

Supplementary data

Interactive responses of *Solanum dulcamara* to drought and insect feeding are herbivore species specific

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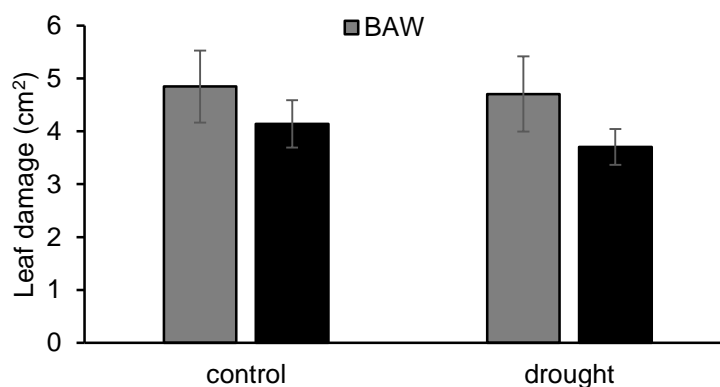


Figure S1. Levels of herbivory damage of leaf samples used for microarray analysis, measurements of hormone concentrations and protease inhibitor contents. *Spodoptera exigua* (BAW, grey bars) and *Leptinotarsa decemlineata* (CPB, black bars) larvae were fed for 48 h on *Solanum dulcamara* plants under well-watering (control) or drought treatments. Error bars are SEM; N = 9 per treatment combination.

Table S1. Univariate test for effects of watering treatments (well-watered and drought) and herbivory treatments (no herbivory or 48-h herbivory by *Spodoptera exigua* or *Leptinotarsa decemlineata*) on concentrations of jasmonic acid (JA), JA-isoleucine (JA-Ile), abscisic acid (ABA) and salicylic acid (SA) in *Solanum dulcamara*. Degree of freedom (df) and *F* values were presented. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$. Bold numbers indicate significance.

| Source | df | JA | | JA-Ile | | ABA | | SA | |
|-------------------|----|--------------|-----|-------------|-----|-------------|-----|-------------|-----|
| | | <i>F</i> | | <i>F</i> | | <i>F</i> | | <i>F</i> | |
| Water | 1 | 4.1 | * | 2.2 | | 58.0 | *** | 0 | |
| Herbivory | 2 | 101.5 | *** | 96.0 | *** | 10.6 | *** | 12.4 | *** |
| Water * Herbivory | 2 | 3.5 | * | 4.6 | * | 6.7 | ** | 1.5 | |

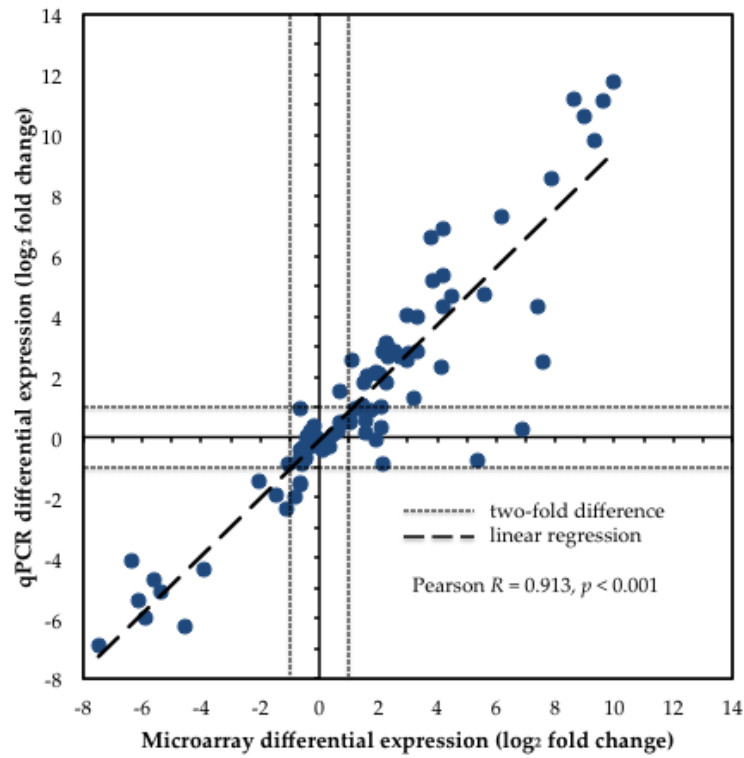


Figure S2. Quantitative PCR validation of microarray analysis of differential gene expression. Correlation plot between log₂ values of expression fold changes of 16 target and four reference genes. Each dot is a comparison between a treatment combination (water availability x herbivory treatments) to the control (well-watering conditions without herbivory).

