

1 Supplementary Materials

2 **Table S1** Relative expression levels and standard errors of each *F. graminearum* gene selected and compound (chitosan
3 hydrochloride C, tebuconazole T, azoxystrobin A, and the mixture of tebuconazole and azoxystrobin T + A). Relative
4 expression values were obtained by using the equation $2^{-\Delta\Delta C_q}$ with *TEF*, *TUB* and *GAPDH* as reference genes and mock
5 treatment used to normalize the relative expression levels. The data represent averages and standard errors for the four
6 independent biological replicates and the four technical replicates examined. The data were subjected to one-way analysis
7 of variance (ANOVA). Different letters among the plant treatments were assessed by means of significant F values by
8 applying the Tukey Honestly Significant Difference Test (Tukey test) at 0.99 confidence level ($p < 0.01$).

Gene		C	T	A	T + A
<i>Erg3</i>	Relative expression	0.01	2.19	2.58	0.92
	Standard error (\pm)	0.044	0.065	0.047	0.05
	$p < 0.01$	b	a	a	ab
<i>Fg03624</i>	Relative expression	0.33	0.59	0.61	0.87
	Standard error (\pm)	0.02	0.12	0.13	0.04
	$p < 0.01$	b	ab	ab	a
<i>Fg03695</i>	Relative expression	0.01	0.38	0.11	0.12
	Standard error (\pm)	0.06	0.38	0.01	0.09
	$p < 0.01$	c	a	bc	b
<i>Fg07551</i>	Relative expression	0.01	0.15	0.50	0.23
	Standard error (\pm)	0.07	0.10	0.13	0.01
	$p < 0.01$	b	b	a	ab
<i>Fg09443</i>	Relative expression	0.04	1.54	0.36	1.18
	Standard error (\pm)	0.06	0.06	0.18	0.11
	$p < 0.01$	c	a	bc	ab
<i>Fg03725</i>	Relative expression	0.01	0.57	0.08	0.88
	Standard error (\pm)	0.01	0.12	0.08	0.07
	$p < 0.01$	c	ab	bc	a
<i>Fg01572</i>	Relative expression	0.04	9.64	2.69	5.69
	Standard error (\pm)	0.05	0.07	0.03	0.03
	$p < 0.01$	c	a	bc	ab
<i>Fg04196</i>	Relative expression	0.01	1.30	0.64	1.58
	Standard error (\pm)	0.02	0.03	0.14	0.09
	$p < 0.01$	b	a	ab	a
<i>Fg06619</i>	Relative expression	0.04	1.23	2.44	0.93
	Standard error (\pm)	0.08	0.06	0.16	0.08
	$p < 0.01$	b	ab	a	ab
<i>Fg10231</i>	Relative expression	0.10	4.00	4.90	4.30
	Standard error (\pm)	0.01	0.03	0.03	0.11

		$p < 0.01$	b	a	a	a
	Relative expression		0.11	3.25	1.33	4.38
<i>FPP</i>	Standard error (\pm)		0.01	0.77	0.22	0.22
		$p < 0.01$	c	ab	bc	a
	Relative expression		0.02	0.03	1.30	0.31
<i>Tri1</i>	Standard error (\pm)		0.07	0.10	0.09	0.09
		$p < 0.01$	b	b	a	b
	Relative expression		0.01	0.82	1.33	0.30
<i>Tri3</i>	Standard error (\pm)		0.04	0.15	0.23	0.08
		$p < 0.01$	c	ab	a	bc
	Relative expression		0.02	0.07	0.21	0.03
<i>Tri4</i>	Standard error (\pm)		0.00	0.18	0.03	0.01
		$p < 0.01$	b	b	a	b
	Relative expression		0.02	1.67	2.76	0.60
<i>Tri5</i>	Standard error (\pm)		0.07	0.15	0.34	0.33
		$p < 0.01$	b	ab	a	b
	Relative expression		0.03	2.09	2.05	0.82
<i>Tri6</i>	Standard error (\pm)		0.08	0.39	0.16	0.16
		$p < 0.01$	c	a	ab	bc
	Relative expression		3.34	19.94	11.52	16.81
<i>Tri8</i>	Standard error (\pm)		0.09	5.23	2.29	2.94
		$p < 0.01$	b	a	ab	a
	Relative expression		0.01	4.98	2.04	0.52
<i>Tri9</i>	Standard error (\pm)		0.00	0.01	0.58	0.13
		$p < 0.01$	c	a	bc	bc
	Relative expression		0.02	2.73	4.19	0.18
<i>Tri10</i>	Standard error (\pm)		0.01	0.84	0.72	0.04
		$p < 0.01$	b	ab	a	b
	Relative expression		0.15	26.84	4.90	1.44
<i>Tri11</i>	Standard error (\pm)		0.01	0.92	0.76	0.55
		$p < 0.01$	c	a	b	c
	Relative expression		0.05	24.95	13.21	5.12
<i>Tri12</i>	Standard error (\pm)		0.03	0.37	1.95	0.76
		$p < 0.01$	c	a	b	c
	Relative expression		0.10	3.39	10.62	2.90
<i>Tri14</i>	Standard error (\pm)		0.01	0.59	1.86	1.01

