

Supplementary Materials

# **Gamma-aminobutyric acid accumulation contributes to *Citrus sinensis* response against ‘*Candidatus Liberibacter asiaticus*’ via modulation of multiple metabolic pathways and redox status**

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**Table S1.** Primers used for gene expression analysis by real time RT-PCR in this study <sup>a</sup>.

Gene	Abbreviation	Pathway	Accession ID		Primer (Forward and Reverse)
$\gamma$ -Aminobutyrate (GABA) permease (aka amino-acid permease BAT1-like)	<i>CsgabP</i>	GABA shunt	XM_006468698.3	F	TTCATCCCCGGACCTTTCAA
				R	CGAGCACTGAAGATCCAAGC
GABA transaminase 3	<i>CsgabT</i>	GABA shunt	XM_006481305.2	F	CTCCTGAATGGGGATAGGT
				R	TGCTGGGACTTGAGTTCCTT
GABA dehydrogenase (aka succinate-semialdehyde dehydrogenase [SSADH])	<i>CsgabD</i>	GABA shunt	XM_006493686.2	F	CAACGTACATGGCGTGTCTC
				R	CTGGCCCATCATTTTCTGTT
Glutamate decarboxylase-like	<i>CsGAD</i>	GABA shunt	NM_001288909.1	F	ATAGCCCGACTGTTCAATGC
				R	ATTTCTCCAGCAGACCTGA
Glutamate decarboxylase 5-like	<i>CsGAD5</i>	GABA shunt	XM_006478039.2	F	CCTTGACGGGAGAATTTGAG
				R	GCCGTACTTGTGACCACTGA
Glutamate dehydrogenase 1	<i>CsGDH1</i>	GABA shunt	XM_006479045.2	F	CTTTGAGTGGGTGCAGAACA
				R	CTCAAGCTTCCCAACCTCTG
Glutamate dehydrogenase 2	<i>CsGDH2</i>	GABA shunt	XM_006477017.2	F	CTCACCAGAGGTGTTACCG
				R	CCAAAACCTTGGATAGCAAA
5-Oxoprolinase	<i>CsOXP1</i>	GABA shunt	XM_006478626.2	F	ATCCCTCCAGGCTCATTTCT
				R	CACCTCCACCTCCGATTGTT
Glutamate synthase [NADH], amyloplastic	<i>CsGS</i>	GABA shunt	XM_006490447.2	F	GCTCAACCCATGCGTATCTT
				R	CGAACCAGAGCTCAAGGAC
Glutamate 5-kinase	<i>CsG5K</i>	GABA shunt	XM_006483017.2	F	ACGGTAACCAGACAGCAACC
				R	CCAGGTCTCTTGCTCCAATC
$\gamma$ -Glutamyltranspeptidase 1-like	<i>Csy-GT1-like</i>	GABA shunt	XM_006464249.2	F	GTGGCTCCAACAACACAGA
				R	GCATAAAGGATCTCCACCA
$\gamma$ -Glutamyltranspeptidase 3	<i>Csy-GT3</i>	GABA shunt	XM_006475300.2	F	TGGAGTTCCCGGTGAGATAG
				R	CCATTTGTGCAAACTTGG
$\gamma$ -Glutamyltranspeptidase 3-like	<i>Csy-GT3-like</i>	GABA shunt	XM_006475299.2	F	TGGAGGACTCTGTTCCAACC
				R	CAGGCTCTGAGCAAGCTTTT
$\gamma$ -Glutamylcyclotransferase-1	<i>Csy-GCT-1</i>	GABA shunt	XM_006478365.2	F	ACTACGAGAGGCTCCCAATT
				R	TCGATTGCCACGTACTCTTG
$\gamma$ -Glutamylcyclotransferase-2	<i>Csy-GCT-2</i>	GABA shunt	XM_006484538.2	F	CAGCTTTATCGATCGCTTCC
				R	GGATCAGTTGTGGTTCGAG
Glutamate-cysteine ligase, chloroplastic <sup>b</sup>	<i>Csy-GCL</i>	GABA shunt	XM_006476514.1	F	CGGAGGATGCTGTTGTTGTA
				R	CTCCCAATCGAACCCTCAG