Table S2. Overrepresentation of gene ontology (GO) terms among genes that were always induced by insect herbivory on *Solanum dulcamara* regardless of watering treatments (part i in Figure 4C). Fisher's exact tests were used with FDR q value cut-off at 0.05. GO categories (Cat.): Molecular Function (F), Biological Process (P), Cellular Component (C).

| GO-ID | Term description | Cat. | q value | #Gene |
|--|---|------|-----------|-------|
| <i>15 top GO terms enriched in upregulated genes</i> | | | | |
| GO:0004866 | endopeptidase inhibitor activity | F | 1.23E-08 | 10 |
| GO:0009505 | plant-type cell wall | C | 1.81E-05 | 24 |
| GO:0009611 | response to wounding | P | 8.29E-05 | 32 |
| GO:0048046 | apoplast | C | 1.11E-04 | 24 |
| GO:0009695 | jasmonic acid biosynthetic process | P | 1.49E-04 | 15 |
| GO:0009605 | response to external stimulus | P | 3.27E-04 | 73 |
| GO:0019373 | epoxygenase P450 pathway | P | 4.11E-04 | 3 |
| GO:0047987 | hydroperoxide dehydratase activity | F | 4.11E-04 | 3 |
| GO:0009269 | response to desiccation | P | 9.42E-04 | 9 |
| GO:0009753 | response to jasmonic acid | P | 1.47E-03 | 28 |
| GO:0009698 | phenylpropanoid metabolic process | P | 2.70E-03 | 18 |
| GO:0009978 | allene oxide synthase activity | F | 2.71E-03 | 3 |
| GO:0044550 | secondary metabolite biosynthetic process | P | 7.18E-03 | 22 |
| GO:0000326 | protein storage vacuole | C | 7.20E-03 | 5 |
| GO:0042807 | central vacuole | C | 8.95E-03 | 4 |
| <i>15 top GO terms enriched in downregulated genes</i> | | | | |
| GO:0009644 | response to high light intensity | P | 8.46E-31 | 35 |
| GO:0042542 | response to hydrogen peroxide | P | 5.47E-30 | 34 |
| GO:0010286 | heat acclimation | P | 1.69E-16 | 20 |
| GO:0051082 | unfolded protein binding | F | 7.61E-16 | 17 |
| GO:0034976 | response to endoplasmic reticulum stress | P | 4.52E-14 | 27 |
| GO:0042026 | protein refolding | P | 9.17E-08 | 7 |
| GO:0001671 | ATPase activator activity | F | 1.34E-07 | 5 |
| GO:0032781 | positive regulation of ATPase activity | P | 1.34E-07 | 5 |
| GO:0006986 | response to unfolded protein | P | 4.81E-07 | 16 |
| GO:0031072 | heat shock protein binding | F | 5.32E-07 | 10 |
| GO:0051087 | chaperone binding | F | 1.06E-06 | 7 |
| GO:0045109 | intermediate filament organization | P | 3.39E-06 | 4 |
| GO:0005730 | nucleolus | C | 2.36E-05 | 24 |
| GO:0005783 | endoplasmic reticulum | C | 4.49E-05 | 21 |
| GO:0005782 | peroxisomal matrix | C | 1.09E-04 | 5 |

Table S3. Univariate test for effects of watering treatments (well-watered and drought) and herbivory treatments (no herbivory or 48-h herbivory by *Spodoptera exigua* or *Leptinotarsa decemlineata*) on serine-type protease inhibitor (serPI) and leaf total protein contents in *Solanum dulcamara*. Degrees of freedom (df) and *F* values are presented. * $p < 0.05$; *** $p < 0.001$. Bold numbers indicate significance.

| Source | df | serPI | | Total protein | |
|-------------------|----|---------------|-----|---------------|---|
| | | <i>F</i> | | <i>F</i> | |
| Water | 1 | 73.315 | *** | 5.605 | * |
| Herbivory | 2 | 4.517 | * | 0.158 | |
| Water * Herbivory | 2 | 1.137 | | 0.499 | |

