

Supplementary Material

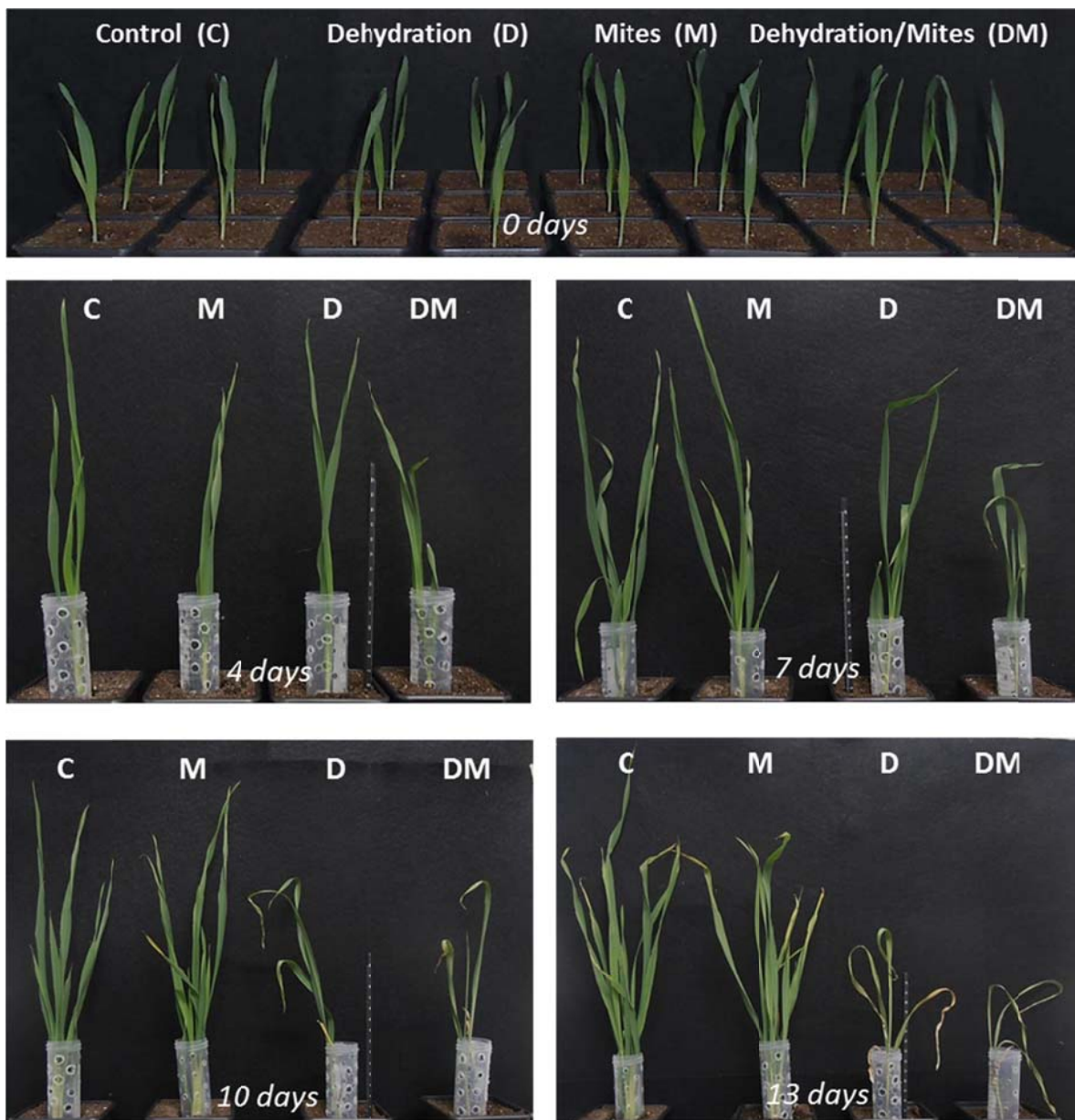
Dehydration stress contributes to enhance plant defense response and mite performance on barley

