

Supporting information

Pinpointing regulatory protein phosphatase 2A subunits involved in beneficial symbiosis between plants and microbes

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Table 1. List of primers

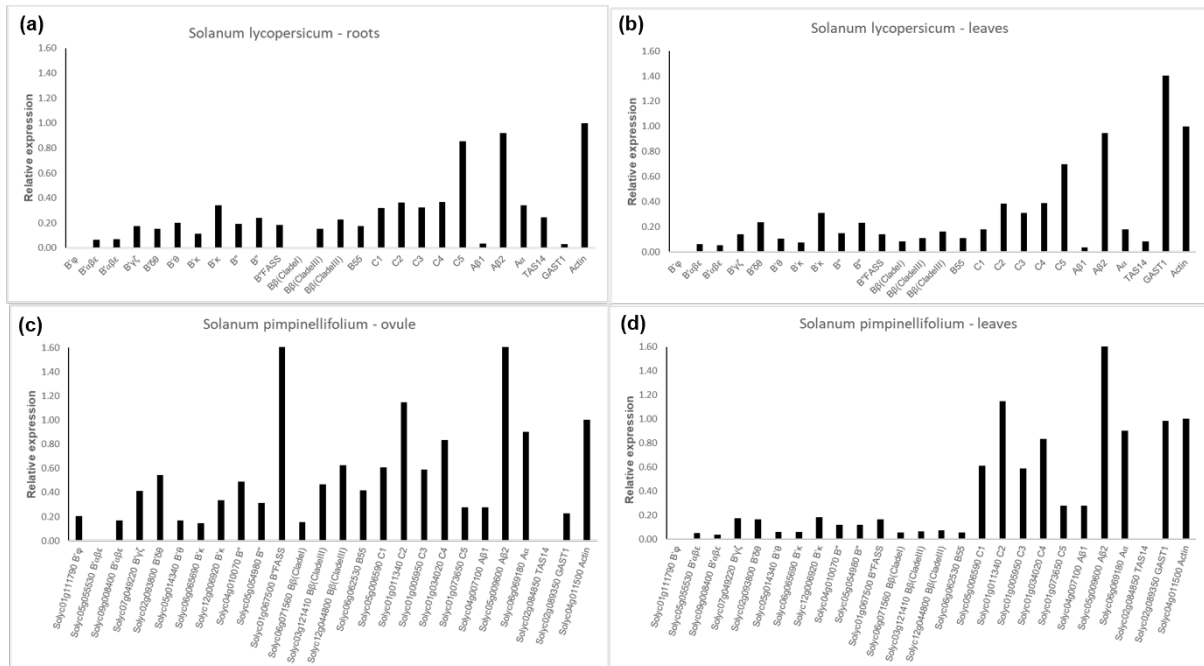
Target gene	Sequence (5' - 3')	Annealing (°C)	PCR Product Size (bp)
pBA002 cloning vector ^{a,b} pBA002-B'φ ox insert ^{a,b}	Forward: CGTCTTCAAAGCAAGTGGATTGATG Reverse: TGCTTAACGTAATTCAACAACAGAAATTAT	54	276 1762
B'φ PP2A-B'φ regulatory subunit (M. A. Booker & A. DeLong, 2017) ^a NCBI Reference Sequence: XM_010317091.2	Forward: ATGACAAATTTTCTTGATTCTGAGACAG ATCG Reverse: TCACATTGCTGCATTTTCAATTTTTTCCC	54	1486
B'φ PP2A-B'φ regulatory subunit ^b NCBI Reference Sequence: XM_010317091.2	Forward: GAGACTGATCAAAGGCACCCTGGAATCG Reverse: ACAATGCGCGTTCAGCAACCTGCGAG	61	406
B'θ PP2A B56 (Clade 6/9/10) ^b NCBI Reference Sequence: XM_004239128.4	Forward: AGGTGTATGGTGCCGTTGTT Reverse: GATGGCACAAGCACAGCTTCCA	55	389
Bβ (Clade I) PP2A B55 (CLADE I, Booker 2017) ^b NCBI Reference Sequence: XM_004241456.4	Forward: CTCACATGGAGTCTTCCCCG Reverse: AAGCCACATGCAGCAACTT	55	373
Bβ (Clade III) PP2A B55 (CLADE III) (M. A. Booker & A. DeLong, 2017) ^b NCBI Reference Sequence: XM_004252324.4, XM_019211570.2, XM_010316006.3 (transcript variant X1, X2, X3)	Forward: GTGGTGATGGTTCGCGAGTA Reverse: CATTTGCATCAACACCGGCA	56	213
B'κ PP2A-B56 (Clade B11) ^b NCBI Reference Sequence: XM_004251542.4 (transcript variant X1), XM_010315410.3 (transcript variant X2), XM_010315411.3 (transcript variant X3), XM_026028819.1 (transcript variant X4), XM_026028820.1 (transcript variant X5)	Forward: ACCTCTGCACAAGCCAAAGT Reverse: TCCAGTGGTTCTGGCTGTTC	56	392
A βI B65 or PP2A-A ^b NCBI Reference Sequence: XM_004236914.4 (transcript variant X1), XM_010321123.3 (transcript variant X2)	Forward: TAGCAAAGGACAGAGTGCCC Reverse: ACTGTTTCCTGGTGTGACGG	56	291