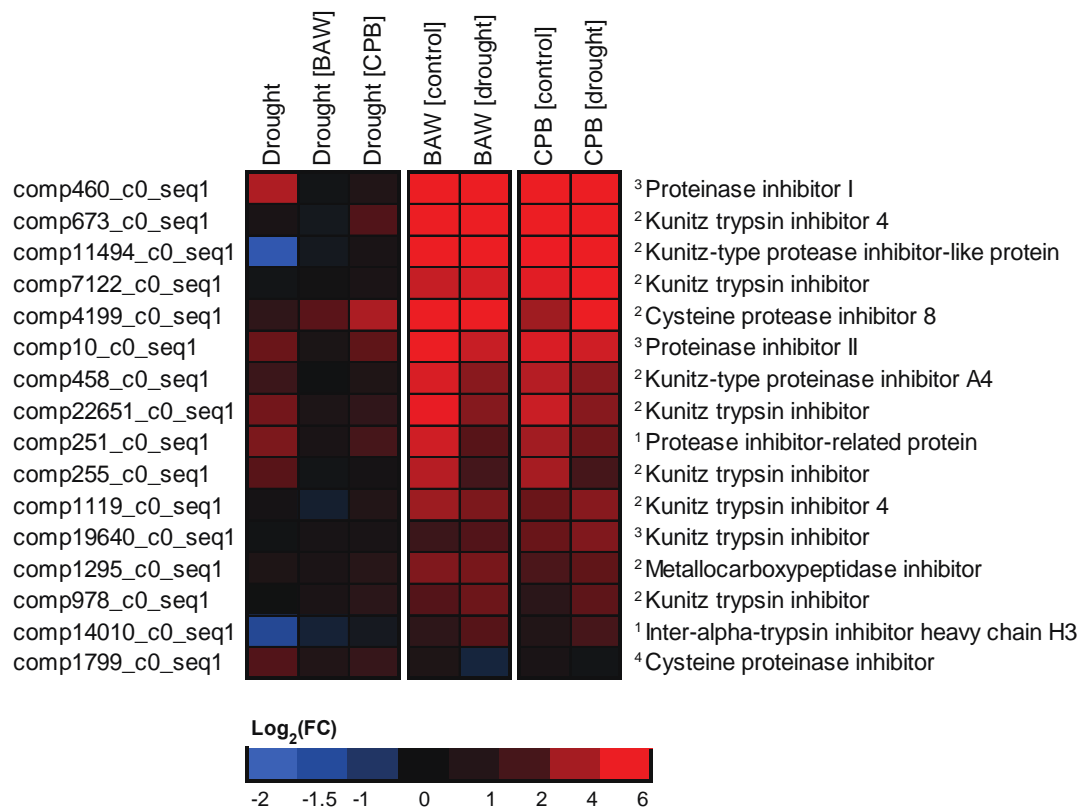
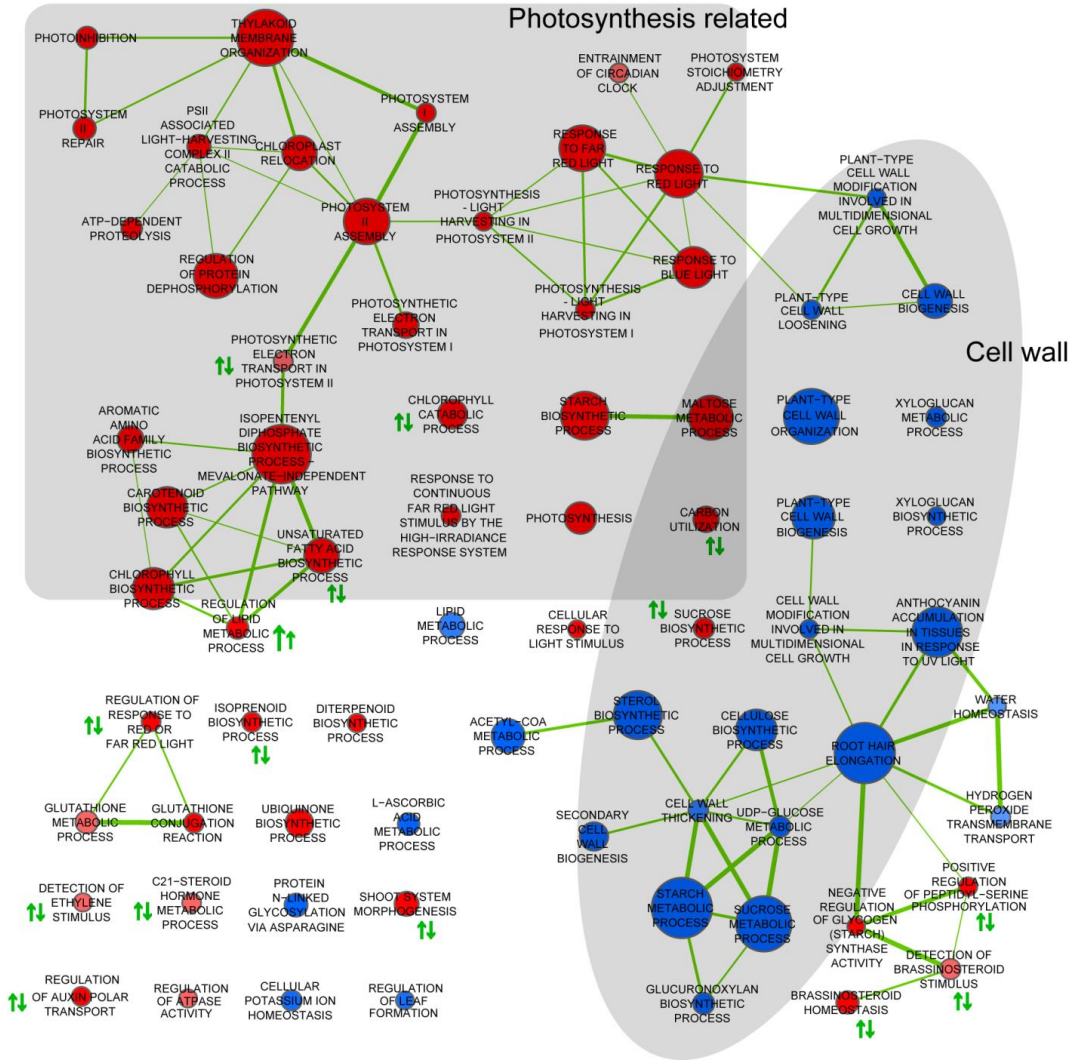


Figure S3. Effects of watering and insect herbivory treatments on the expression of protease inhibitor (PI) genes in *Solanum dulcamara*. Each column is a pairwise comparison between two conditions to show effects of drought treatment on plants that were undamaged (Drought) or fed by *Spodoptera exigua* (Drought [BAW]) or *Leptinotarsa decemlineata* (Drought [CPB]) and effects of herbivory on well-watered (BAW [control] and CPB [control]) or drought-stressed plants (BAW [drought] and CPB [drought]). ¹ GO:0030414, peptidase inhibitor activity; ² GO:0004866, endopeptidase inhibitor activity ³ GO:0004867, serine-type endopeptidase inhibitor activity ⁴ GO:000486, cysteine-type endopeptidase inhibitor activity.