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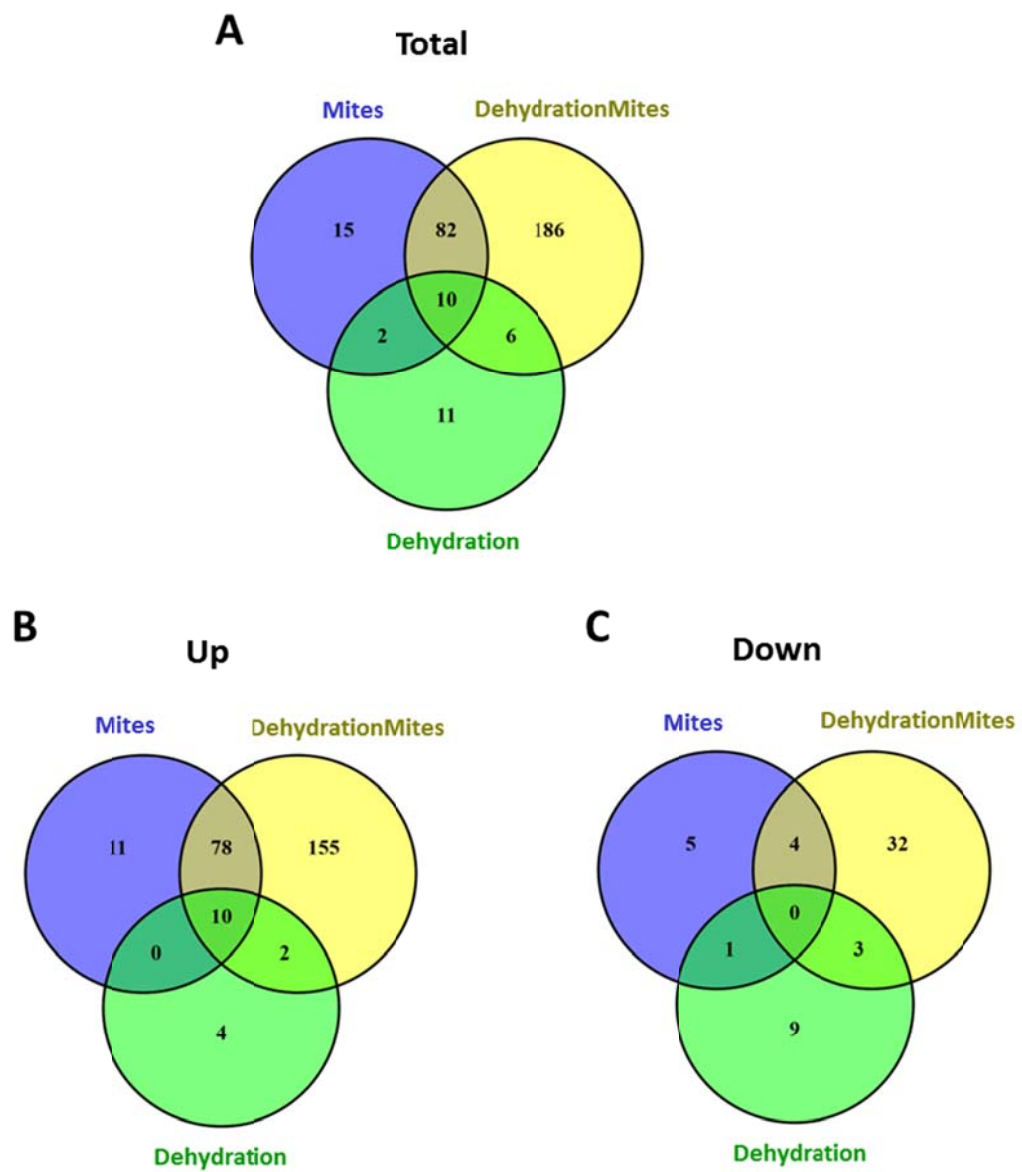
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1 Supplementary Figures and Tables

