

Supplementary Information

Long intergenic non-coding RNAs modulate proximal protein-coding gene expression and tolerance to *Candidatus Liberibacter* spp. in potatoes

Renesh Bedre^{1,§}, Naga Rajitha Kavuri^{1,2,§}, Manikandan Ramasamy¹, Sonia Irigoyen¹, Andrew Nelson³, Mohan Singh Rajkumar¹, Kranthi Mandadi^{1,2,4*}

¹Texas A&M AgriLife Research & Extension Center, Texas A&M University System, 2415 E. Highway 83, Weslaco 78596, TX, USA

²Department of Plant Pathology and Microbiology, Texas A&M University System, 2132 TAMU, College Station 77843, TX, USA

³Boyce Thompson Institute, Cornell University, 533 Tower Rd., Ithaca 14853, NY, USA

⁴Institute for Advancing Health Through Agriculture, Texas A&M AgriLife, College Station, TX, USA

[§]Equal contribution

*Corresponding author: kkmandadi@tamu.edu

Running Title: LincRNAs mediate potato defense responses.

Supplementary Table 1. RNA-Seq data analysis of CT, CLso(-), and CLso(+) conditions at 7, 14, and 21 DAI.

Days after infection (DAI)	Conditions	Biological replicates	Number of pair-end reads	Number of high-quality pair-end reads	Percentage of uniquely mapped reads
7 DAI	CT	1	13,576,628	13,487,676	58.4
		2	11,536,895	11,461,138	59.3
		3	10,794,191	10,716,101	58.8
	CLso(-)	1	11,358,992	11,291,153	59.6
		2	11,273,106	11,169,356	59.8
		3	10,329,479	10,272,722	60.1
	CLso(+)	1	10,271,728	10,197,411	60.7
		2	9,724,422	9,648,296	60.2
		3	11,423,992	11,353,822	60
14 DAI	CT	1	12,290,432	12,216,239	60.6
		2	3,832,745	3,814,875	54
		3	12,771,456	12,638,422	60.1
	CLso(-)	1	11,253,303	11,132,821	60.4
		2	10,870,649	10,781,165	59.9
		3	10,700,381	10,629,605	60.4
	CLso(+)	1	12,899,387	12,820,039	60.6
		2	12,218,065	12,137,821	59.7
		3	12,731,618	12,652,599	60.3
21 DAI	CT	1	12,140,126	12,079,831	58.4
		2	11,905,782	11,817,765	58.6
		3	11,056,344	10,989,709	57.9
	CLso(-)	1	10,486,900	10,423,115	60.5
		2	10,615,938	10,567,584	60.5
		3	13,652,968	13,580,820	60.5
	CLso(+)	1	10,808,607	10,748,725	59.8
		2	11,454,508	11,376,887	60
		3	9,369,277	9,326,282	60

Supplementary Table 2. List of primers used to estimate the expression level of lincRNA and their associated PCGs harboring the same binding sites of miRNA.