(A)



(Figure S4. Continued)

(B)

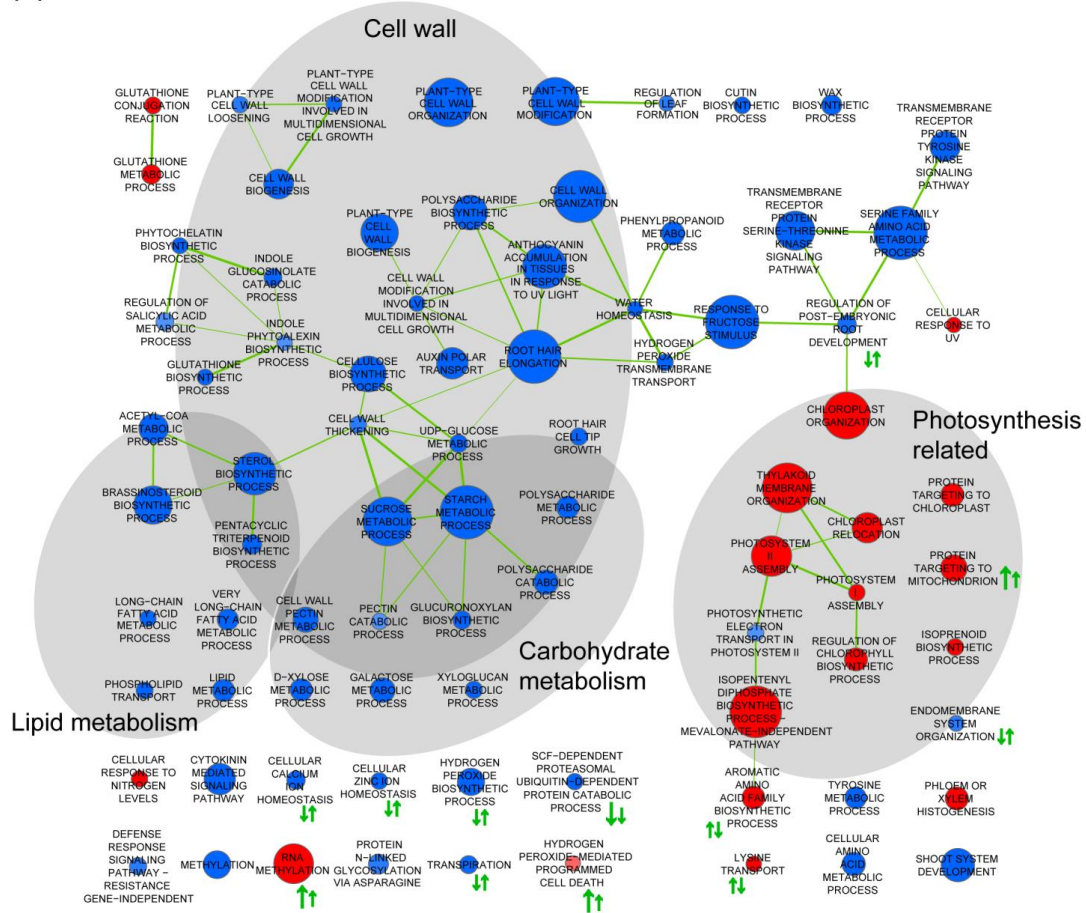


Figure S4. Differences in the transcriptional regulation *Solanum dulcamara* plants subjected to herbivory by *Spodoptera exigua* (BAW) or *Leptinotarsa decemlineata* (CPB). Network of biological processes (BPs), indicated by nodes, in well-watered (A) or drought-stressed (B) plants. Only BPs with a nominal p value ≤ 0.001 , FDR q value ≤ 0.05 , and an overlap coefficient ≤ 0.5 generated from the gene set enrichment analyses were included in the networks. Red or blue nodes are BPs that were downregulated or upregulated, respectively, stronger by BAW than by CPB compared to undamaged plants. Exceptions to this colour coding are nodes with adjacent green arrows indicating inducing directions by CPB (left arrow) and BAW (right arrow) herbivory. Node and edge sizes correspond to numbers of genes of a BP and number of genes that overlap between two connected BPs, respectively. Related clusters and individual BPs are grouped and assigned with labels.

Table S4A. Overrepresentation of gene ontology (GO) terms among the genes that were specifically induced by *Spodoptera exigua* (BAW) herbivory on *Solanum dulcamara* plants under well-watering or drought treatments (parts o + k + g in Figure 4C). Fisher's exact tests were used with FDR q value cut-off at 0.05. GO categories (Cat.): Molecular Function (F), Biological Process (P) and Cellular Component (C).

