

Figure S1.

Accumulation of $m/z = 683.23$ at retention time, 90 s, in roots. Mean (\pm SE) levels of normalized intensity of $m/z = 683.23$ at 90 s in roots. Calculated molecular formula ($C_{24}H_{43}O_{22}^-$) and retention time (90 s) indicated that it is a disaccharide dimer. After W+W (dashed lines with colors) or W+OS (solid lines with colors) treatments, compound levels were examined in roots (green). Gray boxes depict the dark period. Asterisks indicate significant differences among the treatments at the indicated time point (* = $P < 0.05$, one-way ANOVA with Bonferroni *post hoc* test).

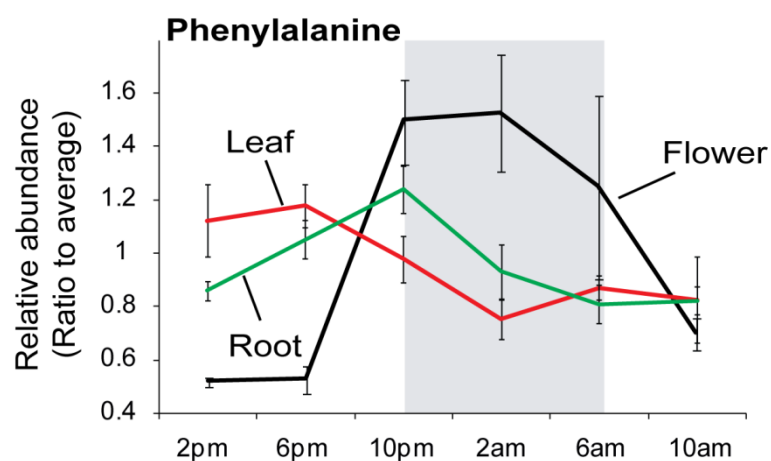


Figure S2.

Accumulation of Phe in leaves, roots and open flowers. Mean (\pm SE) levels of normalized intensity of Phe in different tissues. Phe accumulation was quantified in leaves (red), roots (green), and flowers (black). To calculate relative accumulation, 75th percentile normalized intensity at each harvest time was divided by average value over all time points. We collected open flowers from 7 week-old plants and extracted metabolites with a 40% methanol extraction method. Gray box depicts the dark period.

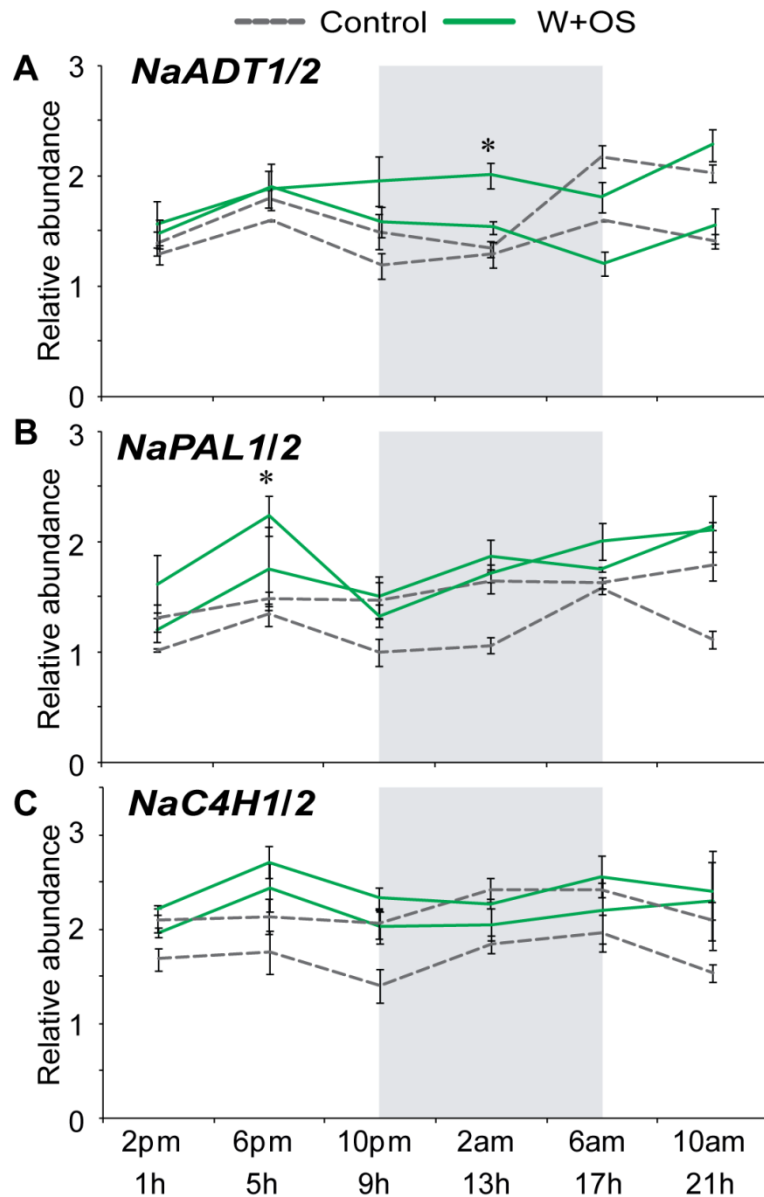


Figure S3.

