

Supplementary data

Table S1 Sequence of the primers in the experiment for qPCR.

Gene name	Forward Primer 5' → 3'	Reverse Primer 5' → 3'
Solyc03g120390.3	tcaccaaactatctaaaaaggggg	tttcattgaaattaaggccggaat
Solyc01g110790.3	gttggggaaaagcagaagaagagat	ttgactaagcaagccttgaaataaa
Solyc03g033590.1	caaacacataactcaaagtatagcc	acatcataaggaagtcattctcatt
Solyc04g052970.3	gtaggagagagccagaagaagaga	gcaggatgtgagatgaacaaacac
Solyc08g068480.1	caaaatccattggtccattagagt	gcagccccatttcctatgtaagat
Solyc03g096670.3	tagtgaagaacgaggttgagagcg	tcagtggacagaggaattgggaca
Solyc01g087460.3	ggcgattcacgtgcagtactcatt	cctttgctttcgactacctctttt
Solyc08g005610.3	tgtggcattgatttcgatatttg	tttctcgccttcattgctttgtt
Solyc03g005500.1	gaggggttcgtgtttggctaggga	tggcattgatgaagaattgttgta
Solyc01g067540.2	gagaacgaggacgtcgtaaacaa	caaaagggtgaaataagcgaaggga
Solyc01g090370.3	aataagggaccccagaggaaag	gaggaggagacgacgatgaaac
Solyc01g079370.4	ccacaagttgccaatgaaagaga	gccgaaccataagggtgaataaa
Solyc09g064160.3 (<i>YUCCA5</i>)	ttccattcccagaacattaccct	caccaaactccttcaatccatc
Solyc09g091090.2 (<i>YUCCA2</i>)	acttcccatttcacaaaacttc	ctacacactgtcttcaccctcca
Solyc09g073015.1 (<i>YUCCA10</i>)	gctttgatctatcgtctccggt	gaaattttcaaggccttccactt
Solyc06g065630.3 (<i>YUCCA2.1</i>)	cacaaaaagcggaggaaacacata	ttacaacaaccattcaaagatca
Solyc08g065700.3 (<i>YUCCA10.1</i>)	ggtttttgttcattaccctttatgc	aaattttcaattcctcccaccttg
Solyc01g080150.3 (<i>IPT5</i>)	atttgaaaaaaaagatggtgaagca	aagggaagttgacgatgaaggaggag
Solyc09g064910.1 (<i>IPT</i>)	actctctatcgacttagccactcaa	ggtacaccgcaacgttcttctctg
Solyc06g071030.3 (<i>ICS</i>)	atattgtcatccgtgcaccctactc	attccaaccgcaaattcactctctt
Solyc01g109160.4 (<i>AOS</i>)	catacttttcattaccgtttgtc	catctctcttgatcccactctctc
Solyc02g085730.3 (<i>AOC</i>)	ttctccttcccactccatactaccc	ctgattctgtgattctaaatccggt
Solyc08g016720.1 (<i>NCED5</i>)	acaatacccccaaaaatcaaccac	ctccattctgacataaaccat
Solyc04g025650.3 (<i>ZEP</i>)	tatctgactggccttcttttgag	tattgagtatgagcacttgggttt
Solyc02g081190.4 (<i>ACO</i>)	acacagtggagaatttaactaaggg	ggaaacaggaagatgtttcaagaag
Solyc02g063540.3 (<i>ACS</i>)	ttctccttcccactccatactaccc	ctgattctgtgattctaaatccggt
NM_001330119.1 (<i>Actin</i>)	tggtgtgatggtgggtatgggt	aagaggggcttcagttaggagg

Table S2 Impacts of cycle aerated subsurface drip irrigation on plant height and stem diameter in

Tomato

treatment	Height/cm	Stem diameter/cm
O1F2	212.5±32.76	1.480±0.080
O2F2	187.17±21.91	1.466±0.065
O3F2	186.67±20.34	1.455±0.116
SF2	177.17±26.72	1.421±0.143

Table S3 Effects of cycle aerated subsurface drip irrigation on photosynthetic pigment content of

leaves

Treatment	Chlorophyll a content	Chlorophyll b content	Total chlorophyll
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	(mg·g ⁻¹)	(mg·g ⁻¹)	content (mg·g ⁻¹)
HAI	0.83±0.013	0.34±0.077	1.17±0.069
MAI	0.72±0.018	0.26±0.020b	0.98±0.031
LAI	0.66±0.044	0.24±0.020	0.90±0.063
CK	0.60±0.093	0.22±0.029	0.81±0.123

Table S4 Impacts of cycle aerated subsurface drip irrigation on plant dry matter in tomato