| GO-ID | Term description | Cat. | q value | # Gene |
|--|---|------|-----------|--------|
| <i>GO terms enriched in BAW-upregulated genes specific to control conditions</i> | | | | |
| GO:0009607 | response to biotic stimulus | P | 3.46E-03 | 71 |
| GO:0030397 | membrane disassembly | P | 3.46E-03 | 4 |
| GO:0009414 | response to water deprivation | P | 3.46E-03 | 35 |
| GO:0051707 | response to other organism | P | 3.46E-03 | 69 |
| GO:0005976 | polysaccharide metabolic process | P | 3.46E-03 | 44 |
| GO:0005985 | sucrose metabolic process | P | 5.49E-03 | 17 |
| GO:0009505 | plant-type cell wall | C | 1.66E-02 | 21 |
| GO:0048509 | regulation of meristem development | P | 2.16E-02 | 22 |
| GO:0016165 | linoleate 13S-lipoxygenase activity | F | 2.16E-02 | 4 |
| GO:0005576 | extracellular region | C | 2.79E-02 | 29 |
| GO:0009695 | jasmonic acid biosynthetic process | P | 2.97E-02 | 13 |
| GO:0071669 | plant-type cell wall organization or biogenesis | P | 2.97E-02 | 30 |
| GO:0071555 | cell wall organization | P | 4.81E-02 | 33 |
| <i>15 top GO terms enriched in BAW-upregulated genes overlapping between control and drought treatments</i> | | | | |
| GO:0045229 | external encapsulating structure organization | P | 2.06E-06 | 45 |
| GO:0009505 | plant-type cell wall | C | 2.06E-06 | 27 |
| GO:0042546 | cell wall biogenesis | P | 1.69E-05 | 29 |
| GO:0010054 | trichoblast differentiation | P | 3.83E-05 | 30 |
| GO:0051753 | mannan synthase activity | F | 4.74E-05 | 5 |
| GO:0009506 | plasmodesma | C | 4.90E-05 | 55 |
| GO:0005886 | plasma membrane | C | 1.81E-04 | 80 |
| GO:0030244 | cellulose biosynthetic process | P | 2.19E-04 | 13 |
| GO:0016760 | cellulose synthase (UDP-forming) activity | F | 3.54E-04 | 6 |
| GO:0005985 | sucrose metabolic process | P | 4.27E-04 | 17 |
| GO:0006011 | UDP-glucose metabolic process | P | 8.64E-04 | 6 |
| GO:0048046 | apoplast | C | 8.66E-04 | 23 |
| GO:0005802 | trans-Golgi network | C | 1.03E-03 | 13 |
| GO:0052546 | cell wall pectin metabolic process | P | 1.73E-03 | 10 |
| GO:0042545 | cell wall modification | P | 1.97E-03 | 22 |
| <i>GO terms enriched in BAW-upregulated genes specific to drought treatment</i> | | | | |
| GO:0005783 | endoplasmic reticulum | C | 2.94E-02 | 44 |
| <i>GO terms enriched in BAW-downregulated genes specific to control conditions</i> | | | | |
| GO:0016556 | mRNA modification | P | 1.59E-03 | 13 |
| GO:0042793 | transcription from plastid promoter | P | 1.51E-02 | 8 |
| GO:0009507 | chloroplast | C | 4.73E-02 | 61 |
| GO:0009902 | chloroplast relocation | P | 4.73E-02 | 10 |
| GO:0019288 | isopentenyl diphosphate biosynthetic process, non-MVA pathway | P | 4.73E-02 | 13 |
| GO:0006098 | pentose-phosphate shunt | P | 4.73E-02 | 12 |
| GO:1903792 | negative regulation of anion transport | P | 4.73E-02 | 4 |

| | | | | |
|--|---|---|----------|----|
| GO:0010362 | negative regulation of anion channel activity by blue light | P | 4.73E-02 | 4 |
| <i>GO terms enriched in BAW-downregulated genes overlapping between control and drought treatments</i> | | | | |
| GO:0016556 | mRNA modification | P | 2.03E-03 | 9 |
| GO:0044434 | chloroplast part | C | 5.97E-03 | 26 |
| GO:0019684 | photosynthesis, light reaction | P | 6.37E-03 | 12 |
| GO:0000959 | mitochondrial RNA metabolic process | P | 4.20E-02 | 5 |
| GO:0031425 | chloroplast RNA processing | P | 4.20E-02 | 5 |
| GO:0009311 | oligosaccharide metabolic process | P | 4.86E-02 | 12 |
| <i>GO terms enriched in BAW-downregulated genes specific to drought treatment</i> | | | | |

Table S4B. Overrepresentation of gene ontology (GO) terms among the genes that were specifically induced by *Leptinotarsa decemlineata* (CPB) herbivory on *Solanum dulcamara* plants under well-watering (control) or drought treatments (parts a + b + c in Figure 4C). Fisher's exact tests were used with FDR q value cut-off at 0.05. GO categories (Cat.): Molecular Function (F), Biological Process (P) and Cellular Component (C).