Glutaminyl-peptide cyclotransferase <sup>c</sup>	<i>CsQPCT</i>	GABA shunt	XM_006490569.2	F	CGGTTCTTCAGTTCGGAGAG
				R	CCCAACCATCTTTCATCTG
Pyrrolidone-carboxylate peptidase 1 <sup>d</sup>	<i>CsPCP1</i>	GABA shunt	XM_006480219.2	F	CCATTTTCTGCTGATGGT
				R	GGCACATGAACGAAGAGTGA
Tyrosine decarboxylase 1	<i>CsTDC1</i>	Amino acids	XM_006479363.2	F	GCTCAGTGCTGCTCTCAACA
				R	CCTTATCACGAGCAGCCAA
Arginine decarboxylase-like	<i>CsADC</i>	Amino acids	XM_006487236.2	F	GTCCCTTCAGTCAGCCTTTG
				R	TGCACAAGCAACTCATAGCC
Argininosuccinate lyase, chloroplastic	<i>CsASL</i>	Amino acids	XM_006472396.2	F	TGAGCCAAAGCACAAGACTG
				R	GTGCTGATCAAACCTGTGT
Argininosuccinate synthase, chloroplastic	<i>CsASS</i>	Amino acids	XM_006476944.2	F	AGTCTCGGGAATCCCTGTGT
				R	AAGGACTCAAGCTCTCTGCAC
$\delta$ -1-Pyrroline-5-carboxylate dehydrogenase 12A1	<i>CsP5CDH</i>	Amino acids	XM_006476581.1	F	TGCCAAAGGTCTCCAATTTT
				R	GGACCATAAGGCCAAGCATA
Proline dehydrogenase 1, mitochondrial-like	<i>CsProDH</i>	Amino acids	XM_006482264.1	F	TTGCAGGGATTCTCCAAC
				R	CTGCAATCCGAGAAAAGAGG
Serine acetyltransferase 1, chloroplastic-like	<i>CsSAT1</i>	Amino acids	XM_006474855.2	F	AAGAGACCTGCGTGCAATA
				R	AAAGTAACCCACGTCCGAT
Serine acetyltransferase 5	<i>CsSAT5</i>	Amino acids	XM_006475346.2	F	GAGCTCAGTACCCATCTCC
				R	AGAGAGTGGAGAGAAGCGTG
Cysteine synthase	<i>CsCysK</i>	Amino acids	XM_006471676.1	F	CCAGCTGCTTGACATTGTT
				R	AGCAGGGTTCATCATCTCC
Methionine synthase 2 <sup>e</sup>	<i>CsMS2</i>	Amino acids	XM_006479085.2	F	GTCCATGGAGAGCCTGAGAG
				R	ATGGTGACAGGGCCAGTAAG
Cystathionine gamma-synthase 1, chloroplastic	<i>CsCGS</i>	Amino acids	XM_006482566.3	F	AGATGGAACCTTTGCCACAC
				R	GAGAGCACCAACCCAAACAT
Cystathionine beta-lyase, chloroplastic	<i>CsCBL</i>	Amino acids	XM_006492446.3	F	GCAGGTGTGCTTGCTGTAAA
				R	GTCCAGGATGTTGAGGAGA
Chorismate synthase	<i>CsCS</i>	Salicylic acid	XM_006485798.2	F	ACTGGAACCCCATCCATGT
				R	GAAATGAAGCCATCCAGAA
Chorismate mutase	<i>CsCM</i>	Salicylic acid	XM_006482655.2	F	GGGAGCTTGCTTGATTCTTG
				R	GTACGCAGCTTGATGTTGGA
Arogenate dehydratase/prephenate dehydratase 1, chloroplastic	<i>CsADT</i>	Salicylic acid	XM_006467360.2	F	TTGGTGCCTAACAGATGTGG
				R	CCTTGTGAAAGCCAGAGGAC
Aspartate aminotransferase, cytoplasmic-like	<i>CsAST</i>	Salicylic acid	XM_006476023.2	F	GCTTCTCCAAGCATCTGTCT
				R	GTTTGAGCGGACTCCATCAT
Tyrosine aminotransferase	<i>CsTAT</i>	Salicylic acid	XM_006469841.1	F	GTGGAATTCAGGGCTATCG
				R	TCGAGATGGTATGTGTTGC
Isochorismate synthase	<i>CsICS</i>	Salicylic acid	XM_006476586.2	F	TGCCGGAACAGGGATAGTAG
				R	CTTGGTGAACTGCACAATGG