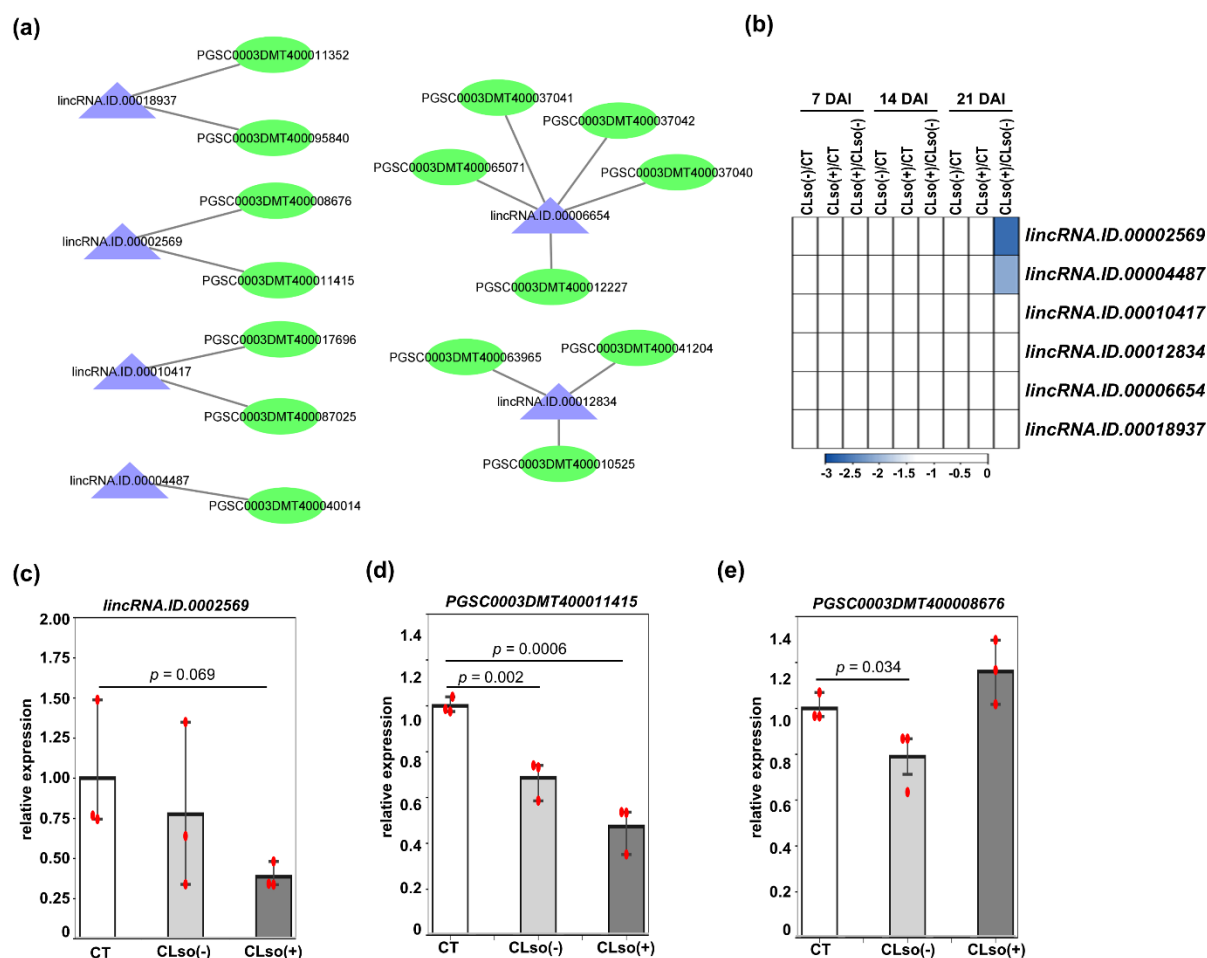
lincRNA/PCG ID	Forward	Reverse
lincRNA.ID.00002569	CTAAACCTTATGAAACCCTAAATCCT	CGTTTAGGATTTAGAGCTTACAGA
PGSC0003DMT400008676	CTCTTTGGTGAAGCGCGAAG	GCTGGTGGCTGTCACACTAT
PGSC0003DMT400011415	CATCGGGTGTCATGCTCTGTA	GCACTCATGAAGCCAAGAGC

Supplementary Table 3. List of primers used for verification of lncRNA overexpression.