<i>A βII</i> B65 or PP2A-A ^b NCBI Reference Sequence: XM_004238897.4 (transcript variant X1), XM_019214032.2 (transcript variant X2)	Forward: TGCACCAGTAATGGGCTCTG Reverse: ACTGGGCCGAATGGTTTCT	56	166
Target gene	Sequence (5'- 3')	Annealing (°C)	PCR Product Size (bp)
<i>C1</i> PP2A catalytic subunit (PP2Ac1) ^b NCBI Reference Sequence: NM_001247587.2	Forward: GCGGCAACGTCCTGATTACTA Reverse: AGGCTCAATCTGTCGTGGAG	56	667
<i>C2</i> PP2A catalytic subunit (PP2Ac2) ^b NCBI Reference Sequence: NM_001246875.2	Forward: ATGCCGTCTCATGCAGATCTA Reverse: CTTCCTTGTGGTGTCTGGGCTCTA	54	900
<i>TAS 14</i> Absciscic acid and environmental stress- inducible protein ^b NCBI Reference Sequence: NM_001247109.1	Forward: CATCACCATGAGGGGCAACA Reverse: GCGTCAGCACACTTTACACG	56	363
<i>NCED-1</i> Nine-cis-epoxycarotenoid dioxygenase 1 ^b NCBI Reference Sequence: NM_001247526.2	Forward: GTGCAGAAAAGCAGCAGCAAT Reverse: CGTAAACCACCGGTGAACCT	55	871
<i>GA3ox-1</i> Gibberellin-3β-hydroxylase-1 ^b NCBI Reference Sequence: AB010991.1	Forward: AGGCCCAAAAGGTGAAACCA Reverse: CCGTACGGATGAAAGTGCCT	56	463
<i>GA3ox-2</i> Gibberellin-3β-hydroxylase-2 ^b NCBI Reference Sequence: NM_001246926.3	Forward: AGGCCCAAAAGGTGAAACCA Reverse: CCGTACGGATGAAAGTGCCT	51	276
<i>GA20ox-1</i> Gibberellin 20-oxidase-1 ^b NCBI Reference Sequence: NM_001247141.1	Forward: AGGCCCAAAAGGTGAAACCA Reverse: CCGTACGGATGAAAGTGCCT	51	451
<i>GA20ox-2</i> Gibberellin 20-oxidase-2 ^b NCBI Reference Sequence: NM_001247699.2	Forward: CTACAAGGCTCGTCCCACAT Reverse: TGAAAGCGCCATAAATGTGTC	51	402
<i>GA20ox-3</i> Gibberellin 20-oxidase-3 ^b NCBI Reference Sequence: NM_001247650.2	Forward: CCGGACCATGAGAAGCCAAA Reverse: GATAGTGCCATAAACGTGTCGC	55	752
<i>GA20ox-4</i> Gibberellin 20-oxidase-4 ^b	Forward: CTACAAGGCTCGTCCCACAT		

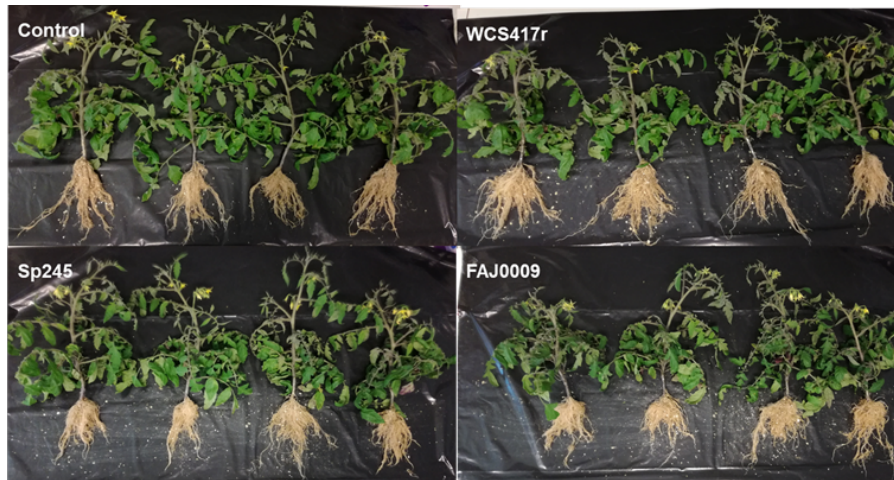
NCBI Reference Sequence: NM_001247434.2	Reverse: TGAAAGCGCCATAAATGTGTC	53	375
<i>GAST1</i> Gibberellin responsive gene NCBI Reference Sequence: NM_001309377.1	Forward: TCAGGTTTCAAGGGCCAACA Reverse: CACTTTGGGCCACCTCTTTTG	56	275
<i>Actin 41</i> Reference gene ^b NCBI Reference Sequence: NM_001330119.1	Forward: CACTGTATGCCAGTGGTCGT Reverse: GCATCTCTGGTCCAGTAGGAAA	58	773

^aPrimers used with **Phire® Hot Start II DNA Polymerase**

^bPrimers used in sqRT-PCR analysis



S1 Figure. Expression of PP2A subunit genes in *S. lycopersicum* roots and leaves, and *S. pimpinellifolium* ovules and leaves. Publicly available data from the Sol genetics database. Genes presented are named according to International Tomato Annotation Group, and orthologues in Arabidopsis. The genes presented are PP2A subunits: eight different B', three B'', four B/B55, five C and three A (A β 2 is 2.23, exceeding the scale), additionally TAS14, GAST1 and Actin. All are normalized to Actin 41 (set to 1).



S2 Figure. Visual phenotype of tomato plants three weeks after treatment with PGPR.

Two-month-old tomato plants not cultivated (upper left photo) and cultivated with WCS417r (upper right photo); Sp245 (lower left photo) and FAJ0009 (lower right photo).