

Supplementary materials

Table S1 The bacterial strains used in this study.

Strain	Culture medium	Source
<i>Vibrio cholerae</i> GIM1.449	TSB	GCCC, China
<i>Vibrio parahaemolyticus</i> ATCC 17802	TSB	ATCC, United States
<i>Klebsiella pneumoniae</i> 8-2-5-4	TSB	LS-SHOU, China
<i>Klebsiella oxytoca</i> 8-3-38	TSB	LS-SHOU, China
<i>Staphylococcus aureus</i> ATCC 25923	TSB	ATCC, United States
<i>Lactobacillus plantarum</i> D27	MRS	LS-SHOU, China

Note: ATCC: American Type Culture Collection, USA; GCCC, Guangdong Culture Collection Center, Guangzhou, China; LS-SHOU, Laboratory stock, Shanghai Ocean University, Shanghai, China.

Table S2 The DEGs in the main altered metabolic pathways of *V. cholerae* GIM1.449 after exposed to the 100 nm PS-MPs.

Metabolic pathway	Gene ID	Fold change	Gene description
Glycolysis / Gluconeogenesis	<i>GTH07_01055</i>	0.162	6-phosphofructokinase
	<i>GTH07_04225</i>	0.12	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>GTH07_02220</i>	0.244	Phosphopyruvate hydratase
	<i>GTH07_01140</i>	0.198	Triose-phosphate isomerase
	<i>GTH07_04320</i>	0.251	PTS glucose transporter subunit IIBC
	<i>GTH07_04385</i>	0.099	D-hexose-6-phosphate mutarotase
	<i>GTH07_04390</i>	0.098	Type I glyceraldehyde-3-phosphate dehydrogenase
	<i>GTH07_11470</i>	0.183	Pyruvate kinase PykF
	<i>GTH07_12095</i>	0.298	Glucose-6-phosphate isomerase
	<i>GTH07_11500</i>	0.279	Phosphoglycerate kinase
	<i>GTH07_11495</i>	0.286	Class II fructose-bisphosphate aldolase
	<i>GTH07_12320</i>	0.231	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
	<i>GTH07_06320</i>	4.428	Galactose-1-epimerase
	<i>GTH07_06480</i>	2.747	6-phospho-beta-glucosidase
	<i>GTH07_17335</i>	2.789	Glyceraldehyde-3-phosphate dehydrogenase
	<i>GTH07_07795</i>	2.193	6-phospho-beta-glucosidase
	<i>GTH07_15895</i>	2.45	Pyruvate:ferredoxin (flavodoxin) oxidoreductase

