. stutzeri</i> A1501-pME6522- <i>P_{d2hgdh}</i>	<i>P. stutzeri</i> A1501 strain harboring the transcriptional fusions plasmid pME6522- <i>P_{d2hgdh}</i>
BL-D2HGDH	<i>E. coli</i> BL21(DE3) strain harboring the expression plasmid pET- <i>d2hgdh</i>
BL-ETF	<i>E. coli</i> BL21(DE3) strain harboring the expression plasmid pET- <i>etfAB</i>
BL-SerA	<i>E. coli</i> BL21(DE3) strain harboring the expression plasmid PET- <i>serA</i>
BL-DmlA	<i>E. coli</i> BL21(DE3) strain harboring the expression plasmid PET- <i>dmlA</i>
<i>E. coli</i> K-12 MG1655-WT	wild strain of <i>E. coli</i> MG1655
<i>E. coli</i> K-12 MG1655- Δ <i>dmlA</i>	<i>E. coli</i> MG1655 strain mutant obtained by exchanging the <i>dmlA</i> gene with the <i>Kana</i>
<i>E. coli</i> K-12 MG1655- Δ <i>dmlA-dmlA</i> ⁺	MG1655- Δ <i>dmlA</i> strain harboring the plasmid pMMB66EH- <i>dmlA</i> ; Ap ^r *
<i>E. coli</i> K-12 MG1655- Δ <i>dmlA-d2hgdh</i> ⁺	MG1655- Δ <i>dmlA</i> strain harboring the plasmid pMMB66EH- <i>d2hgdh</i> ; Ap ^r *
Plasmid	
pk18 <i>mobsacB</i>	Allelic exchange suicide vector mobilized by <i>E. coli</i> S17-1 λ <i>pir</i> ; for selecting double crossover; Km ^r Suc ^s *
pk18- <i>d2hgdh'</i>	pk18 <i>mobsacB</i> carrying <i>d2hgdh'</i>
pk18- <i>etf'</i>	pk18 <i>mobsacB</i> carrying <i>etfAB'</i>
pET28a(+)	vector for protein expression, Km ^r *

pET- <i>dmlA</i>	pET28a(+) carrying <i>dmlA</i> gene
pBBR1MCS-5	broad host range cloning vector; Gm ^r *
pBBR- <i>dmlA</i>	pBBR1MCS-5 carrying <i>dmlA</i> gene
pMMB66EH	broad host range <i>tacP</i> expression vector; <i>lacI</i> ^q ; Ap ^r *
pMM- <i>d2hgdh</i>	pMMB66EH carrying <i>d2hgdh</i> gene
pMM- <i>dmlA</i>	pMMB66EH carrying <i>dmlA</i> gene
pME6522	<i>E. coli</i> - <i>Pseudomonas</i> shuttle vector for transcriptional <i>lacZ</i> fusions and promoter probing, Tc ^r *
pME6522- <i>P</i> _{<i>d2hgdh</i>}	A 199 bp fragment upstream translation initiation site of <i>d2hgdh</i> was ligated into the pME6522

*Km^r, Gm^r, Tc^r and Ap^r indicate resistance to kanamycin, gentamicin sulphate, tetracycline and ampicillin, respectively. Suc^s indicates sensitive to sucrose.

TABLE S2.

Primers used in this study.

Primer	Sequence
PD1	5'- TATCCATGGGCATGATGAAAACGATGCGT - 3' †
PD2	5'- GACGGATCCACGCAAATAATTTTGCAAATCG - 3' †
PBA1	5'- AATTGGATCCATGATGAAAACGATGCG - 3' †
PBA2	5'- AATTAAGCTTTTAACGCAAATAATTT - 3' †
PMD1	5'- AATTGGATCCATGACCGACCCCGCCCTGA - 3' †
PMD2	5'- AATTAAGCTTTCAGGCCGCGAAGATCTTGC - 3' †
PMA1	5'- AATTGGATCCATGATGAAAACGATGCG - 3' †
PMA2	5'- AAGGAAGCTTTTAACGCAAATAATTT - 3' †
6522D1	5'- AATTGAATTCCTGCATTAACCTTAAGGCC - 3' †
6522D2	5'- AATTCTGCAGCACGGAACTTCATACGAT - 3' †

† *Nco*I, *Bam*HI, *Hind*III, *Eco*RI, and *Pst*I restriction sites introduced in the primers are underlined.