	$p < 0.01$	b	b	a	b
	Relative expression	5.00	24.31	0.16	31.40
<i>Tri101</i>	Standard error (\pm)	1.76	3.01	0.01	0.65
	$p < 0.01$	c	b	c	a

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10 **Table S2** Relative expression levels and standard errors of each wheat gene selected for each durum wheat genotype
11 (Marco Aurelio and DBC480) and compound (chitosan C, tebuconazole T, azoxystrobin A, and the mixture of tebuconazole
12 and azoxystrobin T + A). Fg represents the *F. graminearum* inoculated control. Relative expression values were obtained by
13 using the equation $2^{-\Delta\Delta Cq}$ with *TaFNR*, *TaTUB* and *TaACT* as reference genes and mock treatment used to normalize the
14 relative expression levels. The data represent averages and standard errors for the four independent biological replicates
15 and the four technical replicates examined. The data were subjected to two-way analysis of variance (ANOVA). Different
16 letters among the plant treatments were assessed by means of significant F values by applying the Tukey Honestly
17 Significant Difference Test (Tukey test) at 0.99 confidence level ($p < 0.01$).

Gene	Marco Aurelio					DBC480				
	Fg	C	T	A	T + A	Fg	C	T	A	T + A
Relative expression	2.89	1.76	1.16	1.09	0.84	2.62	2.35	0.67	2.29	0.27
<i>TaPAL</i> Standard error (\pm)	0.22	0.29	0.22	0.27	0.23	0.84	0.66	0.10	0.80	0.07
$p < 0.01$	a	b	b	b	c	a	a	c	a	c
Relative expression	3.48	2.91	0.87	0.98	1.05	2.04	2.16	1.21	1.47	0.84
<i>TaPR1</i> Standard error (\pm)	0.27	0.61	0.22	0.18	0.28	0.56	0.59	0.16	0.44	0.12
$p < 0.01$	a	b	c	c	c	b	b	c	bc	c
Relative expression	2.51	2.69	0.47	0.49	0.40	3.41	3.23	1.79	1.04	0.61
<i>TaPR2</i> Standard error (\pm)	0.69	0.34	0.16	0.13	0.05	0.52	0.83	0.26	0.20	0.08
$p < 0.01$	b	b	d	d	d	a	a	b	c	d

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19 **Table S3** A list of *F. graminearum* selected genes, accession numbers, gene functions, primer pairs, amplicon length from
20 DNA and cDNA and primer pairs references.

Gene and Accession Number	Function	Primer Pairs (5'-3')	bp (DNA)	bp (cDNA)	Reference
<i>Erg3</i> - XM_011320132.1	C5-sterol desaturase	ACCAACAACCCTGTCGTCAA TCCGTATAAGTGC GGTTGTCA	239	239	Yun et al., 2014
<i>Fg03624</i> - XM_011323775.1	Xylanase	CTTCCGGTGCTCAGAAGAAGG CGGACCAGTACTGCTGGAAGG	87	87	Carapito et al., 2008
<i>Fg03695</i> - XM_011323698.1	Endoglucanase	GCATCAACCTCAAGGTCCTGG TGC GTAGAGGTTGAAGAGAATGC	127	127	Carapito et al., 2008
<i>Fg07551</i> - XM_011329028.1	Exopolygalacturonase	GGCTCTCTTGGCCAGTACAAGG AAGGTGACGTTGTCTGATGAAGC	126	126	Carapito et al., 2008
<i>Fg09443</i> - XM_011329987.1	Pectin methyl esterase	TGTTGAGGAGAAGACCACCTTCC AGAAGAGCCACCGTTGCTACC	121	121	Carapito et al., 2008