Phenylalanine ammonia-lyase	<i>CsPAL</i>	Salicylic acid	XM_006481431.2	F	GTTCTGGCCTGGCTTCTATG
				R	ATAAGAGCTGCCATCGAGGA
3-Ketoacyl-CoA thiolase 2	<i>CsKAT2</i>	Salicylic acid	XM_006489736.1	F	GGGTACAGTTTGGCACCAG
				R	CAGGCACAGTTTCTGAACCA

Alcohol acyl transferase	<i>CsAAT</i>	Salicylic acid	NM_001288910.1	F	CTCGTGTGTGATGTGCGTCTT
				R	TGGCCTCTCCGGAACATTATA
$\omega$ -3-Fatty acid desaturase	<i>CsFAD</i>	Jasmonic acid	XM_006480990.2	F	CAGATCCCGCATTACCACTT
				R	GGTATCGGTCCCGATTCTT
Lipoxygenase	<i>CsLOX</i>	Jasmonic acid	XM_006483993.1	F	TGGCTGTCCAAGCACTCTG
				R	CAGCACCACATCTGCCTTTA
Allene oxide synthase	<i>CsAOS</i>	Jasmonic acid	NM_001288906.1	F	GTTTCAGCTCGCTCCGTTAC
				R	GAGGTTGTGACACGCTTCCT
Allene oxide cyclase	<i>CsAOC</i>	Jasmonic acid	NW_006260521.1	F	GCGAGTGGGAATTACAGCAG
				R	TTAACCTGCCCACTCACTCC
Acetate/butyrate--CoA ligase AAE7	<i>CsAAE7</i>	Jasmonic acid	XM_006488806.2	F	CCACCAGAGGACACAATCCT
				R	CTGAGCTTCGAAAGGGAGTG
12-Oxophytodienoate reductase 3	<i>CsOPR3</i>	Jasmonic acid	XM_006475468.2	F	TGCCACTTCTCTTGTGTGG
				R	AAATGGTAGCGTCCCTTCT
Acyl-coenzyme A1	<i>CsACX1</i>	Jasmonic acid	XM_006477083.2	F	ACGGATCATTGAGCTTCGTC
				R	CCAGTGGAGATCCGTAAAA
Enoyl-CoA hydratase, mitochondrial-like	<i>CsAIM</i>	Jasmonic acid	XM_006488772.2	F	TAATCCTCGTGACCCGAGAC
				R	CTCTGCTGACGTCAATCCA
3-Ketoacyl-CoA thiolase , peroxisomal-like	<i>CsKAT</i>	Jasmonic acid	XM_006480138.2	F	ATACCTGTGCGGTGAAGTC
				R	AGGATCAAGCCCCAGTTTCT
Anthranilate synthase alpha subunit 1	<i>CsASA</i>	Auxins	XM_015532734.1	F	TTGAGCTTCAACCGGAGACT
				R	ACTGAAAGTTGCTCGGACT
Anthranilate synthase beta subunit 2	<i>CsASB</i>	Auxins	XM_006469235.2	F	CAATCGCACAGTTGCTCAGT
				R	GCTCAGGGATTGCAGAGAGA
Tryptophan synthase alpha chain, chloroplastic-like	<i>CsTSA</i>	Auxins	XM_006470948.2	F	TACGGAAGGAAGCCATCAAG
				R	GGAGTGGTGGGACCTGTAAA
Tryptophan synthase beta chain 1, chloroplastic-like	<i>CsTSB</i>	Auxins	XM_006493882.2	F	GTGTTGCATGGTGCTTTGAG
				R	CAGGTCCAACCTCCAGGGTAA
Tryptophan aminotransferase-related protein 2-like	<i>CsTAA2</i>	Auxins	XM_015529685.1	F	AATGGAACGGGTTGTCTGG
				R	TCATCAGGGATATGGGAAGG
Tryptophan aminotransferase-related protein 4-like	<i>CsTAA4</i>	Auxins	XM_006473060.2	F	CGCATCTGGTTGAGTTTGTG
				R	TAGAGCAGCATGACCACTG
Indole-3-pyruvate monooxygenase YUCCA2	<i>CsYUC2</i>	Auxins	XM_006466708.2	F	CTGGCCCTGTAATTGTGTGGT
				R	ACGAGGGAATGGCACATAAG
Indole-3-pyruvate monooxygenase YUCCA8	<i>CsYUC8</i>	Auxins	XM_006480095.2	F	CTACGGGTACCCGAGCAAT
				R	ATTTCTTTCCAGCCATGTG
Aromatic-L-amino-acid decarboxylase-like (aka tryptophan decarboxylase)	<i>CsTDC1</i>	Auxins	XM_006469752.3	F	CGACTTTATGGCTGGAAAA