| GO-ID | Term description | Cat. | q value | # Gene |
|--|---|------|-----------|--------|
| <i>GO terms enriched in CPB-upregulated genes specific to control conditions</i> | | | | |
| <i>GO terms enriched in CPB-upregulated genes overlapping between control and drought treatments</i> | | | | |
| <i>GO terms enriched in CPB-upregulated genes specific to drought treatment</i> | | | | |
| GO:0006614 | SRP-dependent cotranslational protein targeting to membrane | P | 5.43E-28 | 25 |
| GO:0006415 | translational termination | P | 9.99E-28 | 25 |
| GO:0019083 | viral transcription | P | 1.07E-27 | 25 |
| GO:0006414 | translational elongation | P | 5.17E-27 | 25 |
| GO:0000184 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | P | 2.23E-26 | 25 |
| GO:0044391 | ribosomal subunit | C | 3.67E-25 | 27 |
| GO:0003735 | structural constituent of ribosome | F | 3.33E-24 | 27 |
| GO:0006413 | translational initiation | P | 4.03E-23 | 25 |
| GO:0022625 | cytosolic large ribosomal subunit | C | 1.31E-22 | 21 |
| GO:0001510 | RNA methylation | P | 8.32E-19 | 22 |
| GO:0003723 | RNA binding | F | 2.79E-05 | 20 |
| GO:0022627 | cytosolic small ribosomal subunit | C | 3.82E-04 | 6 |
| GO:0005730 | nucleolus | C | 5.17E-04 | 22 |
| GO:0005794 | Golgi apparatus | C | 9.12E-04 | 25 |
| GO:0015808 | L-alanine transport | P | 2.49E-03 | 2 |
| GO:0015180 | L-alanine transmembrane transporter activity | F | 2.49E-03 | 2 |
| GO:0015812 | gamma-aminobutyric acid transport | P | 7.04E-03 | 2 |
| GO:0015185 | gamma-aminobutyric acid transmembrane transporter activity | F | 7.04E-03 | 2 |
| GO:0000028 | ribosomal small subunit assembly | P | 8.72E-03 | 3 |
| GO:0016020 | membrane | C | 3.19E-02 | 51 |
| <i>GO terms enriched in CPB-downregulated genes specific to control conditions</i> | | | | |
| <i>GO terms enriched in CPB-downregulated genes overlapping between control and drought treatments</i> | | | | |
| <i>GO terms enriched in CPB-downregulated genes specific to drought treatment</i> | | | | |
| GO:0010378 | temperature compensation of circadian clock | P | 1.01E-03 | 3 |
| GO:0048578 | positive regulation of long-day photoperiodism, flowering | P | 1.05E-02 | 3 |

Table S5. The top 10 genes specifically induced by *Spodoptera exigua* (BAW) or *Leptinotarsa decemlineata* (CPB) in drought-stressed *Solanum dulcamara* plants.

| Gene number | Description |
|--|--|
| 10 genes most upregulated by BAW specifically under drought; in part g, Figure 4C | |
| comp4199_c0_seq1 | Cysteine protease inhibitor 8 |
| comp13011_c0_seq2 | Sesquiterpene synthase 1 |
| comp29348_c0_seq1 | Lipid transfer protein |
| comp26311_c0_seq1 | ABC transporter G family member 14 |
| comp26586_c0_seq1 | Limonene synthase |
| comp25136_c0_seq1 | Legumin 11S-globulin |
| comp5470_c0_seq1 | Peroxidase |
| comp11400_c0_seq1 | Multidrug resistance protein mdtK |
| comp13940_c0_seq1 | Pectate lyase |
| comp11103_c0_seq1 | DNA polymerase |
| 10 genes most downregulated by BAW specifically under drought; in part g, Figure 4C | |
| comp17359_c0_seq1 | Protein with unknown function |
| comp904_c0_seq1 | Microtubule-associated protein futsch |
| comp20050_c0_seq1 | Phloem protein |
| comp22520_c0_seq1 | SKP1-like protein |
| comp12519_c0_seq1 | Homeobox-leucine zipper protein |
| comp13007_c0_seq1 | Heat shock protein 1 |
| comp20351_c0_seq1 | Cotton fiber expressed protein 1 |
| comp5436_c1_seq1 | Early nodulin 75 protein |
| comp23666_c0_seq1 | Acetyl esterase |
| comp16023_c0_seq1 | Protein with unknown function |
| 10 genes most upregulated by CPB specifically under drought; in part c, Figure 4C | |
| comp15794_c0_seq1 | Protein with unknown function |
| comp572_c0_seq1 | Osmotin-like protein |
| comp15807_c0_seq1 | Patatin-like protein 3 |
| comp20396_c0_seq1 | Alternative oxidase |
| comp2990_c0_seq1 | Universal stress protein |
| comp10454_c0_seq1 | Tropinone reductase I |
| comp4593_c0_seq1 | N-acetyltransferase |
| comp469_c0_seq1 | Blue copper protein |
| comp19640_c0_seq1 | Kunitz trypsin inhibitor |
| comp4880_c0_seq1 | Protein with unknown function |
| 10 genes most downregulated by CPB specifically under drought; in part c, Figure 4C | |
| comp21048_c0_seq1 | Protein with unknown function |
| comp24351_c0_seq1 | Protein with unknown function |
| comp23146_c0_seq1 | Carotenoid cleavage dioxygenase |
| comp2675_c0_seq2 | Squamosa promoter binding-like protein |
| comp19061_c0_seq1 | BZIP transcription factor family protein |
| comp1493_c0_seq1 | Pathogenesis-related protein PR-1 |
| comp25443_c0_seq1 | Protein with unknown function |
| comp21508_c0_seq1 | Protein with unknown function |
| comp28418_c0_seq1 | Non-LTR retroelement reverse transcriptase |
| comp959_c0_seq1 | Polygalacturonase |