<i>Fg03725 -</i> XM_011323666.1	Multidrug transporter	TGGTCGTC AATACCTCTTCATTGG TACCACCAGCGTTGGTAAGAGG	111	111	Carapito et al., 2008
<i>Fg01572 -</i> XM_011319083.1	Glutamate decarboxylase	GGCCAATACTACCAGCTCATCC CGAACGTTCTGACATGATGACG	115	115	Carapito et al., 2008
<i>Fg04196 -</i> XM_011323131.1	Succinate semialdehyde dehydrogenase	GCCGGATACTTCTTCTCCAAGG CGTAACCGTCTCCTTGACACC	126	126	Carapito et al., 2008
<i>Fg06619 -</i> XM_011327936.1	NADP-dependent alcohol dehydrogenase	CTCAGCCTCCTCGATATTCACG AAGTGAGACGTGCCGATGTAGC	122	122	Carapito et al., 2008
<i>Fg10231 -</i> XM_011320878.1	NADH-ubiquinone oxidoreductase	CCAAGGCCACTGCTACTGATCC CAGATCCTTCTTGTGGTCTCG	115	115	Carapito et al., 2008
<i>FPP -</i> XM_011328132.1	Farnesyl pyrophosphate synthase	TTTGCAAGCCCGAACACATT GCGGATCTGGCCAACAACCTTCT	234	234	Lee et al., 2014
<i>Tri1 -</i> AY339129.1	Cytochrome P450 monooxygenase	GCTCGGAACTAATCACTCC TCCAAACATTGGCAGATGA	185	185	Heidtmann- Bemvenuti et al., 2015
<i>Tri3 -</i> XM_009265280.1	Trichothecene 15-O- acetyltransferase	CTTGCAAGGATATCAAGAAATGTTACGA CTCGCCTGTTGTAGTTCGCTTGATTT	208	208	Lee et al., 2014
<i>Tri4 -</i> EF685280.1	Trichodiene oxygenase	TCGAGGCACAACAGAAGGGTATCC AATGTCGGCCTTGGTGGTGTC	237	237	Lee et al., 2014
<i>Tri5 -</i> XM_011323870.1	Trichodiene synthase	GGAGCGTATCGA GAATTGTC TGCCCAACTGTATACGACCA	168	168	Heidtmann- Bemvenuti et al., 2015
<i>Tri6 -</i> AB017495.1	Trichothecene transcriptional regulator	TCTTTGTGAGCGGACGGGACTTTA ATCTCGCATGTTATCCACCCTGCT	245	245	Horevaj et al., 2011
<i>Tri8 -</i> HG970333.1	Trichothecene 3-O- esterase	GCTACTTTGGACTCAATTCG CATACTGTACCGCAAGTTCTG	139	139	Lee et al., 2014
<i>Tri9 -</i> LT222054.1	Unknown	AGCCGCTAAACTGATCGACTCATA GCTTTGGCTGCGACCCATAT	85	85	Lee et al., 2014
<i>Tri10 -</i> AF365969.1	Regulatory gene	GTGGCCGGGACGCTTCAAT ATCCGTC AAGTCTTCCCATCTCAT	254	254	Brown et al., 2001
<i>Tri11 -</i> XM_009265275.1	Trichothecene C-15 hydroxylase	AAGTACTTCACCCGACCAAACGAC CGGCAAGGCGAATGTCAAAC	192	192	Lee et al., 2014
<i>Tri12 -</i> XM_009265274.1	Trichothecene efflux pump	TCCACAGTCATCTTTCCCCAGTCT CTCCCAGTGCCATAGCGAAGTAGT	172	172	Lee et al., 2014
<i>Tri14 -</i> XM_009265272.1	Unknown	CTGGGAACCTACGCATCAAACATT CGAATGAGCTGCCAATGATGT	165	165	Lee et al., 2014
<i>Tri101 -</i> AB011417.1	Trichothecene 3-O- acetyltransferase	GTGGGACTCTGGGATTACGACTTT GTCCACTCCTTATCCGCTTCAA	130	130	Lee et al., 2014