Butanoate metabolism	<i>GTH07_01060</i>	0.462	Class II fructose-bisphosphatase
	<i>GTH07_05230</i>	2.423	Aldehyde dehydrogenase
	<i>GTH07_04225</i>	0.12	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>GTH07_03950</i>	4.04	Succinate dehydrogenase flavoprotein subunit
	<i>GTH07_03955</i>	4.391	Succinate dehydrogenase iron-sulfur subunit
	<i>GTH07_05005</i>	0.08	Formate C-acetyltransferase
	<i>GTH07_13245</i>	4.79	Fatty acid oxidation complex subunit alpha FadB
	<i>GTH07_00095</i>	3.881	Acetolactate synthase 2 catalytic subunit
	<i>GTH07_08920</i>	3.083	Fatty acid oxidation complex subunit alpha FadJ
	<i>GTH07_17085</i>	0.245	Trans-2-enoyl-CoA reductase family protein
	<i>GTH07_17280</i>	2.736	Acetoacetate--CoA ligase
	<i>GTH07_03945</i>	3.15	Succinate dehydrogenase, hydrophobic membrane anchor protein
	<i>GTH07_00090</i>	7.644	Acetolactate synthase 2 small subunit
	<i>GTH07_15895</i>	2.45	Pyruvate:ferredoxin (flavodoxin) oxidoreductase
	<i>GTH07_16665</i>	2.162	Acetyl-CoA C-acetyltransferase
Fatty acid degradation	<i>GTH07_16670</i>	2.118	SDR family oxidoreductase
	<i>GTH07_05600</i>	10.093	Acyl-CoA dehydrogenase
	<i>GTH07_04225</i>	0.12	Bifunctional acetaldehyde-CoA/alcohol dehydrogenase
	<i>GTH07_13245</i>	4.79	Fatty acid oxidation complex subunit alpha FadB
	<i>GTH07_13250</i>	5.432	Acetyl-CoA C-acyltransferase FadA
	<i>GTH07_03225</i>	5.843	Acyl-CoA dehydrogenase
	<i>GTH07_02045</i>	0.326	Long-chain fatty acid-CoA ligase
	<i>GTH07_08920</i>	3.083	Fatty acid oxidation complex subunit alpha FadJ
	<i>GTH07_08925</i>	2.581	Acetyl-CoA C-acyltransferase FadI
	<i>GTH07_16665</i>	2.162	Acetyl-CoA C-acetyltransferase
Citrate cycle (TCA cycle)	<i>GTH07_03950</i>	4.04	Succinate dehydrogenase flavoprotein subunit
	<i>GTH07_03955</i>	4.391	Succinate dehydrogenase iron-sulfur subunit
	<i>GTH07_03960</i>	4.988	2-oxoglutarate dehydrogenase E1 component
	<i>GTH07_03965</i>	5.416	2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase
	<i>GTH07_03970</i>	6.197	ADP-forming succinate-CoA ligase subunit beta
	<i>GTH07_03975</i>	6.2	Succinate-CoA ligase subunit alpha
	<i>GTH07_01190</i>	0.297	Fumarate reductase subunit FrdD
	<i>GTH07_01200</i>	0.396	Succinate dehydrogenase/fumarate reductase iron-sulfur subunit
	<i>GTH07_01205</i>	0.359	Fumarate reductase (quinol) flavoprotein subunit

Biosynthesis of siderophore group nonribosomal peptides	<i>GTH07_08470</i>	2.032	NADP-dependent isocitrate dehydrogenase
	<i>GTH07_06420</i>	26.509	Class II fumarate hydratase
	<i>GTH07_03945</i>	3.15	Succinate dehydrogenase, hydrophobic membrane anchor protein
	<i>GTH07_01195</i>	0.424	Fumarate reductase subunit FrdC
	<i>GTH07_15895</i>	2.45	Pyruvate:ferredoxin (flavodoxin) oxidoreductase
	<i>GTH07_10200</i>	51.917	Vibriobactin biosynthesis bifunctional isochorismatase/aryl carrier protein VibB
Propanoate metabolism	<i>GTH07_03325</i>	18.217	Non-ribosomal peptide synthetase
	<i>GTH07_10185</i>	43.968	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
	<i>GTH07_10190</i>	39.822	Isochorismate synthase MenF
	<i>GTH07_10195</i>	10.823	(2,3-dihydroxybenzoyl) adenylate synthase
	<i>GTH07_10155</i>	6.11	4'-phosphopantetheinyl transferase superfamily protein
	<i>GTH07_10180</i>	7.483	Norspermidine-2,3-dihydroxybenzoate synthase VibH
	<i>GTH07_03970</i>	6.197	ADP-forming succinate--CoA ligase subunit beta
	<i>GTH07_03975</i>	6.2	Succinate--CoA ligase subunit alpha
	<i>GTH07_14420</i>	0.086	Acetate/propionate family kinase
	<i>GTH07_05005</i>	0.08	Formate C-acetyltransferase
	<i>GTH07_08680</i>	0.138	Acetate kinase
	<i>GTH07_08685</i>	0.137	Phosphate acetyltransferase
	<i>GTH07_13245</i>	4.79	Fatty acid oxidation complex subunit alpha FadB
	<i>GTH07_08920</i>	3.083	Fatty acid oxidation complex subunit alpha FadJ
	<i>GTH07_07550</i>	3.095	Fe/S-dependent 2-methylisocitrate dehydratase AcnD
	<i>GTH07_00070</i>	2.496	Oxidoreductase
	<i>GTH07_07540</i>	3.634	Propionyl-CoA synthetase
	<i>GTH07_07545</i>	3.957	2-methylaconitate cis-trans isomerase PrpF
Valine, leucine and isoleucine degradation	<i>GTH07_07560</i>	2.751	Methylisocitrate lyase
	<i>GTH07_07555</i>	2.783	2-methylcitrate synthase
	<i>GTH07_13245</i>	4.79	Fatty acid oxidation complex subunit alpha FadB
	<i>GTH07_13250</i>	5.432	Acetyl-CoA C-acyltransferase FadA
	<i>GTH07_08920</i>	3.083	Fatty acid oxidation complex subunit alpha FadJ
	<i>GTH07_17280</i>	2.736	Acetoacetate--CoA ligase
	<i>GTH07_00085</i>	3.49	Branched-chain-amino-acid transaminase
	<i>GTH07_08925</i>	2.581	Acetyl-CoA C-acyltransferase FadI
	<i>GTH07_16665</i>	2.162	Acetyl-CoA C-acetyltransferase