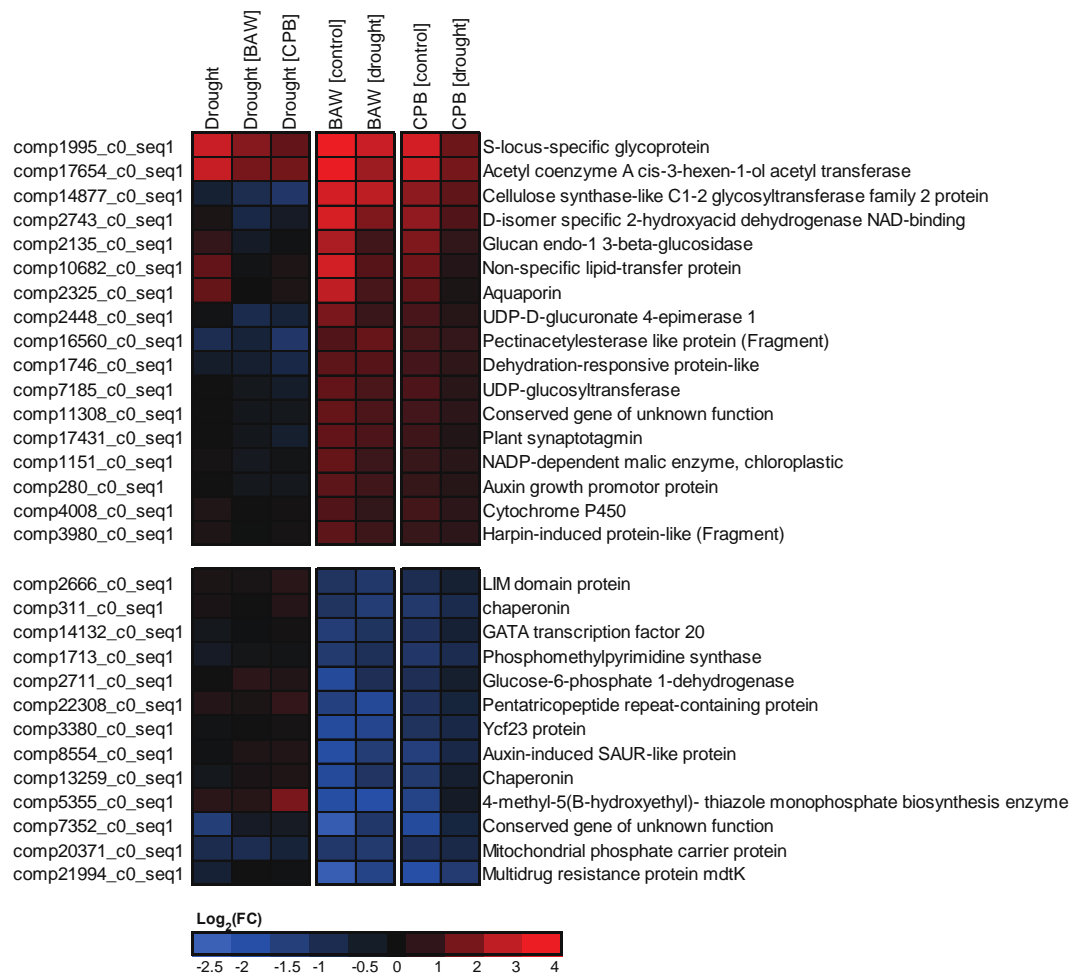


Figure S5. Herbivore-induced genes in *Solanum dulcamara* that were no longer significantly induced by *Leptinotarsa decemlineata* (CPB) feeding on drought-stressed plants. Each column is a pairwise comparison between two conditions to show effects of drought on plants that were undamaged (drought) or fed by *Spodoptera exigua* (drought [BAW]) or *L. decemlineata* (drought [CPB]) and effects of herbivory on well-watered (BAW [control] and CPB [control]) or drought-stressed plants (BAW [drought] and CPB [drought]).

Table S6. Overrepresentation of gene ontology (GO) terms among the genes that were consistently induced by drought and specifically in a 2x2 treatment combinations with *Leptinotarsa decemlineata* herbivory on *Solanum dulcamara* plants. Fisher's exact tests were used with FDR q value cut-off at 0.05. GO categories (Cat.): Molecular Function (F), Biological Process (P) and Cellular Component (C).