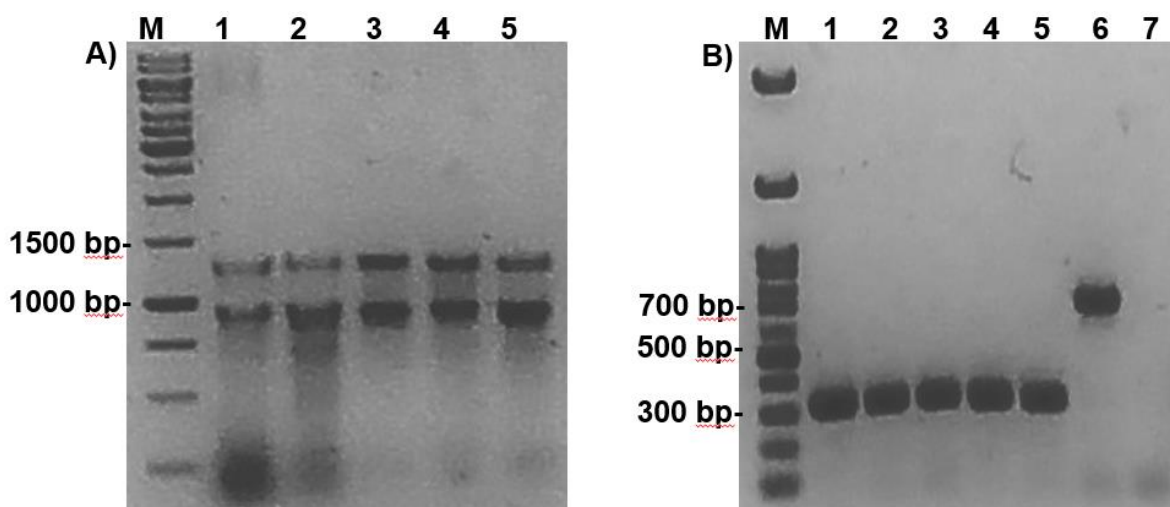
<i>TEF</i> - MH572267.1	Translational elongation factor 1- α	ATGGGTAAGGAGGACAAGAC GGAAGTACCAGTGATCATGTT	700	324	Geiser et al., 2004
<i>TUB</i> - XM_011329885	β -tubulin	TTGCATTGGTACACTGGTGAGG AGGCAGCTCCTCCTCGTACTCC	110	110	Carapito et al., 2008
<i>GAPDH</i> - XM_011326605.1	Glyceraldehyde-3- phosphate dehydrogenase	TGACTTGACTGTTTCGCCTCGAGAA ATGGAGGAGTTGGTGTGCGCGTTA	160	160	Harris et al., 2016

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22 **Table S4** A list of wheat selected genes, accession numbers, gene functions, primer pairs, amplicon length from DNA and
23 cDNA and primer pairs references.

Gene and Accession Number	Function	Primer Pairs (5'-3')	bp (DNA)	bp (cDNA)	Reference
<i>TaPAL</i> - X99705	Phenylalanine ammonia-lyase	CGATGCTCGTCCGAGTCAAT CATGACCTCACAGAAGACGC	407	407	<i>De novo</i> designed
<i>TaPR1</i> - AJ007348	Pathogenesis related protein-1	ACTACGACTACGGGTCCAACA TCGTAGTTGCAGGTGATGAAG	145	145	Lu et al., 2006
<i>TaPR2</i> - Y18212	β -1,3-glucanase	AACGTGCGCCCCTACTACC CGCTCGAACAGGCTCGTGTA	398	398	Francesconi et al., 2020
<i>TaFNR</i> - AJ457980	Ferredoxin-NADP(H)- oxidoreductase	CACCGGCCAGTGATCTT AAGGGCGTCTGCTCCAAC	259	69	Tenea et al., 2011
<i>TaTUB</i> - TAU76745	β -tubulin	CGAGGAGGGCGAGTACGA AGCAAAGCACGACATGGACAT	79	79	Tenea et al., 2011
<i>TaACT</i> - AB181991	Actin	TCCTGTGTTGCTGACTGAGG GGTCCAAACGAAGGATAGCA	350	236	Mandalà et al., 2019