Starch and sucrose metabolism	<i>GTH07_16510</i>	0.424	Glycoside hydrolase family 32 protein
	<i>GTH07_16500</i>	0.242	PTS sucrose transporter subunit IIBC
	<i>GTH07_12095</i>	0.298	Glucose-6-phosphate isomerase
	<i>GTH07_13435</i>	2.563	Glycogen/starch/alpha-glucan phosphorylase
	<i>GTH07_18180</i>	2.125	Glycogen debranching protein GlgX
	<i>GTH07_13440</i>	3.453	4-alpha-glucanotransferase
	<i>GTH07_06480</i>	2.747	6-phospho-beta-glucosidase
	<i>GTH07_17405</i>	2.826	Alpha-amylase
	<i>GTH07_07795</i>	2.193	6-phospho-beta-glucosidase
	<i>GTH07_16515</i>	0.49	Aminoimidazole riboside kinase
Fructose and mannose metabolism	<i>GTH07_07800</i>	2.004	PTS lactose/cellobiose transporter subunit IIA
	<i>GTH07_01055</i>	0.162	6-phosphofructokinase
	<i>GTH07_15830</i>	2.435	PTS fructose transporter subunit IIBC
	<i>GTH07_01140</i>	0.198	Triose-phosphate isomerase
	<i>GTH07_11495</i>	0.286	Class II fructose-bisphosphate aldolase
	<i>GTH07_18240</i>	4.61	Phospho-sugar mutase
	<i>GTH07_15835</i>	2.47	1-phosphofructokinase
	<i>GTH07_18260</i>	2.29	Mannitol-1-phosphate 5-dehydrogenase
	<i>GTH07_01060</i>	0.462	Class II fructose-bisphosphatase
	<i>GTH07_16515</i>	0.49	Aminoimidazole riboside kinase
Bacterial chemotaxis	<i>GTH07_17810</i>	4.046	Maltose/maltodextrin ABC transporter substrate-binding protein MalE
	<i>GTH07_07605</i>	4.187	Galactose/glucose ABC transporter substrate-binding protein MglB
	<i>GTH07_13945</i>	6.39	Ribose ABC transporter substrate-binding protein RbsB
	<i>GTH07_05040</i>	2.718	Methyl-accepting chemotaxis protein
	<i>GTH07_18190</i>	0.406	Methyl-accepting chemotaxis protein
	<i>GTH07_18205</i>	2.74	Methyl-accepting chemotaxis protein
	<i>GTH07_04995</i>	2.868	Methyl-accepting chemotaxis protein
	<i>GTH07_17955</i>	2.929	Methyl-accepting chemotaxis protein
	<i>GTH07_18485</i>	2.755	Chemotaxis protein CheA
	<i>GTH07_18470</i>	2.609	HAMP domain-containing protein
	<i>GTH07_13420</i>	2.049	HAMP domain-containing protein
	<i>GTH07_18465</i>	3.213	Protein-glutamate O-methyltransferase CheR
	<i>GTH07_07270</i>	2.955	Chemotaxis protein CheW
	<i>GTH07_07265</i>	2.385	Chemotaxis protein
	<i>GTH07_08750</i>	2.056	Chemotaxis protein CheC

