

Trypan blue staining of *Fusarium graminearum* macroconidia

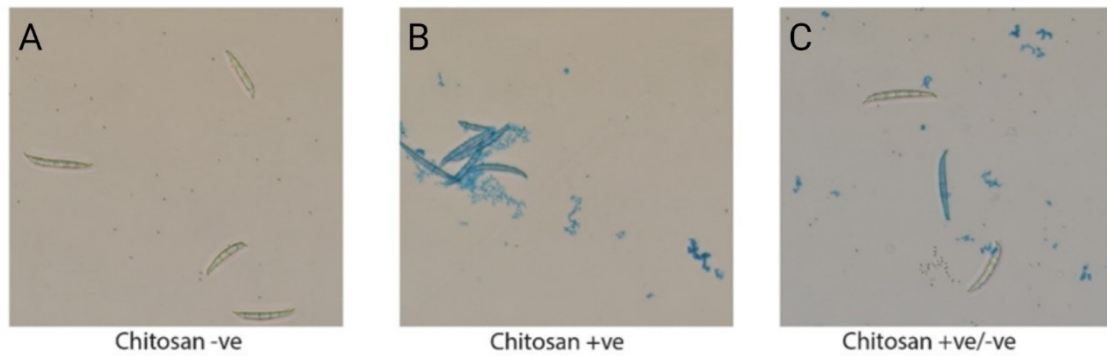


Figure S1. Light microscope picture (200x magnification) of trypan blue staining of *F. graminearum* macroconidia cultured in PDB medium with CS_10 at a concentration of 200 ppm. (A) Negative control culture (no CS_10 application) of *Fg* showing no staining with Trypan blue and indicates live *Fg* macroconidia. (B) Positive culture (CS_10 application) of killed and stained *Fg* macroconidia showing the antifungal impact of CS_10. (C) A mixed culture of negative and positive *Fg* macroconidia showing the authenticity of the Trypan blue staining method.

RNA-Seq Data Outputs

Ensemble ID	Function	Log2 Fold Change	Regulation
FGSG_03842	carbohydrate metabolic process-calcium ion binding	-2.85	Down
FGSG_00571	carbohydrate metabolic process-cellulose binding	-7.52	Down
FGSG_06605	carbohydrate metabolic process	-1.49	Down
FGSG_00007	iron ion binding	1.52	Up