Transcript abundance of *NaADT1/2*, *NaPAL1/2*, and *NaC4H1/2* in roots. Mean (\pm SE) levels of normalized intensity of *NaADTs*, *NaPALs* and *NaC4Hs* in roots. ADT, arogenate dehydratase; PAL, phenylalanine ammonia lyase; C4H, cinnamate 4-hydroxylase. Gray boxes depict the dark period. Asterisks indicate significant differences between control plants and *M. sexta* oral secretions-treated plants (W+OS) at indicated time points (* = $P < 0.05$, as determined by Student's t-test).

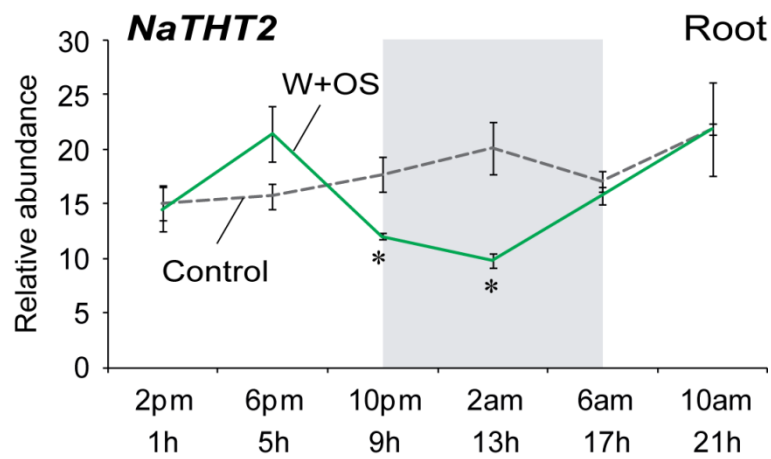


Figure S4.

Transcript abundance of *NaTHT2* in roots. Mean (\pm SE) levels of normalized intensity of *NaTHT2* in roots. THT, tyramine N-hydroxycinnamoyltransferase. Gray box depicts the dark period. Asterisks indicate significant differences between control plants and *M. sexta* oral secretions-treated plants (W+OS) at indicated time points (* = $P < 0.05$, as determined by Student's t-test).

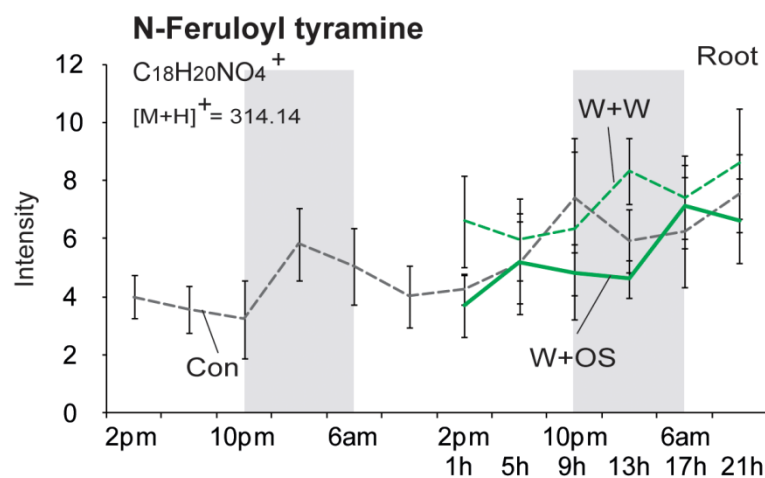


Figure S5.

Accumulation of N-feruloyl tyramine in roots. Mean (\pm SE) levels of normalized intensity of N-feruloyl tyramine in roots. Gray boxes depict the dark period. Asterisks indicate significant differences between control plants and *M. sexta* oral secretions-treated plants (W+OS) at indicated time points (* = $P < 0.05$, as determined by Student's t-test).

Table S1. Proposed molecular formulas of oscillating compounds detected in leaves and roots