	<i>GTH07_17425</i>	0.467	PAS domain S-box protein
	<i>GTH07_07295</i>	2.485	Chemotaxis protein CheA
	<i>GTH07_18460</i>	2.64	Chemoreceptor glutamine deamidase CheD
	<i>GTH07_18480</i>	2.584	Purine-binding chemotaxis protein CheW
	<i>GTH07_13670</i>	2.08	Methyl-accepting chemotaxis protein
	<i>GTH07_18000</i>	3.468	Methyl-accepting chemotaxis protein
	<i>GTH07_18475</i>	2.707	Ppurine-binding chemotaxis protein CheW
	<i>GTH07_07275</i>	2.287	Chemotaxis protein CheB
	<i>GTH07_18490</i>	2.559	Response regulator
	<i>GTH07_07305</i>	5.88	Response regulator
	<i>GTH07_07285</i>	2.023	Protein-glutamate O-methyltransferase CheR
Histidine metabolism	<i>GTH07_08175</i>	2.188	Urocanate hydratase
	<i>GTH07_08180</i>	2.369	Histidine ammonia-lyase
	<i>GTH07_08480</i>	2.331	Bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase HisIE
	<i>GTH07_08510</i>	2.04	Histidinol dehydrogenase
	<i>GTH07_08505</i>	2.287	Histidinol-phosphate transaminase
	<i>GTH07_08485</i>	2.169	Imidazole glycerol phosphate synthase subunit HisF
	<i>GTH07_08495</i>	2.264	Imidazole glycerol phosphate synthase subunit HisH
Ascorbate and aldarate metabolism	<i>GTH07_14485</i>	2.905	L-ascorbate 6-phosphate lactonase
	<i>GTH07_17065</i>	2.036	Nucleotide sugar dehydrogenase
	<i>GTH07_14450</i>	0.419	L-ribulose-5-phosphate 3-epimerase
	<i>GTH07_14455</i>	0.45	3-keto-L-gulonate-6-phosphate decarboxylase UlaD
	<i>GTH07_14465</i>	0.463	L-ribulose-5-phosphate 4-epimerase

Table S3 The oligonucleotide primers designed and used in the RT-qPCR assay.

Target gene	Primer	Sequence (5' to 3')	Predicted size (bp)	Reference
16s RNA	16s RNA-F	GACACGGTCCAGACTCCTAC	179	In this study
	16s RNA-R	GGTGCTTCTTCTGTCGCTAAC		
<i>GTH07_14620</i>	<i>glyA</i> -F	ACTAACAAATACGCCGAAGG	215	In this study
	<i>glyA</i> -R	GCATCTAGCGACATACCCATA		
<i>GTH07_00095</i>	<i>ilvB</i> -F	CCCGTGCTGGTGGACATA	238	In this study
	<i>ilvB</i> -R	TGCTCACTGAAGGCATAGGAT		

<i>GTH07_08750</i>	<i>cheC</i> -F	GCGTCATCGTGGATTTGT	112	In this study
	<i>cheC</i> -R	TGATTGGTCAGGGTCGTG		
<i>GTH07_07305</i>	<i>cheY</i> -F	AAGATGGCGTTGAAGCAG	125	In this study
	<i>cheY</i> -R	GGGTAAAGCGATAAGCAC		
<i>GTH07_10180</i>	<i>vibH</i> -F	TAAACAGTCAGGGCAAGCG	225	In this study
	<i>vibH</i> -R	GGTGAGCCACGAAAGGTAA		

Table S4 The relative expression of representative DEGs in *V. cholerae* GIM 1.449 by the RT-qPCR assay.

Gene_ID	Encoding protein	Fold change	
		RNA-Seq.	RT-qPCR
<i>GTH07_14620</i>	Serine hydroxymethyltransferase	2.881	3.636
<i>GTH07_00095</i>	Acetolactate synthase 2 catalytic subunit	3.881	5.316
<i>GTH07_08750</i>	Chemotaxis protein CheC	2.056	2.800
<i>GTH07_07305</i>	Response regulator	5.88	7.608
<i>GTH07_10180</i>	Norspermidine-2,3-dihydroxybenzoate synthase VibH	7.483	5.443