Treatments	Stems dry matter accumulation (g/ plant)	Leaves dry matter accumulation (g/ plant)	Fruit dry matter accumulation (g/ plant)	Total dry matter accumulation (g/ plant)
HAI	39.38±11.43	44.56±7.45	3.56±1.29	89.37±20.03
MAI	36.39±1.33	36.82±4.88b	4.34±0.32	79.20±13.74
LAI	30.70±5.88	38.10±5.46	2.57±0.19	72.99±22.17
CK	26.41±5.39	37.58±4.59	2.22±0.17	67.88±15.60

Table S5 DEGs analysis of tomato root metabolic pathway under aeration irrigation

ID	log2FoldChange	regulated	Gene funtion
Solyc01g059965.1	-2.36	down	glucan endo-1,3-beta-glucosidase B
Solyc01g080750.3	-1.938	down	crecserin-1
Solyc01g099910.4	-1.048	down	bifunctional epoxide hydrolase 2
Solyc02g080220.3	-1.517	down	pectinesterase-like
Solyc02g087770.3	-1.133	down	aldose 1-epimerase-like
Solyc02g093250.3	-1.625	down	caffeoyl-CoA O-methyltransferase
Solyc03g121470.4	-1.341	down	phospholipase D alpha 4
Solyc04g054950.3	-1.691	down	tropinone reductase homolog
Solyc07g005100.4	-1.21	down	chitotriosidase-1
Solyc07g052370.4	-4.662	down	premnaspirodiene oxygenase-like
Solyc07g053270.3	-1.113	down	bifunctional riboflavin kinase/FMN phosphatase-like
Solyc08g079420.3	-1.903	down	ferruginol synthase-like
Solyc09g098320.1	-2.544	down	12-oxophytodienoate reductase-like protein
Solyc10g012370.3	-1.557	down	bifunctional L-3-cyanoalanine synthase/cysteine synthase 1, mitochondrial
Solyc11g040340.3	-1.833	down	endo-1,4-beta-D-glucanase precursor
Solyc12g049030.1	-2.248	down	delta(12)-fatty-acid desaturase FAD2-like
Solyc02g084980.3	1.526	up	galactinol synthase
Solyc03g031440.4	1.233	up	NAD(P)H dehydrogenase (quinone) FQR1-like 1
Solyc03g034220.3	2.077	up	ribulose biphosphate carboxylase small chain 2A, chloroplastic
Solyc03g083870.4	7.605	up	Pectin methylesterase inhibitor
Solyc05g054350.3	1.181	up	alpha/beta hydrolase family protein
Solyc06g008920.3	1.451	up	probable acyl-activating enzyme 1,

Solyc06g072740.1	1.103	up	peroxisomal inositol-tetrakisphosphate 1-kinase 5-like
Solyc08g005720.4	2.619	up	santalene and bergamotene synthase, chloroplastic
Solyc08g008430.4	1.08	up	short-chain type dehydrogenase/reductase-like
Solyc09g005690.3	1.014	up	type I inositol polyphosphate 5-phosphatase 8 isoform X1
Solyc09g008970.1	1.25	up	uncharacterized protein
Solyc09g091030.3	1.985	up	beta-amylase
Solyc10g083990.2	1.188	up	uncharacterized protein
Solyc11g010480.2	1.046	up	uncharacterized protein
Solyc12g008650.2	1.552	up	myo-inositol oxygenase
Solyc12g096800.1	4.424	up	vinorine synthase-like
Solyc01g079160.4	1.683	up	GDSL esterase/lipase LIP-4-like
Solyc01g096280.2	3.233	up	cytochrome P450 78A3-like
Solyc01g098490.3	2.501	up	sugar transporter ERD6-like 5
Solyc03g026210.4	1.081	up	dihydrodipicolinate reductase-like protein CRR1
Solyc03g097440.3	1.895	up	11-beta-hydroxysteroid dehydrogenase 1B
Solyc03g097600.3	2.651	up	bidirectional sugar transporter SWEET10-like
Solyc03g097620.1	7.171	up	bidirectional sugar transporter SWEET14-like
Solyc04g051150.3	2.659	up	sterol 3-beta-glucosyltransferase UGT80A2-like
Solyc07g006870.4	3.125	up	xyloglucan endotransglucosylase/hydrolase protein 25
Solyc07g014680.4	2.499	up	Na ⁺ transporter
Solyc07g062810.4	1.563	up	D-amino-acid transaminase, chloroplastic-like isoform X2
Solyc08g079040.1	1.499	up	probable xyloglucan galactosyltransferase GT19
Solyc09g055860.1	2.768	up	2,3-bisphosphoglycerate-independent phosphoglycerate mutase
Solyc11g005560.3	1.141	up	cellulose synthase A catalytic subunit 5
Solyc11g066880.2	6.872	up	putative phytosulfokines 6-like precursor