Peak No.	R.T.	m/z	M.F.	Error (mDa)	SigmaFit (mσ)	Name
L1	129 s	191.02	C ₆ H ₇ O ₇ ⁻	0.76	4.9	Citric acid
L2/R3	137 s	243.06	C ₉ H ₁₁ N ₂ O ₆ ⁻	0.28	19.7	
L3	143 s	180.07	C ₉ H ₁₀ NO ₃ ⁻	0.85	19.1	Tyrosine
L4	167 s	282.08	C ₉ H ₁₆ NO ₉ ⁻	-0.56	24.1	
L5/R5	192 s	164.07	C ₉ H ₁₀ NO ₂ ⁻	-1.20	10.7	Phenylalanine
L6	261 s	463.22	C ₂₁ H ₃₅ O ₁₁ ⁻	1.99	15.3	
L7	306 s	691.34	C ₃₂ H ₅₁ O ₁₆ ⁻	-0.28	26.7	
L8	317 s	227.13	C ₁₂ H ₁₉ O ₄ ⁻	1.44	10.7	
L9	325 s	673.34	C ₃₃ H ₅₃ O ₁₄ ⁻	1.61	60.5	
L10	340 s	629.35	C ₃₂ H ₅₃ O ₁₂ ⁻	-0.79	17.2	Lyciumoside I
L11	352 s	715.35	C ₃₅ H ₅₅ O ₁₅ ⁻	-3.08	16.8	
L12	361 s	689.34	C ₃₃ H ₅₃ O ₁₅ ⁻	2.63	12.2	
R1	88s	341.10	C ₁₂ H ₂₁ O ₁₁ ⁻	1.27	3.3	Dissacharide
R2	99 s	259.02	C ₈ H ₇ N ₂ O ₈ ⁻	0.07	13.8	
R4	138 s	243.06	C ₉ H ₁₁ N ₂ O ₆ ⁻	0.71	6.7	
R6	197 s	315.07	C ₁₃ H ₁₅ O ₉ ⁻	0.71	3.7	
R7	354 s	329.23	C ₁₈ H ₃₃ O ₅ ⁻	0.07	1.3	
R8	367 s	209.12	C ₁₂ H ₁₇ O ₃ ⁻	0.81	6.6	Jasmonic acid
R9	396 s	327.22	C ₁₈ H ₃₁ O ₅ ⁻	0.32	2.4	
R10	433 s	309.21	C ₁₈ H ₂₉ O ₄ ⁻	0.35	83.8	
R11	437 s	341.23	C ₁₉ H ₃₃ O ₅ ⁻	1.08	11.8	
R12	446 s	311.22	C ₁₈ H ₃₁ O ₄ ⁻	1.01	21.8	
R13	458 s	311.22	C ₁₈ H ₃₁ O ₄ ⁻	1.41	4.8	
R14	478 s	291.19	C ₁₈ H ₂₇ O ₃ ⁻	1.04	56.6	OPDA

Molecular formulas (M.F.) were calculated using Bruker SmartFormula software. Blanks in name column indicate unknown compounds. L, leaf; R, root; R.T., retention time.

Table S2. Oscillating transcripts involved in sugar metabolism of *N. attenuata*.

Probe Name	Peak	Gene Annotation
Na_454_03214	Night	alpha-amylase
Na_454_06724	Night	beta-amylase
Na_454_08612	Night	beta-amylase
Na_454_10779	Night	beta-amylase
Na_454_35633	Night	beta-amylase
Na_454_12641	Night	sucrose invertase
Na_454_41936	Night	sucrose invertase
Na_454_01065	Night	sucrose synthase
Na_454_05247	Night	sucrose transporter
Na_454_02704	Night	sugar exporter (SWEET)
Na_454_05391	Night	sugar exporter (SWEET)
Na_454_16634	Night	sugar exporter (SWEET)
Na_454_28050	Night	sugar exporter (SWEET)
Na_454_14081	Day	beta-amylase
Na_454_18724	Day	beta-amylase
Na_454_20797	Day	beta-amylase
Na_454_22181	Day	beta-amylase
Na_454_34221	Day	beta-amylase
Na_454_39081	Day	beta-amylase
Na_454_00622	Day	maltose transporter
Na_454_11568	Day	sucrose phosphate synthase
Na_454_39731	Day	sucrose phosphate synthase
Na_454_40855	Day	sucrose phosphate synthase
Na_454_16096	Day	sucrose synthase
Na_454_27568	Day	sucrose synthase
Na_454_04103	Day	sugar exporter (SWEET)
Na_454_05017	Day	sugar exporter (SWEET)
Na_454_06723	Day	sugar exporter (SWEET)

Table S3. Oscillating transcripts involved in Phe/Tyr metabolism of *N. attenuata*.

Probe Name	Gene Annotation
Na_454_02400	arogenate dehydratase (ADT)
Na_454_09000	arogenate dehydrogenase (TyrA)
Na_454_00178	Phe ammonia lyase 1 (PAL1)
Na_454_00083	Phe ammonia lyase 2 (PAL2)
Na_454_00021	4-coumarate:CoA ligase (4CL)
Na_454_00101	cinnamic acid-4-hydroxylase (C4H)
Na_454_00269	cinnamic acid-4-hydroxylase (C4H)
Na_454_00315	S-adenosylmethionine decarboxylase (SAMDC)
Na_454_00797	S-adenosylmethionine decarboxylase (SAMDC)
Na_454_36134	spermidine synthase (SPS)
Na_454_07429	tyramine N-hydroxycinnamoyltransferase (THT)

Table S4. Oscillating transcripts involved in jasmonic acid metabolism and signaling of *N. attenuata*.

Probe Name	Gene Annotation
Na_454_00565	allene oxide synthase (AOS)
Na_454_04958	coronatine insensitive 1 (COI1)
Na_454_02978	jasmonate-ZIM-domain (JAZ)
Na_454_13225	jasmonate-ZIM-domain (JAZ)
Na_454_14633	jasmonate-ZIM-domain (JAZ)
Na_454_19886	jasmonate-ZIM-domain (JAZ)
Na_454_41896	jasmonate-ZIM-domain (JAZ)