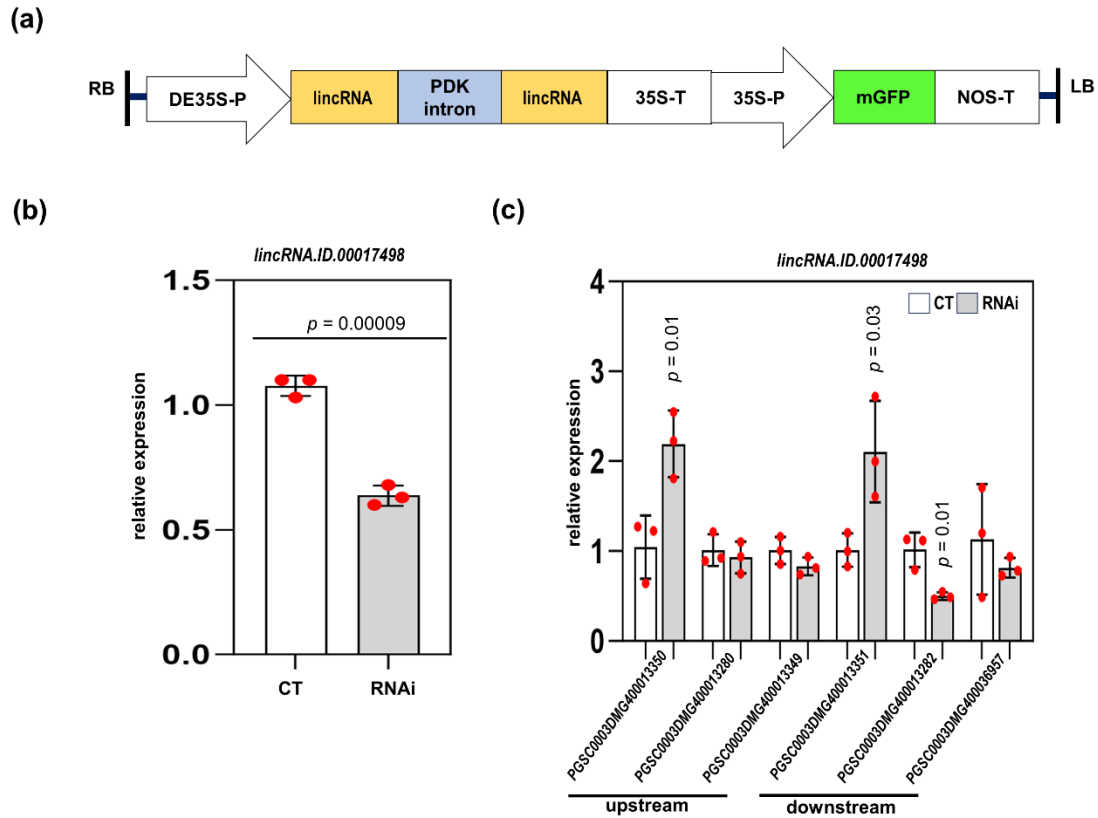
lincRNA ID	Forward	Reverse
lincRNA.ID.00017902	ACCGTTACGTGTGTGGACAG	TTTCTCTAATGGGCTAAGAGATCC
lincRNA.ID.00017498	CAATGGCCAGTGTTGAGGTTG	GGCTGGTTCCTCCACCTCTG
lincRNA.ID.00013924	AGAAGAAGTGATTGAGAGGGGA	ACGAGTAAATTCAGGCGTCCA
lincRNA.ID.00013620	CACTCATTGCAACCATGGCA	GGTCTTCCCCAATCCTCCAA

Supplementary Table 4. List of primers used to determine the expression level of proximal PCGs located either in up- or downstream regions of the overexpressed lncRNAs.