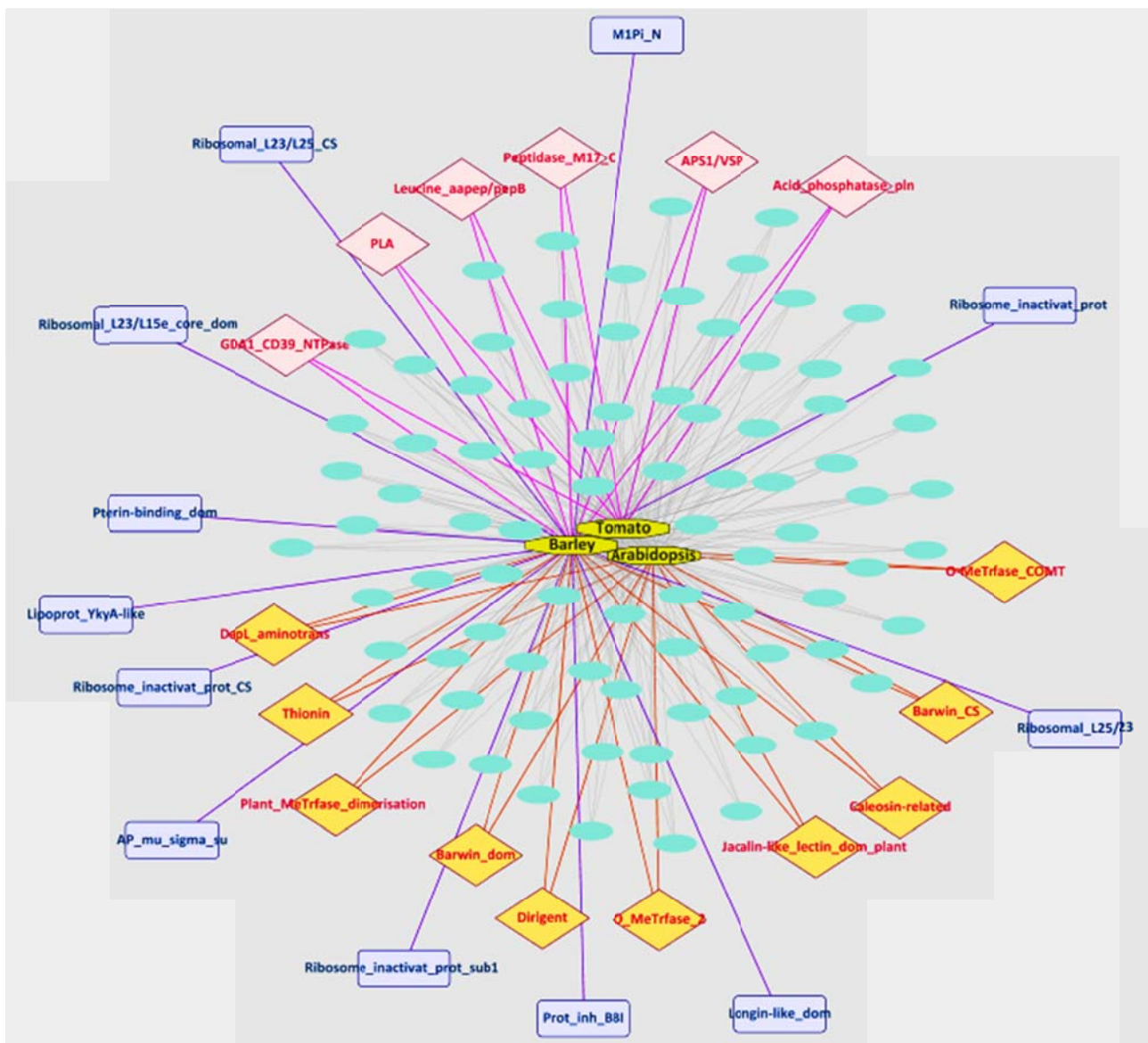
1.1 Supplementary Figures



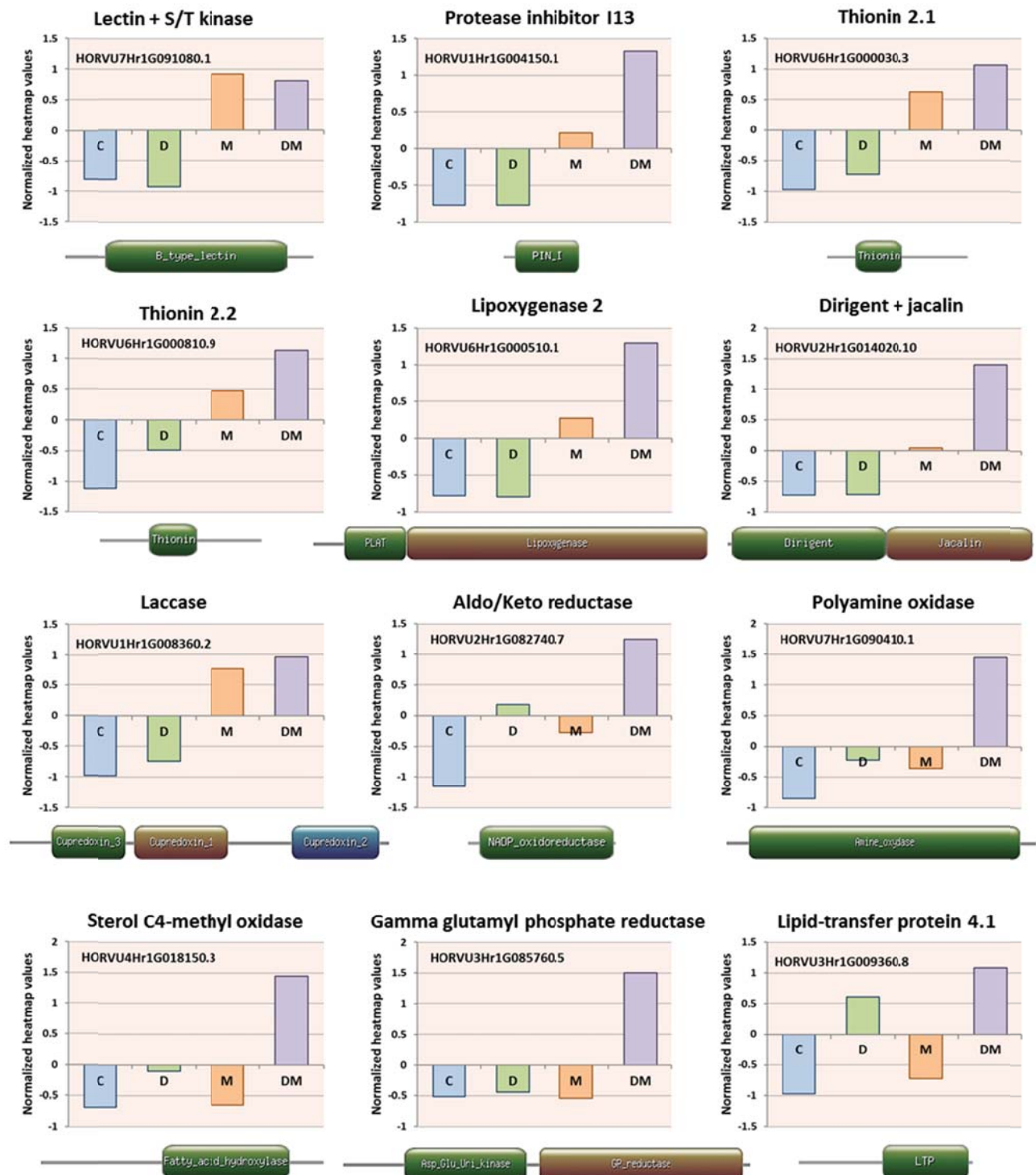
Supplementary Figure 1. Phenotype of barley plants 0, 4, 7, 10 and 13 days post treatment. Control (C), mites (M), dehydration (D) and dehydration + mites (DM).



Supplementary Figure 2. Venn diagrams showing the number of specific and shared differential expressed genes among the different treatments and non-treated plants. **(A)** Total number of DEGs. **(B)** Up-regulated DEGs. **(C)** Down-regulated DEGs.



Supplementary Figure 3. Network showing the conservation of Interpro identifiers from DEGs after mites treatment in barley in the DEGs after mites treatment in tomato and Arabidopsis. Unique barley identifiers (purple), shared barley and tomato identifiers (pink), shared barley and Arabidopsis identifiers (orange), shared barley, tomato and Arabidopsis identifiers (blue-green).



Supplementary Figure 4. RNA-seq expression of the selected DEGs after the different treatments. Values were normalized as heatmap values (see Figure 3). C, control. D, dehydration. M, mites. DM, dehydration and mites. A schematic representation of each gene showing the Interpro domains identified is located under the expression graphics.