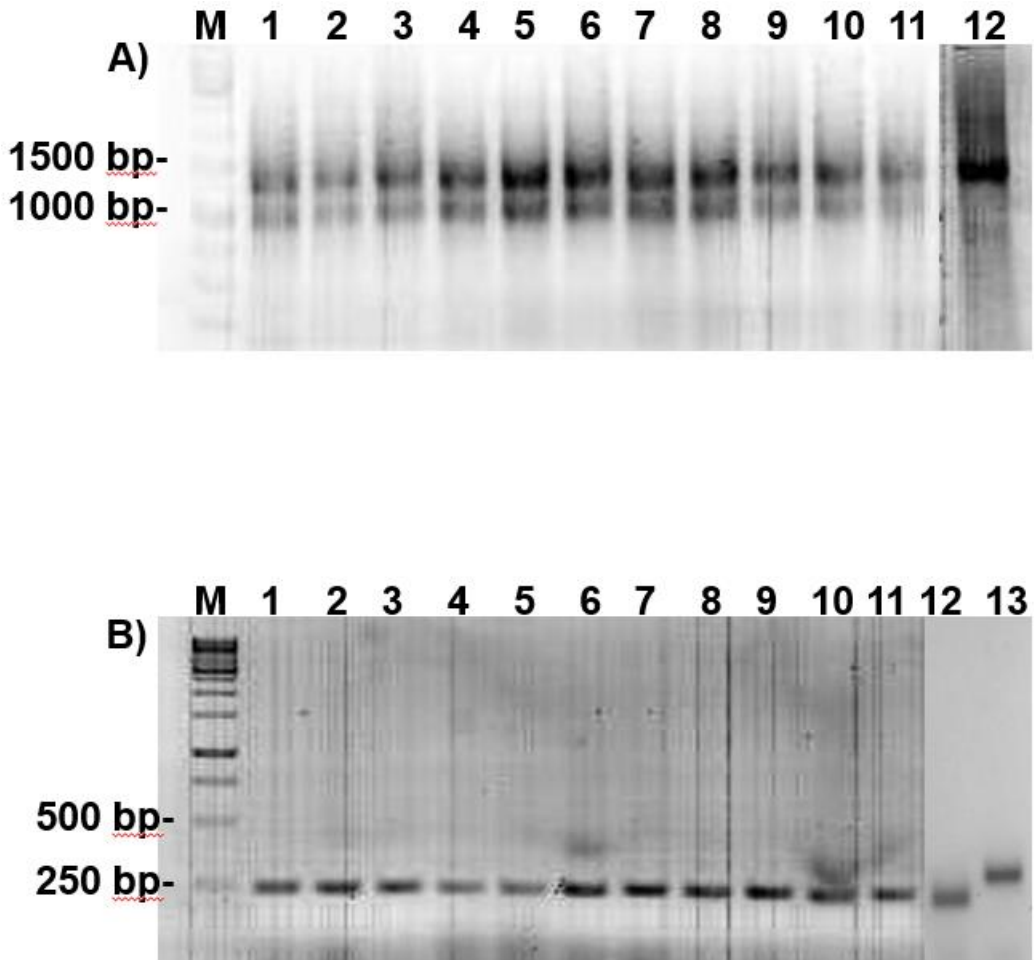
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26 **Figure S1** 1.5% agarose gel of total extracted RNA (A) and RT-PCR (B) from *F. graminearum*. M) GeneRuler™ 1 kb DNA
27 Ladder (Thermo Fisher Scientific) and ExcelBand™ 100 bp + 3K DNA Ladder (Smobio); (1) Chitosan hydrochloride; (2)
28 Tebuconazole; (3) Azoxystrobin; (4) Tebuconazole+Azoxystrobin; (5) Mock; (6) Genomic DNA (gDNA); (7) No template
29 control (NTC). The figure represents the original pictures of the gels.
30

31 **Figure S2** Durum seedlings at 14 days after the coating with chitosan hydrochloride at 0.5% (C). M represents the mock
32 control.



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 34 **Figure S3** 1.5% agarose gel of total extracted RNA (A) and RT-PCR (B) from the spikes of Marco Aurelio and DBC480
 35 subjected to the different compounds' treatments at the flag leaf level. M) GeneRuler™ 1 kb DNA Ladder (Thermo Fisher
 36 Scientific); (1) Marco Aurelio, chitosan; (2) Marco Aurelio, tebuconazole; (3) Marco Aurelio, azoxystrobin; (4) Marco
 37 Aurelio, tebuconazole+azoxystrobin; (5) Marco Aurelio, *F. graminearum* inoculated control; (6) Marco Aurelio, mock
 38 control; (7) DBC480, chitosan; (8) DBC480, tebuconazole; (9) DBC480, azoxystrobin; (10) DBC480,
 39 tebuconazole+azoxystrobin; (11) DBC480, *F. graminearum* inoculated control; (12) DBC480, mock control; (13) Genomic
 40 DNA (gDNA). The figure represents the pictures of three gels. The original pictures of the gels are available if requested.