				R	GGGGTGACAACCTATCCTCA
Indole-3-acetaldehyde oxidase-like (aka Acetaldehyde oxidase)	<i>CsAO1</i>	Auxins	XM_006487737.2	F	GGGATCAGACAGGAATCGAA
				R	CCGCCCCAAGAAGTATTGTA
Zeaxanthin epoxidase	<i>CsZEP</i>	Absciscic acid	XM_006466537.2	F	CGCGTTGTGCTTCTAGGTTT
				R	CGATCACCTTAACCCGAAAA
Violaxanthin de-epoxidase	<i>CsVDE</i>	Absciscic acid	NM_001288881.1	F	AATCGCATACCAACCTGCTC
				R	GGTTTGAAGGCAAGCAACAT
Neoxanthin synthase	<i>CsNSY</i>	Absciscic acid	NM_001288932.1	F	AACGTTGACCAAAACCAGACC
				R	CTCACTGAGCACCGAAAGTG
9-cis-Epoxycarotenoid dioxygenase 3	<i>CsNCED</i>	Absciscic acid	NM_001288935.1	F	ATGGCGGCAGCACTACTAC
				R	CTGCAGGTGATGGAGGGTAT
Short chain alcohol dehydrogenase	<i>CsABA2</i>	Absciscic acid	NM_001288867.1	F	GCAATCTGCTGGCAATAGT
				R	ATGCCAGTAGCTCCACCTGT
Absciscic aldehyde oxidase	<i>CsAAO3</i>	Absciscic acid	XM_006487736.2	F	TTCTTTCAGGGGATTCTGTG
				R	CAACCTGTTGGGGTACCAG
1-Aminocyclopropane-1-carboxylate (ACC) synthase-like	<i>CsACS</i>	Ethylene	NM_001288902.1	F	CGAATCCAGGTTGGTTTAGA
				R	TCCTTCGAGATGACATGCTG
ACC oxidase	<i>CsACO</i>	Ethylene	NM_001288883.1	F	ACCTCGGTGACCAAAATTGAG
				R	TTTTTCAAGCAATGCTGGTG
S-Adenosylmethionine decarboxylase	<i>CsSAMDC</i>	Ethylene	NM_001288936.1	F	CCTGAAGGAAAGGCCCTTAG
				R	GGTGGGATTGAAAGAAGCAA
L-ascorbate peroxidase, cytosolic isoform X1	<i>CsAPX</i>	Antioxidant	XM_015533381.2	F	CATAGCGAGCTTGTGCTCTG
				R	ATGAGTGGAGCGCAGTTCTT
phospholipid hydroperoxide glutathione peroxidase	<i>CsGPX</i>	Antioxidant	XM_006476535.2	F	CAAGCATCTGAAATCCAGCA
				R	GCAAGAAGCTGATCATGCAA
cationic peroxidase 1-like	<i>CscPOX</i>	Antioxidant	XM_006481093.2	F	GTGGCCACACTATTGGCTTT
				R	AGTAGCCCTCGTTTCTGCAA
lignin-forming anionic peroxidase-like	<i>CsliPOX</i>	Antioxidant	XM_006470880.2	F	GCTACCAAAGGCTTGAATGC
				R	ACCATTAGCCGGCACTGAC
peroxidase A2-like	<i>CsPOX-A2</i>	Antioxidant	XM_006494741.3	F	GCAATCCAGACCCAACACTT
				R	TATTGACAATGGCAGCGGTA
peroxidase 3	<i>CsPOX3</i>	Antioxidant	XM_006469646.3	F	TTGAAATGGACCCCTGGTAGC
				R	CAGACTTGGCAAATTCAGCA
superoxide dismutase [Cu-Zn], chloroplastic	<i>CsSOD-Cu/Zn</i>	Antioxidant	XM_006487937.3	F	GGCTCACGTTCTCCTCGTAG
				R	AGAGGGGAATTGAGGGAGA
superoxide dismutase [Mn], mitochondrial	<i>CsSOD-Mn</i>	Antioxidant	XM_006486115.2	F	GGGCTATTGACACGCATTTT
				R	ACCAGTGGATCCTGATTTGC
superoxide dismutase [Fe] 2, chloroplastic-like	<i>CsSOD-Fe</i>	Antioxidant	XM_006484979.3	F	CAGTGCCCAATTACACATTGC
				R	TCTCATGGAAATTGGAAGC