1.2 Supplementary Tables

Supplementary Table 1. Primer sequences used for the amplification of barley genes by RT-qPCR assays.

Gene ID	Description	Primer name	Sequence (5' → 3')
<i>Hv1Hr1G004150</i>	Protease inhibitor I13	Hv1Hr1G004150-F	TCAAGGACATGCCTGAAGTG
		Hv1Hr1G004150-R	CGACAGTGTCAACGAGGATG
<i>Hv1Hr1G008360</i>	Laccase	Hv1Hr1G008360-F	AGGCCCACTACAACAACGTC
		Hv1Hr1G008360-R	TCGACTTGGTCGTGTACTGC
<i>Hv2Hr1G014020</i>	Jasmonate-induced protein (Dirigent + jacalin)	Hv2Hr1G014020-F	GCCGCGTTTGTAGAGATCA
		Hv2Hr1G014020-R	CCAGTAGTGGCATTGGAGTCT
<i>Hv2Hr1G082740</i>	Aldo/Keto reductase	Hv2Hr1G082740-F	GACATCTACGGTCCCCACAC
		Hv2Hr1G082740-R	GTGGCCAACCTGGACCTTCT
<i>Hv3Hr1G009360</i>	Lipid transfer protein 4.1	Hv3Hr1G009360-F	CAGAGCACCGCTGACAATC
		Hv3Hr1G009360-R	TTAGAGCAGTCGACGGAAGC
<i>Hv3Hr1G085760</i>	Gamma glutamyl phosphate reductase	Hv3Hr1G085760-F	GCTCTAGCAATCCGAAGTGG
		Hv3Hr1G085760-R	CAACACCATCTGGAATCAGC
<i>Hv4Hr1G018150</i>	Sterol C4-methyl oxidase	Hv4Hr1G018150-F	CCAGTACCTGCGTTCTGACA
		Hv4Hr1G018150-R	GTAGTCACCACCACGCCTTT
<i>Hv6Hr1G000030</i>	Thionin 2.1	HvThionin 2.1-F	GACGGGCAGAACTGCTACAAC
		HvThionin 2.1-R	ACCGGATTGAGGAGAAGAT
<i>Hv6Hr1G000510</i>	Lipoxygenase 2	Hv6Hr1G000510-F	AGAAGGGCGAAATGTACGTG
		Hv6Hr1G000510-R	CACCTTCAAGCCAGTGCATA
<i>Hv6Hr1G000810</i>	Thionin 2.2	HvThionin 2.2-F	TCAATCCAACATAGCCATTTC
		HvThionin 2.2-R	CAACTTTTTCCCTCACCTG
<i>Hv7Hr1G090410</i>	Polyamine oxidase	Hv7Hr1G090410-F	GTACAAGCTGCAGCCCAAG
		Hv7Hr1G090410-R	GATGATGAGCAGCGAGACC
<i>Hv7Hr1G091080</i>	Lectin + Serine/threonine-protein kinase	Hv7Hr1G091080-F	AGCCACAGACATACGTGCAG
		Hv7Hr1G091080-R	GCGAGAGTATCGCCTTTTGT
<i>Hv6Hr1G012570</i>	Cyclophilin	Hv6Hr1G012570-F	TCCACCGGAGAGGAAGTACAGT
		Hv6Hr1G012570-R	AATGTGCTCAGAGATGCAAGGA
<i>tetur18g03590</i>	RP49	tetur18g03590-F	CTTCAAGCGGCATCAGAGC
		tetur18g03590-R	CGCATCTGACCCTTGAACCTC
<i>tetur43g00010</i>	VTG	tetur43g00010-F	ACGTCGCTATTGGTGAAACC
		tetur43g00010-R	TGTTGATTCGGGATGGGTAT
<i>tetur03g03240</i>	ATG13	tetur03g03240-F	ATGGCGGTGATAAGCTATGC
		tetur03g03240-R	AAGAAGCACCTGGCGAAGTA

Supplementary Table 2. List of the top ten significant results obtained from the enrichment gene ontology (GO) analysis of the Biological Process assigned to the DEGs.