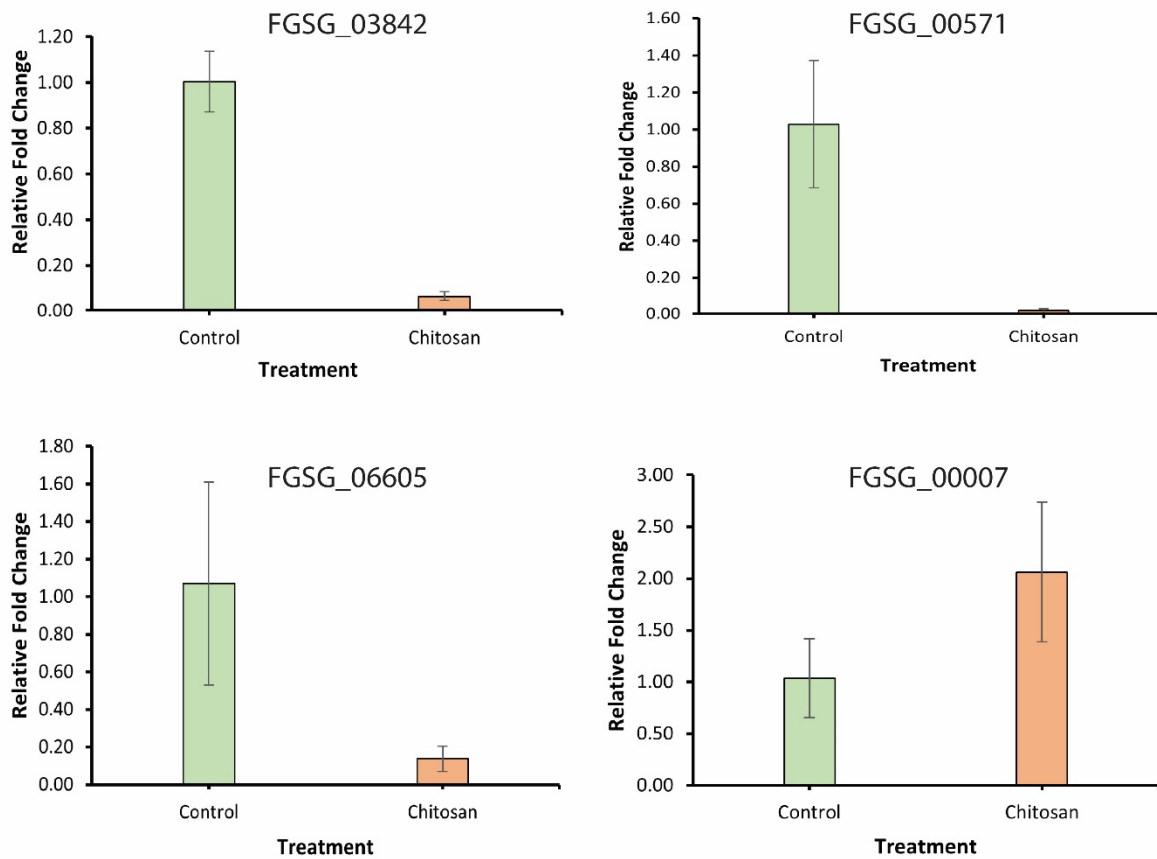


Figure S2. qPCR expression of *F. graminearum* genes in response to chitosan treatment. Relative expression levels of the *Fg* were normalized using the beta-tubulin gene as internal control and were measured through the $2^{-\Delta\Delta C_t}$ method. The bar plots represent the relative fold change expression of three biological replicates and error bars represent the average means. The qPCR expression is in line with the RNA-Seq Data and confirms the validity of the expression.

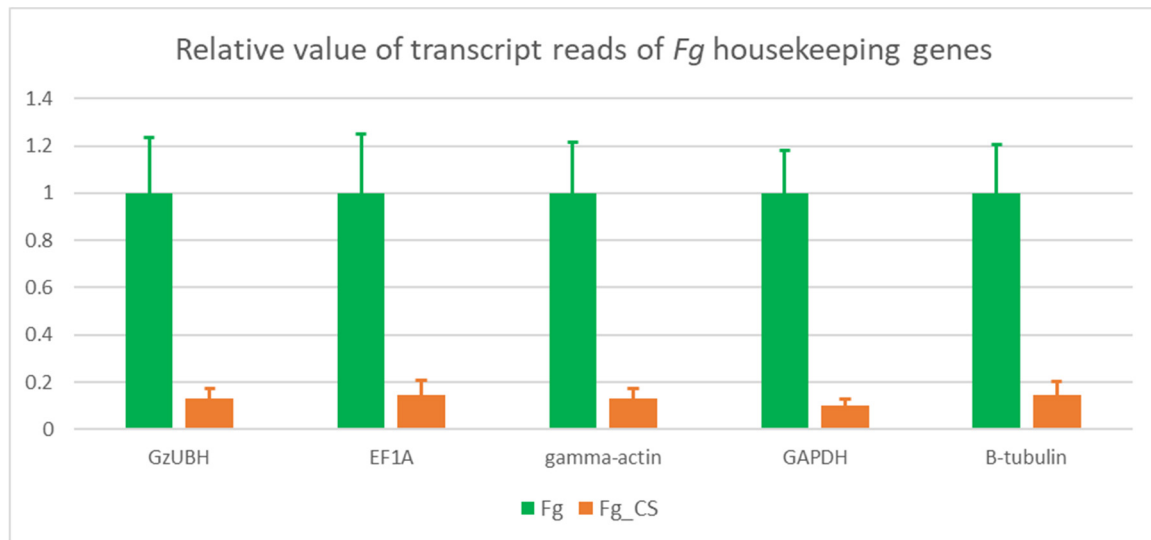


Figure S3. Relative value of transcript reads of *F. graminearum* housekeeping genes. Number of transcripts reads for each of selected housekeeping genes has been estimated based on transcriptomics results. The number of transcripts reads of the *Fg* sample has been counted as '1' while the sample treated with CS (*Fg_CS*) is shown as relative value.

Table S1: The list of Primers used for qPCR experiment based on Harris et al. (2016).