lincRNA ID	Forward	Reverse
PGSC0003DMG400000425	ACCCTATGGACCTCGTTGGA	TGACCTAGCTCATTGGCACG
PGSC0003DMG400000422	ACTTTCAGCCCTCAAAGCCA	AGGGCCCCATGAAAACACAA
PGSC0003DMG400000460	GATGATCGACGCCGGAGAAA	AGATTGCACCGTTGATGGGT
PGSC0003DMG400000427	GCGGTGAAGTTTCCTGCTCT	CAACGACGCCTTTGATGCTT
PGSC0003DMG401000428	CGACAAACTCGTCTGCTCCT	TGCAATAACCGACAAGCCCT
PGSC0003DMG403000428	ATGAGATCAGATACAGGGGATTAC	AGTGCCCCCAATCTAGTTATGA
PGSC0003DMG400013351	TCAATAGCAGAGCAGGTCGC	CCAGAAGAAGGACCAAAGCCT
PGSC0003DMG400013282	CACCAATAGTGGCCATCGGA	CTGTCCCGGTCAACGTAATC
PGSC0003DMG400036957	TGCTTCCACCTTCTGTCTTGC	TCTTAGTTGCCTCCTTCACCG
PGSC0003DMG400013350	AATTGAGCCACTTAGATTGGTGAGTG	GACGATCCAAGAATAATTTGTTGACTC
PGSC0003DMG400013280	AGCTCGGAGCAAACTTGGA	AGAAATAAGCTGCGGTGGCT
PGSC0003DMG400013349	AAACGAAGGGAGGAAGCAGG	GGGCTTCCTGCCAAAATGG
PGSC0003DMG400012137	CGCCATTGGCTTCGTTCAA	GTGGTTGTTGTGGAGGTTGC
PGSC0003DMG400012136	AAATGCTGATGAGCCACCGA	AGCAACCAGCAACTCTTCGT
PGSC0003DMG400012259	CGCAGAGTGCTTTGGACAAC	GCACTCAACACCCTGTGGTA
PGSC0003DMG400012261	GAGAGAGCGCCTCCAAACAT	GGTAACCGCAAATGGCCTTG
PGSC0003DMG400012262	GATCGGTGTCTTGGTTGGGT	AGCCAACAATGCTGATCCCA
PGSC0003DMG400012138	TCAGTGACCAGCTTCGTCTG	TTGAGGTCACCACCTACCCT
PGSC0003DMG400021736	AGGTGTTGAACATCGACCAGT	TGAGGCTTGATGCTGGACTT
PGSC0003DMG400045276	GCATCACACAGGACGAACAC	GCAGGGTGGGTTTTGATGC
PGSC0003DMG400042381	AGAGTCTTTGGCTGATGGTGA	AAAGCCTCCCAGTTCAGTGC
PGSC0003DMG400021737	CGACAAGTCGGTCAATGCAC	GGATACTCCTTCACGTCCGC
PGSC0003DMG400021738	GCAAATCGGCTCGAAATCCC	TCTAAAGCCCATGGCACGAA
PGSC0003DMG400021747	ACCCTCGAAGTTACAGTGCC	GGCAAGCTCTCTGTGCATTC



Supplementary Fig. 1 LincRNAs may act as possible decoys of miRNA. (a) The lincRNAs and associated PGs harboring the same binding site of the potato stu-miR482a-5p are depicted. (b) The differential expression profile of the lincRNAs is shown via heatmap. The scale represents the differential in log₂ fold-change. (c) The relative expression level of lincRNA.ID.0002569 (d) and their associated PGs (d, e) in CT, CLso (-), and CLso (+) conditions at 21 DAI estimated via qPCR is shown in bar plots. Statistical significance (*p*-value) was calculated using Student's *t*-test. The error bars represent the standard error among the three biological replicates.



Supplementary Fig. 2 Effects of lincRNA knockdown on PCG expression. (a) Schematic diagram showing plasmid vector employed for RNAi-mediated knockdown (RNAi) of lincRNA. (b) The relative expression level of the lincRNAs between the CT and RNAi tissues was estimated by RT-qPCR. (c) The relative expression level of the proximal PCGs located either in upstream or downstream regions of the lincRNA compared between CT and RNAi plants was estimated by RT-qPCR. Statistical significance (p -value) was calculated using Student's t -test. The error bars represent the standard error among the three biological replicates.