superoxide dismutase [Fe] 3, chloroplastic isoform X1	<i>CsSOD-Fe3</i>	Antioxidant	XM_006484439.3	F	GGAATGACATCCCCATCATC
				R	ACATCCTTTGCTTGACGCTT
catalase-like isoform X1	<i>CsCAT</i>	Antioxidant	XM_006473726.2	F	AAGGCTTGCAATTGAGAAGGA
				R	CGGCCTGAGACCAGTAAGAG

Elongation factor-1 alpha	CsEF1	Reference gene	AY498567.1	F	GGAAGTTCGAGACCACCAAG
				R	ACACCAAGGGTGAAGCAAG
F-Box/kelch-repeat protein	CsF-box	Reference gene	XM_006482390.1	F	ACTTGACAGATGGGCTGTCC
				R	CAGCAACCAATACCGTCT

- <sup>a</sup> The listed genes were assembled based on recent available data in GenBank, National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).
- <sup>b</sup>  $\gamma$ -Glutamylcysteine synthetase ( $\gamma$ -GCS) from *Arabidopsis thaliana* has been matched as PREDICTED: *Citrus sinensis* glutamate-cysteine ligase, chloroplastic (CsGCL) using the protein-protein BLAST, based on recent available data in GenBank, National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).
- <sup>c</sup> Glutaminy cyclase (QC) from *Arabidopsis thaliana* has been matched as PREDICTED: *Citrus sinensis* glutaminy-peptide cyclotransferase (CsQPCT) using the protein-protein BLAST, based on recent available data in GenBank, National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).
- <sup>d</sup> Pyroglutamyl-peptidase (PGP) from *Arabidopsis thaliana* has been matched as PREDICTED: *Citrus sinensis* pyrrolidone-carboxylate peptidase 1 (CsPCP1) using the protein-protein BLAST, based on recent available data in GenBank, National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).
- <sup>e</sup> Methionine synthase 2 (MS2) from *Arabidopsis thaliana* has been matched as PREDICTED: *Citrus sinensis* 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase 1 using the protein-protein BLAST, based on recent available data in GenBank National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).
- <sup>f</sup> Ornithine transcarbamylase (OTC) from *Arabidopsis thaliana* has been matched as PREDICTED: *Citrus sinensis* ornithine carbamoyltransferase, chloroplastic (CsOTC) using the protein-protein BLAST, based on recent available data in GenBank, National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).
- <sup>g</sup> Para-aminobenzoic acid synthase (PABA synthase) from *Arabidopsis thaliana* has been matched as PREDICTED: *Citrus sinensis* aminodeoxychorismate synthase, chloroplastic (CsADCS) using the protein-protein BLAST, based on recent available data in GenBank National Center for Biotechnology Information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>).