Control/Mites						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0006952	defense response	143	11	0.41	1.40E-13
2	GO:0006950	response to stress	694	13	1.99	2.90E-08
3	GO:0050896	response to stimulus	1171	13	3.36	1.20E-05
4	GO:0009617	response to bacterium	5	2	0.01	8.00E-05
5	GO:0042742	defense response to bacterium	5	2	0.01	8.00E-05
6	GO:0009620	response to fungus	7	2	0.02	0.00017
7	GO:0050832	defense response to fungus	7	2	0.02	0.00017
8	GO:0043207	response to external biotic stimulus	10	2	0.03	0.00036
9	GO:0051707	response to other organism	10	2	0.03	0.00036
10	GO:0098542	defense response to other organism	10	2	0.03	0.00036
Control/Dehydration and mites						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0006952	defense response	143	14	1.02	1.20E-12
2	GO:0006950	response to stress	694	19	4.93	3.00E-07
3	GO:0044710	single-organism metabolic process	3207	45	22.78	3.60E-07
4	GO:0043207	response to external biotic stimulus	10	4	0.07	4.80E-07
5	GO:0051707	response to other organism	10	4	0.07	4.80E-07
6	GO:0098542	defense response to other organism	10	4	0.07	4.80E-07
7	GO:0009605	response to external stimulus	18	4	0.13	6.70E-06
8	GO:0009607	response to biotic stimulus	30	4	0.21	5.70E-05
9	GO:0055114	oxidation-reduction process	1986	29	14.11	6.70E-05
10	GO:0002682	regulation of immune system process	3	2	0.02	0.00015
Control/Dehydration						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0006952	defense response	143	4	0.11	3.20E-06
2	GO:0006950	response to stress	694	4	0.55	0.0015
3	GO:0050896	response to stimulus	1171	4	0.93	0.0101
						7

Mites/Dehydration and mites						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0001101	response to acid chemical	20	2	0.01	5.10E-05
2	GO:0009415	response to water	20	2	0.01	5.10E-05
3	GO:0010035	response to inorganic substance	31	2	0.02	0.00012
4	GO:1901700	response to oxygen-containing compound	31	2	0.02	0.00012
5	GO:0009628	response to abiotic stimulus	37	2	0.02	0.00018
6	GO:0006560	proline metabolic process	6	1	0	0.00335
7	GO:0006561	proline biosynthetic process	6	1	0	0.00335
8	GO:0006950	response to stress	694	3	0.39	0.005
9	GO:0042221	response to chemical	213	2	0.12	0.00571
10	GO:0046394	carboxylic acid biosynthetic process	218	2	0.12	0.00597
Dehydration/Dehydration and mites						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0043207	response to external biotic stimulus	10	3	0.03	4.40E-06
2	GO:0051707	response to other organism	10	3	0.03	4.40E-06
3	GO:0098542	defense response to other organism	10	3	0.03	4.40E-06
4	GO:0044710	single-organism metabolic process	3207	24	11	2.40E-05
5	GO:0009605	response to external stimulus	18	3	0.06	3.00E-05
6	GO:0002682	regulation of immune system process	3	2	0.01	3.40E-05
7	GO:0002831	regulation of response to biotic stimulus	3	2	0.01	3.40E-05
8	GO:0009627	systemic acquired resistance	3	2	0.01	3.40E-05
9	GO:0009814	defense response, incompatible interaction	3	2	0.01	3.40E-05
10	GO:0010112	regulation of systemic acquired resistance	3	2	0.01	3.40E-05
Mites/Dehydration						
	GO.ID	Term	Annotated	Significant	Expected	classicFisher
1	GO:0043207	response to external biotic stimulus	10	3	0.03	2.80E-06
2	GO:0051707	response to other organism	10	3	0.03	2.80E-06
3	GO:0098542	defense response to other organism	10	3	0.03	2.80E-06
4	GO:0009605	response to external stimulus	18	3	0.05	1.90E-05
5	GO:0006952	defense response	143	5	0.42	5.90E-05
6	GO:0009617	response to bacterium	5	2	0.01	8.40E-05
7	GO:0042742	defense response to bacterium	5	2	0.01	8.40E-05
8	GO:0009607	response to biotic stimulus	30	3	0.09	9.10E-05
9	GO:0006950	response to stress	694	9	2.05	0.00014
10	GO:0009620	response to fungus	7	2	0.02	0.00018