Gene Name	Sequence	Gene involved in
FGSG_03842	F: GAACACGGATGGTGGATACC R: CCCTTTACCCATGTGGTTTG	Starch synthesis pathways
FGSG_00571	F: GGCTCCCATGGTTCTTGTTA R: GTTGGGGACGTTCTTCTCAA	Starch synthesis pathways
FGSG_06605	F: TCTGGAGTCATTGCTTGTGC R: GCGAAAGGCCAGTTGTAGAG	Starch synthesis pathways
FGSG_00007	F: GTGCGGTTTTGACCAGATTT R: TATCAAGAGAGCGCAGCAGA	Cytochrome Synthesis
<i>Fg</i> -Elongation Factor 1 (FGSG_08811)	F: CCTCCAGGATGTCTACAAGA R: CTCAACGGACTTGACTTCAG	Housekeeping gene (Harris, et al. 2016)

Harris, L. J., Balcerzak, M., Johnston, A., Schneiderman, D., & Ouellet, T. (2016). Host-preferential *Fusarium graminearum* gene expression during infection of wheat, barley, and maize. *Fungal Biol*, 120(1), 111-123.

Table S2. The list of differentially expressed genes discussed in the manuscript.

Gene ID	log2fold change	fold change	Annotation
FGSG_00071	1.424	2.684	TRI1
FGSG_00571	-7.522	0.005	exoglucanase 1 precursor
FGSG_01403	-0.791	0.578	minor allergen alt a 7
FGSG_01419	-1.209	0.433	long-chain acyl- synthetase
FGSG_01786	-2.273	0.207	ent-kaurene oxidase
FGSG_01959	0.277	1.212	cytochrome P450 61
FGSG_02113	-0.816	0.568	cytochrome p450 3a7
FGSG_02327	5.203	36.843	flavin adenine dinucleotide (FAD)
FGSG_02328	4.090	17.036	multicopper oxidase
FGSG_02366	1.724	3.302	sterigmatocystin biosynthesis
FGSG_02367	1.565	2.959	trichodiene oxygenase cytochrome P450
FGSG_02371	2.863	7.276	cytochrome P450 monooxygenase
FGSG_03049	-5.749	0.019	alpha-n-arabinofuranosidase 2
FGSG_03532	1.781	3.436	TRI8
FGSG_03533	1.519	2.865	TRI7
FGSG_03534	1.541	2.911	TRI3
FGSG_03535	1.390	2.620	TRI4
FGSG_03537	1.645	3.128	TRI5
FGSG_03540	1.300	2.461	TRI11
FGSG_03624	-2.485	0.179	XYLB
FGSG_03628	-6.517	0.011	exoglucanase-6A precursor
FGSG_03795	-6.930	0.008	endoglucanase 3 precursor
FGSG_03796	0.406	1.325	prostacyclin synthase
FGSG_05140	-1.372	0.386	acyl- dehydrogenase
FGSG_05551	-1.198	0.436	trans-enoyl- isomerase
FGSG_06445	-6.595	0.010	glycosyl hydrolase family 10
FGSG_06554	2.663	6.332	catalase 1
FGSG_06605	-1.491	0.356	beta-glucosidase 1 precursor
FGSG_06733	2.007	4.021	catalase 3
FGSG_07274	-2.827	0.141	probable beta-glucosidase
FGSG_07695	-6.928	0.008	xylosidase glycosyl
FGSG_07765	-2.553	0.170	trichothecene c-15 hydroxylase
FGSG_07896	1.025	2.035	TRI10
FGSG_08011	-6.584	0.010	endo-beta- -glucanase d
FGSG_08800	0.347	1.272	bzip transcription factor (Fgap1)
FGSG_09786	0.665	1.586	NADPH-cytochrome P450 reductase
FGSG_09895	-0.159	0.896	neutral trehalase
FGSG_10571	-2.089	0.235	O-methylsterigmatocystin oxidoreductase
FGSG_10571	-2.089	0.235	O-methylsterigmatocystin oxidoreductase
FGSG_10999	-6.697	0.010	XYLA
FGSG_11208	-5.928	0.016	xyloglucanase
FGSG_11258	-7.085	0.007	endo-1,4-beta-xylanase B
FGSG_11428	-5.812	0.018	feruloyl esterase B
FGSG_11656	5.596	48.370	fatty acid synthase beta subunit
FGSG_12369	1.127	2.184	catalase 4
FGSG_12551	-6.376	0.012	hypothetical protein
FGSG_13855	5.667	50.825	hypothetical protein