| GO-ID | Term description | Cat. | q value | # Gene |
|---|--|------|----------|--------|
| <i>GO terms enriched in upregulated genes</i> | | | | |
| GO:0009570 | chloroplast stroma | C | 7.38E-07 | 24 |
| GO:0019288 | isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway | P | 9.06E-04 | 11 |
| GO:0009941 | chloroplast envelope | C | 1.10E-03 | 20 |
| GO:0009535 | chloroplast thylakoid membrane | C | 1.43E-03 | 13 |
| GO:0009657 | plastid organization | P | 1.20E-02 | 15 |
| GO:0009767 | photosynthetic electron transport chain | P | 2.80E-02 | 6 |
| GO:0015995 | chlorophyll biosynthetic process | P | 3.44E-02 | 8 |
| GO:0043229 | intracellular organelle | C | 3.64E-02 | 65 |
| GO:0009234 | menaquinone biosynthetic process | P | 3.64E-02 | 2 |
| GO:0042254 | ribosome biogenesis | P | 4.35E-02 | 12 |
| GO:0044422 | organelle part | C | 4.53E-02 | 47 |
| <i>GO terms enriched in downregulated genes</i> | | | | |
| GO:1901701 | cellular response to oxygen-containing compounds | P | 7.79E-05 | 22 |
| GO:0071229 | cellular response to acid chemical | P | 1.13E-04 | 19 |
| GO:0080181 | lateral root branching | P | 1.56E-04 | 3 |
| GO:0015398 | high-affinity secondary active ammonium transmembrane transporter activity | F | 2.59E-04 | 3 |
| GO:0010311 | lateral root formation | P | 2.93E-03 | 5 |
| GO:0009751 | response to salicylic acid | P | 2.93E-03 | 13 |
| GO:0072488 | ammonium transmembrane transport | P | 3.73E-03 | 3 |
| GO:0015843 | methylammonium transport | P | 4.71E-03 | 3 |
| GO:0098542 | defence response to other organism | P | 9.22E-03 | 18 |
| GO:0001666 | response to hypoxia | P | 2.61E-02 | 6 |
| GO:0031347 | regulation of defence response | P | 3.20E-02 | 13 |
| GO:0009954 | proximal/distal pattern formation | P | 3.28E-02 | 3 |
| GO:0033554 | cellular response to stress | P | 3.46E-02 | 20 |
| GO:0009737 | response to abscisic acid | P | 3.54E-02 | 14 |
| GO:0009753 | response to jasmonic acid | P | 4.03E-02 | 11 |
| GO:0043647 | inositol phosphate metabolic process | P | 4.06E-02 | 4 |
| GO:0009755 | hormone-mediated signalling pathway | P | 4.07E-02 | 15 |
| GO:0009627 | systemic acquired resistance | P | 4.14E-02 | 10 |
| GO:0009605 | response to external stimulus | P | 4.15E-02 | 24 |
| GO:0080183 | response to photooxidative stress | P | 4.93E-02 | 2 |

Table S7. Primer sequences used for quantitative validation of microarray analysis.

| Gene name | Primer name | Sequence (5'-3') |
|------------------------|--------------|-------------------------|
| Target genes | | |
| comp14877_c0_seq1 | comp14877F | CTGGCGCGTACCTCTTCTTCTG |
| | comp14877R | TTGGGCATGAAAGTTCCAACGT |
| comp10_c0_seq1 | PIN_20346F | AGCGCTGATGGAACTTTCATTT |
| | PIN_20346R | CATCAATGGAATCATCATTGTGC |
| comp15183_c0_seq1 | comp15183F | GACGAACACGGTAAACGAGGAG |
| | comp15183R | GGGCAATACTTCATCCAACGAG |
| comp17670_c0_seq1 | comp17670F | TCAGTGGTGGGATTTCTGGTCT |
| | comp17670R | TACAAGAGACGTCGGCATCTGA |
| comp2069_c0_seq1 | comp2069F | GCACCAGAGCCATTAGCAATCT |
| | comp2069R | GGATTCAAGTCTCCCATTCACG |
| comp15724_c0_seq1 | comp15724F | CCTGGCATGTCAAACCTCATTT |
| | comp15724R | AACGGAGGATGTTGGGTACAGA |
| comp702_c0_seq1 | comp702F | AAACTCTCCGCACATCTCGAAC |
| | comp702R | GTTCTGGGCTGCTCGTAACATT |
| comp955_c0_seq1 | comp955F | GCATAGTCCAGCCGTTATTCCA |
| | comp955R | GGAAGCCCTGCTTATCTTCGAT |
| comp28407_c0_seq1 | comp28407F | TCCAACCTCTCGCAATACGTTCA |
| | comp28407R | GGCATATGGAATGGAAGTCGAG |
| comp2135_c0_seq1 | comp2135F | AAATCCTCTTGCTTCGGGTTGT |
| | comp2135R | CCCGGTTGGGATGTAGGTATTT |
| comp572_c0_seq1 | comp572F | GAAC TGGTCCAAGGCATATTCG |
| | comp572R | TGCTGGTAGAGGTTCTGTCTAG |
| comp15807_c0_seq1 | comp15807F | ATTCGGAGCTTCCTTTCTCTG |
| | comp15807R | AGAAACAGGCCGATACGAACAA |
| comp13011_c0_seq2 | comp13011F | ATATGGAGCGTCGAAGCAAGAG |
| | comp13011R | GACCTCGTTCGAGAGCAAACAT |
| comp2617_c0_seq1 | comp2617F | TGATTGCTCATCTTGCGTCATT |
| | comp2617R | AAGGTCCAGGGAACAACCTCTCC |
| comp3079_c0_seq1 | comp3079F | TGGACAAGTCATGCACACTCCT |
| | comp3079R | AGCTGGAAGTTGAACCTGACGA |
| comp1495_c0_seq1 | comp1495F | GGTTTCTCGAATCTCAGGCAGA |
| | comp1495R | GGTGGGAAAGGAAAGCAAATCT |
| Reference genes | | |
| comp28_c0_seq4 | EF1a_48212F | TGGTACCTCCCAGGCTGACTGTG |
| | EF1a_48212R | GCAACGCATGTTACGGGTCT |
| comp3969_c0_seq2 | CAC_00903F | GGTAGTGTGCTCCGTTGCGATG |
| | CAC_00903R | GCGGGATTAAAGCTGCGACTCT |
| comp10185_c0_seq4 | TIP_26454F | CCTTTGCAACAGGTGGTGCTCG |
| | TIP_26454R | CCCACTGAATGCAGCTGCTTCC |
| comp141_c0_seq1 | GAPDH_13565F | ATTGGTGGCTCGGGTTGCTCTC |
| | GAPDH_13565R | ATGATGCTTCCACTGGCCGTGT |